

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2477.8	99.4	2617	7	Aah34812	Human col
2	2477.8	99.4	2617	4	Abv75370	Human IGF
3	2472	99.1	2472	7	Adc25638	Human GDN
4	2461.8	98.7	2617	7	Abx63775	Human GDN
5	2456	98.5	2496	6	Aas94940	Human DNA
6	2452.4	98.3	2465	9	Adh18437	Human pro
7	2446.2	98.1	2499	6	ABX04173	Human mRN
8	2446.2	98.1	2499	7	Acf12873	Human cer
9	2445.8	98.1	2506	7	ACC51197	Human Plk
10	2441.4	97.9	2549	1	AAh91467	Sequence
11	2430.4	97.4	2474	2	AQg99244	insulin 1
12	2430.4	97.4	2474	4	Aaf45143	IGFSP-3 c
13	2361.8	94.7	2448	7	ADA52925	Human cod
14	2143.4	85.9	2191	2	Az421960	Human myo
15	2099.8	84.2	2327	9	ADB66292	Human GDN
16	1738.4	69.7	1833	3	ACG77920	Human can
17	1459.8	58.5	10874	7	Abv75373	Human IGF
18	1459.8	58.5	10884	6	ABn95848	Gene #234
19	1459.8	58.5	10884	9	ADb71028	Human ins
20	1307	52.4	1575	5	ABv28334	Human pro
21	1307	52.4	1575	5	ABv22519	Human pro
22	983.8	39.4	998	2	AQO4796	Sequence
23	948	38.0	994	9	ADe40107	Human NOV

CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the proteins. N and P
 CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922
 XX

SQL Sequence 2617 BP; 663 A; 672 C; 685 G; 595 T; 0 U; 2 Other;

Query Match	99.4%	Score 2478.4	DB 4	Length 2617
Best Local Similarity	99.8%	Pred No. 0		
Matches 2490	Conservative 1	Mismatches 2	Indels 1	Gaps 1
QY 1	GGCTGAGGATCAGCGGTTCTGCTGGATTCACAGCTTCGCGCGGTGACTGTGCGC	60		
DB 98	GGCTGAGGATCAGCGGTTCTGCTGGATTCACAGCTTCGCGCGGTGACTGTGCGC	157		
QY 61	CCATCCCTGGCGCCAGCCTGCCAAGCAGCGTGCCCGGTTGAGGGGTCATCAGCGG	120		
DB 138	CCATCCCTGGCGCCAGCCTGCCAAGCAGCGTGCCCGGTTGAGGGGTCATCAGCGG	217		
QY 121	GGCGACCCACGCTCTGGGCGGCTCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180		
DB 218	GGCGACCCACGCTCTGGGCGGCTCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	277		
QY 181	GTGGCGGGGCTGGCGGAGCTCGGGGGCTGGGTCCTGCTGCTGCTGCTGCTGCTGCTG	240		
DB 278	GTGGCGGGGCTGGCGGAGCTCGGGGGCTGGGTCCTGCTGCTGCTGCTGCTGCTGCTG	337		
QY 241	GACGCGGCTGCACTGGCGCCAGTCGCGGCTCGCGCCGCTCGCGCGGCTGGTGGCG	300		
DB 338	GACGCGGCTGCACTGGCGCCAGTCGCGGCTCGCGCCGCTCGCGCGGCTGGTGGCG	397		
QY 301	GAGCGGGGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360		
DB 398	GAGCGGGGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	457		
QY 361	TACACCGAGCGTGTGGCTCCGGCTTCGCTGCGAGCGCTCGCGCCGAGCGCGGACCG	420		
DB 458	TACACCGAGCGTGTGGCTCCGGCTTCGCTGCGAGCGCTCGCGCCGAGCGCGGACCG	517		
QY 421	CTGACGGCGTGTGAGCGCGCGCGGCTCTGGCTCAAGCTAGTCCGCTGAGCGCGCTG	480		
DB 518	CTGACGGCGTGTGAGCGCGCGCGGCTCTGGCTCAAGCTAGTCCGCTGAGCGCGCTG	577		
QY 481	CGCGCTTACTGCTGCGAGCGCGCGCTCCAGGAAATGCTAGTGAAGTCGAGGAGAC	540		
DB 578	CGCGCTTACTGCTGCGAGCGCGCGCTCCAGGAAATGCTAGTGAAGTCGAGGAGAC	637		
QY 541	CGAGCGCGGAGTGTGAGAGCGCGCTGCTGCTGCGAGCGCTCGCGCCGAGCGCGGAC	600		
DB 638	CGAGCGCGGAGTGTGAGAGCGCGCTGCTGCTGCGAGCGCTCGCGCCGAGCGCGGAC	697		
QY 601	AAGTTCACCCCTCCATTCAGAGAAATCATCATCAAGAAAGGCGATGCTAAAGACAGC	660		
DB 698	AAGTTCACCCCTCCATTCAGAGAAATCATCATCAAGAAAGGCGATGCTAAAGACAGC	757		
QY 661	CAGCGCTTACAAAGTGTGACTACGAGTCTCAGAGCACAGATCCAGAACTTCTCTCCGAG	720		
DB 758	CAGCGCTTACAAAGTGTGACTACGAGTCTCAGAGCACAGATCCAGAACTTCTCTCCGAG	817		
QY 721	TCCAGCGGAGACAGAAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780		
DB 818	TCCAGCGGAGACAGAAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	877		
QY 781	CTGAAGTTCCTCAATGTGCTGAGTCCAGGGGTGTACACATTCCTCAATGTGACAGAG	840		
DB 878	CTGAAGTTCCTCAATGTGCTGAGTCCAGGGGTGTACACATTCCTCAATGTGACAGAG	937		
QY 841	GGATTTTATAGAAAGACAGTGTGCGCTTCCAAAGGACAGGAGCGGGCTTCTGCTGG	900		

DB 938	GGATTTTATAGAAAGACAGTGTGCGCTTCCAAAGGACAGGAGCGGGCTTCTGCTGG	997
QY 901	TGTGTGATAGTATGGCAGCCTCTCCAGCTACACACCAAGGGGAGAGAGCGTG	960
DB 998	TGTGTGATAGTATGGCAGCCTCTCCAGCTACACACCAAGGGGAGAGAGCGTG	1057
QY 961	CACCTGTACAGCATCAGAGCAAGTAGACGCTGCGCAAGGTTAATGTGAGCTCAAT	1020
DB 1058	CACCTGTACAGCATCAGAGCAAGTAGACGCTGCGCAAGGTTAATGTGAGCTCAAT	1117
QY 1021	ATGCTTATTTTGCAAAAGACTCCCAAGACATGACAGCAGCTGCTACAGCTCGA	1080
DB 1118	ATGCTTATTTTGCAAAAGACTCCCAAGACATGACAGCAGCTGCTACAGCTCGA	1177
QY 1081	TTTATATTTCTGTTGTGTAACATGATTTTTTTTAAACCAAGTTTAGAAAGGTTT	1140
DB 1178	TTTATATTTCTGTTGTGTAACATGATTTTTTTTAAACCAAGTTTAGAAAGGTTT	1236
QY 1141	TTGAATGCTATGTTTCTTTGAATGTAACATGTAACCTTTCCTTTCCTAGTAGT	1200
DB 1237	TTGAATGCTATGTTTCTTTGAATGTAACATGTAACCTTTCCTTTCCTAGTAGT	1296
QY 1201	CAGCAAGAGCAGTTTGAATTTTCTGCTTCTCTATCAAAATATTTCAGAGACTCGAG	1260
DB 1297	CAGCAAGAGCAGTTTGAATTTTCTGCTTCTCTATCAAAATATTTCAGAGACTCGAG	1356
QY 1261	ACAGCACCCAGACTTCATGCGCCCGTGGAAATGCTCACCATGTTGGTGAAGCGCGA	1320
DB 1357	ACAGCACCCAGACTTCATGCGCCCGTGGAAATGCTCACCATGTTGGTGAAGCGCGA	1416
QY 1321	CCACTGACTTTGTGACTTAGGGGCTGCTGCTGCTATGTAGAGAACACCTTTCACCCCA	1380
DB 1417	CCACTGACTTTGTGACTTAGGGGCTGCTGCTGCTATGTAGAGAACACCTTTCACCCCA	1476
QY 1381	CTCCCGTACAGTGCACAGCGCTTTATCGAGAAATAGGAAACCTTTTAAACCCGCTAT	1440
DB 1477	CTCCCGTACAGTGCACAGCGCTTTATCGAGAAATAGGAAACCTTTTAAACCCGCTAT	1536
QY 1441	CCGAGCATCCCAAGCATGCTCTGAGCTCAGAGCTTCTGCTGCTGCTATTTCTCAAAAC	1500
DB 1537	CCGAGCATCCCAAGCATGCTCTGAGCTCAGAGCTTCTGCTGCTGCTATTTCTCAAAAC	1596
QY 1501	AAGGGCGTGAATCCCTCAACCAAGAAATGTTTATGCTTCAAGTGACCTGTACTGCTT	1560
DB 1597	AAGGGCGTGAATCCCTCAACCAAGAAATGTTTATGCTTCAAGTGACCTGTACTGCTT	1656
QY 1561	GGGACTATTGGAGAAATAGGTTGGAGTCTTCTTAAATAATATGATCTAAGAA	1620
DB 1657	GGGACTATTGGAGAAATAGGTTGGAGTCTTCTTAAATAATATGATCTAAGAA	1716
QY 1621	TGTTCTAGGGCACTTGGGAACTTAAAGGCAAGTATTTTCGGGCGCTCTCTTTCAGGAA	1680
DB 1717	TGTTCTAGGGCACTTGGGAACTTAAAGGCAAGTATTTTCGGGCGCTCTCTTTCAGGAA	1776
QY 1681	TCTTCTGAGACATGCGCCAGTCCGAGGCGCAGGATGCTTTTGTGCGGCGCCCGTGGG	1740
DB 1777	TCTTCTGAGACATGCGCCAGTCCGAGGCGCAGGATGCTTTTGTGCGGCGCCCGTGGG	1836
QY 1741	GTAGGAGGACAGAGACAGGAGAGTCAAGCTCCACATTCAGAGCATCAAGATTAAT	1800
DB 1837	GTAGGAGGACAGAGACAGGAGAGTCAAGCTCCACATTCAGAGCATCAAGATTAAT	1896
QY 1801	GGCAAAATCTTCGGATGACTGCGAGAAATAGTGTGTTTGTAGTTCACAACTCAAGACGA	1860
DB 1897	GGCAAAATCTTCGGATGACTGCGAGAAATAGTGTGTTTGTAGTTCACAACTCAAGACGA	1956
QY 1861	AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAGGCTTTTATTTCTCTCATCTTTT	1920
DB 1957	AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAGGCTTTTATTTCTCTCATCTTTT	2016
QY 1921	GTCTCTTCTAGCAAAATGTAAAAAAGAAATAGTAATATCAGAACAGGAGGAGTGGCT	1980
DB 2017	GTCTCTTCTTAGCAAAATGTAAAAAAGAAATAGTAATATCAGAACAGGAGGAGTGGCT	2076

1991 TCTGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTACCCATGTTTGTGAAC 2040
b TCTGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTACCCATGTTTGTGAAC 2136
Y TTAGAGTCACTTCTCATGTTTCTTTTATAATTCACATATATCGAGAGATATGTTTC 2100
b TTAGAGTCACTTCTCATGTTTCTTTTATAATTCACATATATCGAGAGATATGTTTC 2196
Y TTGTTAACTTGTATACATACATAGCCCAATATAGTAAGATCTATATAGTAATCTCTA 2160
b TTGTTAACTTGTATACATACATAGCCCAATATAGTAAGATCTATATAGTAATCTCTA 2256
Y GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCGCATGCTGAGGAAAGAGCTCA 2220
b GATGAAATGTTAGAGATGCTATATGATACAACTGTGCGCATGCTGAGGAAAGAGCTCA 2316
Y CCGCCAGAGACTGGGCTGCTCTCCGAGGCGCAACCCAGAAAGTCTGCAAGTCAAG 2280
b CGCCAGAGACTGGGCTGCTCTCCGAGGCGCAACCCAGAAAGTCTGCAAGTCAAG 2376
Y CTCAGGAGACTCTGCCCTGCTGACAGACTCGGTGTGACACACGCTGCATAGAGCTCTC 2340
b CTCAGGAGACTCTGCCCTGCTGACAGACTCGGTGTGACACACGCTGCATAGAGCTCTC 2436
Y CTTGAAACAGAGGGGTCTCAAGACATTTCTGCTACCTATTTCTTTATTTT 2400
b CTTGAAACAGAGGGGTCTCAAGACATTTCTGCTACCTATTTCTTTATTTT 2496
Y AACTTTTGGGGGAAAAGTATTTTGAAGAGTTTGTCTTGCATGATTTTAAATAGT 2460
b AACTTTTGGGGGAAAAGTATTTTGAAGAGTTTGTCTTGCATGATTTTAAATAGT 2556
Y AATAAAGTTTTTACCATTAAAAA 2494
b AATAAAGTTTTTACCATTAAAAA 2590

RESULT 2
ABV75370
ID ABV75370 standard; DNA; 2497 BP.
AC ABV75370;
XX
DT 07-MAR-2003 (first entry)
XX Human IGFBP-3 polypeptide encoding DNA.
DE Insulin-like growth factor binding protein; IGFBP; cytostatic; liver;
KW cancer; human; IGFBP-3; gene; ds.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 108..983
FT /tag= a
FT /product= "IGFBP-3"
FT /note= "insulin-like growth factor binding protein"
XX
PN WO200290580-A1.
XX
PD 14-NOV-2002.
PF 03-MAY-2002; 2002WO-AU000558.
XX
PR 03-MAY-2001; 2001US-0288441P.
XX (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.
PA (SIG-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (ARGA/) ARGAET V P.
XX
PI Huynh TH, Chow PKH, Soo KC;
XX

DR WPI; 2003-103522/09.
XX P-PSDB; ABB82756.
PT Detecting the presence or diagnosing the risk of a liver cancer in a
PT patient comprises detecting aberrant expression of a gene encoding an
PT insulin-like growth factor binding protein.
XX Example; Page 99-101; 142pp; English.
XX The invention relates to detecting the presence or diagnosing the risk of
CC a liver cancer in a patient. The method involves detecting in a
CC biological sample obtained from the patient aberrant expression of a gene
CC encoding an insulin-like growth factor binding protein (IGFBP). The
CC method is useful for detecting the presence or diagnosing the risk of a
CC liver cancer or for screening agents in a patient. The agent is useful
CC for the manufacture of a medicament for treating and/or preventing liver
CC cancer. The present sequence represents a human IGFBP-3 polypeptide
CC encoding DNA (GenBank Accession No. BC000013)
XX
SQ Sequence 2497 BP; 620 A; 642 C; 654 G; 581 T; 0 U; 0 Other;
Query Match 99.4%; Score 2477.8; DB 7; Length 2497;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2479; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 14 GCGCTTCCTGCTGGATTCCACAGCTTCGCGCGTGTACTGTGCGCCCATCCCTCGCG 73
DB 10 GCGCTTCCTGCTGGATTCCACAGCTTCGCGCGTGTACTGTGCGCCCATCCCTCGCG 69
QY 74 CCCAGCTGCCCAACGCGTCCCGGTTGCGAGCGTTCATGCGAGCGGCGGCGACCCACGC 133
DB 70 CCCAGCTGCCCAACGCGTCCCGGTTGCGAGCGTTCATGCGAGCGGCGGCGACCCACGC 129
QY 134 TCTGGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 193
DB 130 TCTGGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 189
QY 194 GCGAGAGTCTGGGGGCTTGGTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
DB 190 GCGAGAGTCTGGGGGCTTGGTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 249
QY 254 TGGCCCAAGTGTGCGGCTTCCCGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 313
DB 250 TGGCCCAAGTGTGCGGCTTCCCGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 309
QY 314 GCTGCTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373
DB 310 GCTGCTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369
QY 374 GTGCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 433
DB 370 GTGCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
QY 434 TGGAGCGCGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 493
DB 430 TGGAGCGCGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489
QY 494 TGGAGCGCGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
DB 490 TGGAGCGCGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
QY 554 GTGTGGAGAGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
DB 550 GTGTGGAGAGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609
QY 614 TCCATTCAAGATATATCATCATCAAGAGGGGATGCTAAAGACGCCAGCGGTACAAAG 673
DB 610 TCCATTCAAGATATATCATCATCAAGAGGGGATGCTAAAGACGCCAGCGGTACAAAG 669
QY 674 TTGACTACGAGTCTCAGACACAGATACCCAGAACTTCTCTCCGAGTCCAAAGCGGAGA 733
DB 670 TTGACTACGAGTCTCAGACACAGATACCCAGAACTTCTCTCCGAGTCCAAAGCGGAGA 729

QY		1501	AAGGGCGTGGATCCCTCAACCAAGAAGATGTTATATGTCTTCAAGTGACCTGTACTGTCTT	1560
Dδ		1501	AAGGGCGTGGATCCCTCAACCAAGAAGATGTTATATGTCTTCAAGTGACCTGTACTGTCTT	1560
QY		1561	GGGGACTATTGGAGAAAAATAAGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAAGAA	1620
Dδ		1561	GGGGACTATTGGAGAAAAATAAGTGGAGTCCTACTTGTTTAAAAAATATGTATCTAAAGAA	1620
QY		1621	TGTTCTAGGGCACTCTGGGAAACCTATAAAGGCAGAGTAATTTCCGGGCCCTCCTCTCAGNA	1680
Dδ		1621	TGTTCTAGGGCACTCTGGGAAACCTATAAAGGCAGAGTAATTTCCGGGCCCTCCTCTCAGNA	1680
QY		1681	TCTTCTCTGAAGACAATCGGCCAGTCGAAGCCACCAGGATGGCTTTTGTCTGGCCCCCGTGGG	1740
Dδ		1681	TCTTCTCTGAAGACAATCGGCCAGTCGAAGCCACCAGGATGGCTTTTGTCTGGCCCCCGTGGG	1740
QY		1741	GTAGGAGGCACAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAGTAAT	1800
Dδ		1741	GTAGGAGGCACAGAGACAGGGAGAGTCAGCCTCCACATTCAGAGGCATCACAGTAAT	1800
QY		1801	GGCACAAATCTTCGGATGACTCGCAGAAAATAGTGTGTTTTGTAGTTCAAACAACTCAAGACGA	1860
Dδ		1801	GGCACAAATCTTCGGATGACTCGCAGAAAATAGTGTGTTTTGTAGTTCAAACAACTCAAGACGA	1860
QY		1861	AGGTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCACTCTCACTCTTTT	1920
Dδ		1861	AGGTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAGCTTTATTTTCACTCTCACTCTTTT	1920
QY		1921	GTCCCTCTTAGCACAATGTAAAAAGAAATAGTAATATCAGAACGAGAAAGGGAATGGCT	1980
Dδ		1921	GTCCCTCTTAGCACAATGTAAAAAGAAATAGTAATATCAGAACGAGAAAGGGAATGGCT	1980
QY		1981	TGCTGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCCATGTTTGTGTGAAC	2040
Dδ		1981	TGCTGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACCCCATGTTTGTGTGAAC	2040
QY		2041	TTAGAGTCATTCCTCATGCTTTTCTTTATAATTCACACATATATCGCAGAGAAGATATGTTTC	2100
Dδ		2041	TTAGAGTCATTCCTCATGCTTTTCTTTATAATTCACACATATATCGCAGAGAAGATATGTTTC	2100
QY		2101	TTGTTAACATGTATACAAACATAGCCCACCAATATAGTAAGATCTATCTAGATAATTCCTTA	2160
Dδ		2101	TTGTTAACATGTATACAAACATAGCCCACCAATATAGTAAGATCTATCTAGATAATTCCTTA	2160
QY		2161	GATGAATGTTAGAGATGCTATTGTGACAACTGTGGCCCATGACTGAGGAAAGGAGCTCA	2220
Dδ		2161	GATGAATGTTAGAGATGCTATTGTGACAACTGTGGCCCATGACTGAGGAAAGGAGCTCA	2220
QY		2221	CGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAGAGAGGTCGCGCAAGTCAGG	2280
Dδ		2221	CGCCCAGAGACTGGGCTGCTCTCCCGGAGGCCAAACCCAGAGAGGTCGCGCAAGTCAGG	2280
QY		2281	CTCAGGAGACTCTGCCCTGCTCAGACACCTCGGTGTGGACACACGCTGCAATAGAGCTCTC	2340
Dδ		2281	CTCAGGAGACTCTGCCCTGCTCAGACACCTCGGTGTGGACACACGCTGCAATAGAGCTCTC	2340
QY		2341	CTTGAAAAACAGAGGGTCTCAAGACATTCGCTCTACCTATTTAGCTTTTCTTTATTTTTT	2400
Dδ		2341	CTTGAAAAACAGAGGGTCTCAAGACATTCGCTCTACCTATTTAGCTTTTCTTTATTTTTT	2400
QY		2401	AACTTTTTGGGGGAAAGATATTTTGGAGAAGTTTGTCTTCCAATGTATTTATAAATAGT	2460
Dδ		2401	AACTTTTTGGGGGAAAGATATTTTGGAGAAGTTTGTCTTCCAATGTATTTATAAATAGT	2460
QY		2461	AAATAAAGTTTTT 2472	
Dδ		2461	AAATAAAGTTTTT 2472	

RESULT 4
ABX63775
ID ABX63775 standard; cDNA; 2617 BP.
XX

AC	ABX63775;
XX	
DT	26-FEB-2003 (first entry)
DE	Human cDNA #775 differentially expressed in activated vascular tissue.
DE	
XX	Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
XX	hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;
KW	gene therapy; vascular disease; cancer; coronary; artery disease;
KW	hypertension; diabetes; pre-eclampsia; restenosis;
KW	ischaemia-reperfusion injury; stroke.
XX	
XX	Homio sapiens.
OS	
XX	
PN	US2002137081-A1.
DE	
PD	26-SEP-2002.
XX	
PD	
XX	08-JAN-2002; 2002US-00044090.
PF	
XX	28-JUL-2000; 2000US-0222469P.
PR	
PR	08-JAN-2001; 2001US-0260483P.
XX	
XX	(BAND/) BANDMAN O.
PA	
XX	
PI	Bandman O;
XX	
DR	WPI; 2003-110597/10.
XX	
XX	Combination for diagnosing, staging, treating, or monitoring the
PPT	progression of treatment of a vascular disease, e.g. atherosclerosis,
PPT	comprises several cDNAs that are differentially expressed in activated
PPT	vascular tissue.

Sequence 2617 BP: 649 A; 661 C; 675 G; 632 T; 0 U; 0 Other;

Qy 1 GCCTGAGGATCAGCGCTTCTGCCTGGATTCCACAGCTTCGCCCGTACTGTGCC 60

2y 2220 ACGCCAGAGCTGGGCTCTCCCGAGGCGCAACCCAGAGGTCTGCAAGTCAG 2279
 2b 2237 ACGCCAGAGCTGGGCTCTCCCGAGGCGCAACCCAGAGGTCTGCAAGTCAG 2296
 2y 2280 GCTCAGGAGACTCTGCTCTGTCGACAGCTCGGTGTGGACACACGCTGCATAGAGTCT 2339
 2b 2297 GCTCAGGAGACTCTGCTCTGTCGACAGCTCGGTGTGGACACACGCTGCATAGAGTCT 2356
 2y 2340 CCTTGAACACAGAGGGTCTCAGACATCTGCTACCTATTAGCTTTCTTTATTTT 2399
 2b 2357 CCTTGAACACAGAGGGTCTCAGACATCTGCTACCTATTAGCTTTCTTTATTTT 2416
 2y 2400 TAACCTTTTGGGGGAAAAGTATTGAGAGTTGCTTCCAAATGATTTATAATAG 2459
 2b 2417 TAACCTTTTGGGGGAAAAGTATTGAGAGTTGCTTCCAAATGATTTATAATAG 2476
 2y 2460 TAAATAAAGTTTACCATTAATAAAAAA 2488
 2b 2477 TAAATAAAGTTTACCATTAATAAAAAA 2505

RESULT 5
 ID AAS94940 standard; DNA; 2496 BP.
 AC AAS94940;
 XX
 XX
 DT 14-FEB-2002 (first entry)

XX Human DNA sequence #195 expressed during foam cell differentiation.
 XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;
 KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
 XX
 XX Homo sapiens.

XX W0200177389-A2.
 XX 18-OCT-2001.
 XX 04-APR-2001; 2001WO-US011128.
 XX 05-APR-2000; 2000US-0195106P.
 XX (INCYTE) INCYTE GENOMICS INC.
 XX Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T,
 PI Tai J;
 XX WPI; 2002-010925/01.

XX Composition useful for diagnosis of conditions, disorders or diseases
 PT associated with atherosclerosis, comprises several polynucleotides that
 PT are differentially expressed in foam cell development.

XX Claim 1; Page 246-247; 315pp; English.

XX The present invention relates to the isolation of human polynucleotide
 CC sequences that are differentially expressed during foam cell
 CC differentiation. The polynucleotide sequences of the invention or a
 CC composition comprising these polynucleotides are useful as a high
 CC throughput method for detecting altered expression of one or more
 CC polynucleotides in a sample. The polynucleotides can be used in the
 CC diagnosis of disorders associated with foam cell development such as
 CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
 CC coronary artery disease. The polynucleotide sequences can also be used as
 CC PCR primers and probes. The polynucleotides of the invention are also
 CC useful in gene therapy. AAS94746-AAS95021 represent the human
 CC polynucleotide sequences of the invention which are differentially
 CC expressed during foam cell differentiation

XX Sequence 2496 BP; 600 A; 648 C; 664 G; 584 T; 0 U; 0 Other;

Query Match 98.5%; Score 2456; DB 6; Length 2496;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2478; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
 QY 1 GGGCTGAGGATCAGCGCTTCTGCTGGATTCCACAGCTTCGCGCGCTGTACTGTGCGC 60
 Db 18 GCGCTGAGGATCAGCGCTTCTGCTGGATTCCACAGCTTCGCGCGCTGTACTGTGCGC 77
 QY 61 CCATCCCTCGCGCCCGCCAGCTGCCAA-CCAGGCTGCCCGCTTCAGGCGCTCATGACGCG 119
 Db 78 CCATCCCTCGCGCCCGCCAGCTGCCAAAGCGCTGCCCGCTTCAGGCGCTCATGACGCG 137
 QY 120 GCGCGAACCCAGCTCTCGGCGCGCTGCTGACTCTCTGCTGTGCTGTCCGCGCGCGCC 179
 Db 138 GCGCGAACCCAGCTCTCGGCGCGCTGCTGACTCTCTGCTGTGCTGTCCGCGCGCGCC 197
 QY 180 GGTGCGCGGGCTGCGCGAGCTCGGGGGCTTGGTCCCGTGTGCTGCGAGCGCTG 239
 Db 198 GGTGCGCGGGCTGCGCGAGCTCGGGGGCTTGGTCCCGTGTGCTGCGAGCGCTG 257
 QY 240 CGAGCGCGTGCATGCGCCAGTGGCGCTTCCCGCGCGCTGTGCGCGAGCTGTGCG 299
 Db 258 CGAGCGCGTGCATGCGCCAGTGGCGCTTCCCGCGCGCTGTGCGCGAGCTGTGCG 317
 QY 300 CGAGCGCGCTGCGGCTGCTGCTGACGTGCGACTGAGCGAGGCGCAGCGTGCAGCAT 359
 Db 318 CGAGCGCGCTGCGGCTGCTGCTGACGTGCGACTGAGCGAGGCGCAGCGTGCAGCAT 377
 QY 360 CTACACCGAGCGCTGTGCTCGGCTTTCGTGCGCGCTGCGCGCGCTGTGCGCGAGCG 419
 Db 378 CTACACCGAGCGCTGTGCTCGGCTTTCGTGCGCGCTGCGCGCGCTGTGCGCGAGCG 437
 QY 420 GGTGCGAGCGCTGCTGCGAGCGCGCGGCTCTGCTGCTCAACGCTAGTGCCTGCGCGCT 479
 Db 438 GGTGCGAGCGCTGCTGCGAGCGCGCGGCTCTGCTGCTCAACGCTAGTGCCTGCGCGCT 497
 QY 480 GCGCGCTTACTGCTGCGCGCGCGCTGCTGCGCGCTGCGCGCGCTGTGCGCGAGCG 539
 Db 498 GCGCGCTTACTGCTGCGCGCGCGCTGCTGCGCGCTGCGCGCGCTGTGCGCGAGCG 557
 QY 540 CCGCAGCGCGCGAGTGTGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
 Db 558 CCGCAGCGCGCGAGTGTGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
 QY 600 CAAGTTCACCCCTCCATTCAAGATATCATCATCAAGAAAGGCGATGCTTAAGACAG 659
 Db 618 CAAGTTCACCCCTCCATTCAAGATATCATCATCAAGAAAGGCGATGCTTAAGACAG 677
 QY 660 CCAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCTCCGA 719
 Db 678 CCAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCTCCGA 737
 QY 720 GTCCAGCGGAGACAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
 Db 738 GTCCAGCGGAGACAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
 QY 780 CCGTGAAGTTCCTCAATGTGCTGAGTCCCGAGGGGTGTACATTCCTCAACTGTGACAGAA 839
 Db 798 CCGTGAAGTTCCTCAATGTGCTGAGTCCCGAGGGGTGTACATTCCTCAACTGTGACAGAA 857
 QY 840 GCGATTTTAAAGAAAGCAGTGTGCGCTTCCAAAGCGAGGAGCGGGCTTCTGCTG 899
 Db 859 GCGATTTTAAAGAAAGCAGTGTGCGCTTCCAAAGCGAGGAGCGGGCTTCTGCTG 917
 QY 900 GTGTGTGATAGTATGGCGAGCTTCTCCAGGCTACACCAAGGGGAGGAGGACGT 959
 Db 918 GTGTGTGATAGTATGGCGAGCTTCTCCAGGCTACACCAAGGGGAGGAGGACGT 977
 QY 960 GCACGTCTACAGCATGACAGCAAGTAGCGCTGCGCAAGGTATATGTGGAGCTCAA 1019
 Db 978 GCACGTCTACAGCATGACAGCAAGTAGCGCTGCGCAAGGTATATGTGGAGCTCAA 1037
 QY 1020 TATGCTTTATTTTGCAAAAAGACTGCGCAAGGACATGACCCAGCTGGCTACAGCGCTCG 1079

allow the development of gene therapy. The methods of the invention
 useful for characterizing prostate tissue in a subject, screening
 compounds, characterizing inconclusive prostate biopsy tissue in a
 subject, detecting AMAR (alpha-methylacyl-coenzyme A racemase)
 expression in a bodily fluid, characterizing tissue in a subject,
 diagnosing cancer in a subject and inhibiting the growth of cells. The
 present sequence is a DNA sequence which is preferably utilised in the
 method of the invention.

SQ Sequence 2465 BP; 595 A; 641 C; 649 G; 580 T; 0 U; 0 Other;

Query Match 98.3%; Score 2452.4; DB 9; Length 2465;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2464; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 14 GCGCTTCCTGCTGGATTCCACAGCTTCGCGCGGTACTGTCGCCCATCCCTGCGCG 73
 DB 1 GCGCTTCCTGCTGGATTCCACAGCTTCGCGCGGTACTGTCGCCCATCCCTGCGCG 60

QY 74 CCAGCTGCAAGACAGCTGTCGCCGTTGACGCGTCAATGACGGGGGAGCCAGCC 133
 DB 61 CCAGCTGCAAGACAGCTGTCGCCGTTGACGCGTCAATGACGGGGGAGCCAGCC 120

QY 134 TCTGGGCGCTGCGCTGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 193
 DB 121 TCTGGGCGCTGCGCTGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

QY 194 GCGGAGCTGCGGGGCTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
 DB 181 GCGGAGCTGCGGGGCTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY 254 TGGCCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 313
 DB 241 TGGCCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

QY 314 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
 DB 301 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 374 GTGGCTCCGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 433
 DB 361 GTGGCTCCGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 434 TGGACGCGCGGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 493
 DB 421 TGGACGCGCGGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 494 TGGACGCGCGGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
 DB 481 TGGACGCGCGGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

QY 554 GTGTGGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
 DB 541 GTGTGGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY 614 TCCATTCAAGAGATAATCATCATCAAGAGAGGAGGATGCTAAAGACAGCCAGCGCTACAAG 673
 DB 601 TCCATTCAAGAGATAATCATCATCAAGAGAGGAGGATGCTAAAGACAGCCAGCGCTACAAG 660

QY 674 TTGACTACGAGTCTCAGAGCAGATACCCAGNACTTCTCCTCCAGTCCAGCGGAGAGA 733
 DB 661 TTGACTACGAGTCTCAGAGCAGATACCCAGNACTTCTCCTCCAGTCCAGCGGAGAGA 720

QY 734 CAGAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
 DB 721 CAGAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

QY 794 ATGTGCTGAGTCCAGGGGTGACATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853
 DB 781 ATGTGCTGAGTCCAGGGGTGACATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 854 AAAAGCAGTGTGCGCTTCCTCAAGAGGAGGAGCGGGCTTCTGCTGCTGCTGCTGCTGCTG 913

DB 841 AAAAGCAGTGTGCGCTTCCTCAAGAGGAGGAGCGGGCTTCTGCTGCTGCTGCTGCTGCTG 900
 QY 914 ATGGGAGAGCTTCCAGGCTACACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 973
 DB 901 ATGGGAGAGCTTCCAGGCTACACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960

QY 974 TSCAGAGCAAGTAGACGCTGCGCAAGGTTAAATGTGGAGCTCAAAATATGCTTATTTTG 1033
 DB 961 TSCAGAGCAAGTAGACGCTGCGCAAGGTTAAATGTGGAGCTCAAAATATGCTTATTTTG 1020

QY 1034 CACAAAGACTGCCAAGGACATGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1093
 DB 1021 CACAAAGACTGCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080

QY 1094 TTGTGGTGAACCTGATTTTAAACCAAGGTTTAAAGAGGTTTAAAGAGGTTTAAAGAGG 1153
 DB 1081 TTGTGGTGAACCTGATTTTAAACCAAGGTTTAAAGAGGTTTAAAGAGGTTTAAAGAGG 1139

QY 1154 GGTTCCTTTGAATGTAACCTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAGAGGAG 1213
 DB 1140 GGTTCCTTTGAATGTAACCTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAGAGGAG 1199

QY 1214 TTTGAATTTTCTGCTGCTTCTATCAAAATATTTCAGAGACTTCAGAGCAGCAGCAGCAG 1273
 DB 1200 TTTGAATTTTCTGCTGCTTCTATCAAAATATTTCAGAGACTTCAGAGCAGCAGCAGCAG 1259

QY 1274 TTATGCGCGCGTGGAAATGCTCACCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1333
 DB 1260 TTATGCGCGCGTGGAAATGCTCACCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1319

QY 1334 GACTTAGGCGGCTGTGTTTCCCTATGTAGAGAACACGCTTACCCCGCTTCCCGCTTACAGT 1393
 DB 1320 GACTTAGGCGGCTGTGTTTCCCTATGTAGAGAACACGCTTACCCCGCTTCCCGCTTACAGT 1379

QY 1394 GGCACAGCTTTATCGAAGTAGAAGAACCTTTAAACCCCGCTTCCCGCTTCCCGCTTCCCG 1453
 DB 1380 GGCACAGCTTTATCGAAGTAGAAGAACCTTTAAACCCCGCTTCCCGCTTCCCGCTTCCCG 1439

QY 1454 CGATGCTCTCTGAGACTCACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1513
 DB 1440 CGATGCTCTCTGAGACTCACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1499

QY 1514 CTTCAACCAAGAGAGATGTTTATGTTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1573
 DB 1500 CTTCAACCAAGAGAGATGTTTATGTTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1559

QY 1574 GAAATTAAGGTGAGTCTTCTGTTTAAATAATGTTTAAATAATGTTTAAATAATGTTTAA 1633
 DB 1560 GAAATTAAGGTGAGTCTTCTGTTTAAATAATGTTTAAATAATGTTTAAATAATGTTTAA 1619

QY 1634 TCTGGAGACCTTAAAGGAGGATTTTGGGCGCTTCTGCTGAGGATCTTCTGAGGATCTTCT 1693
 DB 1620 TCTGGAGACCTTAAAGGAGGATTTTGGGCGCTTCTGCTGAGGATCTTCTGAGGATCTTCT 1679

QY 1694 ATGGCCCAAGTCCAGGCGCCAGGATGGCTTTTTCGCGCGCGCGCGCGCGCGCGCGCGAG 1753
 DB 1680 ATGGCCCAAGTCCAGGCGCCAGGATGGCTTTTTCGCGCGCGCGCGCGCGCGCGCGCGAG 1739

QY 1754 AGAGCAGGAGAGTCAAGGCTCCACATTCAGAGGATCAAGGATCAAGGATCAAGGATCAAG 1813
 DB 1740 AGAGCAGGAGAGTCAAGGCTCCACATTCAGAGGATCAAGGATCAAGGATCAAGGATCAAG 1799

QY 1814 GGATGATGTCAGAAATAGTGTGTTTGTAGTTTCAACCACTCAAGACGAGGCTTATTTCTGA 1873
 DB 1800 GGATGATGTCAGAAATAGTGTGTTTGTAGTTTCAACCACTCAAGACGAGGCTTATTTCTGA 1859

QY 1874 GGATGATGTCAGAAATAGTGTGTTTGTAGTTTCAACCACTCAAGACGAGGCTTATTTCTGA 1933
 DB 1860 GGATGATGTCAGAAATAGTGTGTTTGTAGTTTCAACCACTCAAGACGAGGCTTATTTCTGA 1919

QY 1934 CAATGTAAAAAAGATAGTAATATACAGAACAGGAGGAGGATGCTTGTGGGAGGCC 1993
 DB 1920 CAATGTAAAAAAGATAGTAATATACAGAACAGGAGGAGGATGCTTGTGGGAGGCC 1979

1994	ATCCAGGACACTGGGACCATATAGAGATTCA	2053	TTTGTGTTGAACCTTAGAGTCATTCT
1995		2054	
1996		2055	
1997		2056	
1998	ATCCAGGACACTGGGACCATATAGAGATTCA	2059	TTTGTGTTGAACCTTAGAGTCATTCT
1999		2060	
2000		2061	
2001		2062	
2002		2063	
2003		2064	
2004	CATGCTTTTCTTTATTAATTCACACATATAT	2113	CGTGTGTTGTTTGAACCTTAGAGTCATTGT
2005		2114	
2006		2115	
2007		2116	
2008		2117	
2009		2118	
2010	ATACCAATAGCCCCCAATATAGTAAGATCTA	2159	TCTAGATGAATGTTAG
2011		2160	
2012		2161	
2013		2162	
2014	ATACCAATAGCCCCCAATATAGTAAGATCTA	2233	TCTAGATGAATGTTAG
2015		2234	
2016		2235	
2017	AGATGCTATTTGATACAACTGTGGCCCATG	2279	CTGAGGAGAGCTCAGCCAGAGACTG
2018		2280	
2019		2281	
2020	AGATGCTATTTGATACAACTGTGGCCCATG	2293	CTGAGGAGAGCTCAGCCAGAGACTG
2021		2294	
2022		2295	
2023	GGCTGTCTCTCCGGAGGCCAAACCCCAAGAG	2353	CTGAGGAGAGCTCAGCCAGAGACTG
2024		2354	
2025		2355	
2026	GGCTGTCTCTCCGGAGGCCAAACCCCAAGAG	2399	CTGAGGAGAGCTCAGCCAGAGACTG
2027		2400	
2028		2401	
2029		2402	
2030		2403	
2031		2404	
2032		2405	
2033		2406	
2034		2407	
2035		2408	
2036		2409	
2037		2410	
2038		2411	
2039		2412	
2040		2413	
2041		2414	
2042		2415	
2043		2416	
2044		2417	
2045		2418	
2046		2419	
2047		2420	
2048		2421	
2049		2422	
2050		2423	
2051		2424	
2052		2425	
2053		2426	
2054		2427	
2055		2428	
2056		2429	
2057		2430	
2058		2431	
2059		2432	
2060		2433	
2061		2434	
2062		2435	
2063		2436	
2064		2437	
2065		2438	
2066		2439	
2067		2440	
2068		2441	
2069		2442	
2070		2443	
2071		2444	
2072		2445	
2073		2446	
2074		2447	
2075		2448	
2076		2449	
2077		2450	
2078		2451	
2079		2452	
2080		2453	
2081		2454	
2082		2455	
2083		2456	
2084		2457	
2085		2458	
2086		2459	
2087		2460	
2088		2461	
2089		2462	
2090		2463	
2091		2464	
2092		2465	
2093		2466	
2094		2467	
2095		2468	

RESULT 7	
ABX04173	
ID	ABX04173 standard; cDNA; 2499 BP.
XX	
XX	
XX	ABX04173;
XX	
XX	
XX	10-JAN-2003 (first entry)
XX	
DE	Human mRNA differentially expressed in mesenchymal cells #20.
XX	
XX	Human; ss; gene; skeletal growth; cartilage degeneration disorder;
XX	chondroblastic phenotype; mesenchymal cell; cartilage formation;
XX	bone formation; arthritis; osteoarthritis; rheumatoid arthritis;
XX	gout; arthritis; adjuvant arthritis; arthritis deformans; anigout;
XX	infectious arthritis; osteochondrosis; RDA; anti-arthritis; osteopathic;
XX	antirheumatic; antiinflammatory; representational difference analysis.
XX	
XX	Homo sapiens.
XX	
XX	W0200271927-A2.
XX	
XX	19-SEP-2002.
XX	
PF	12-MAR-2002; 2002WO-US007787.
XX	
XX	12-MAR-2001; 2001US-0274980P.
XX	
XX	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PI	
PI	Yates KE, Mizuno S, Glowacki J;
XX	
XX	WPI; 2002-723276/78.
XX	
XX	New nucleic acid molecules capable of promoting chondrogenesis, useful
XX	for diagnosing and treating cartilaginous tissue degeneration conditions.

e.g. osteoarthritis, rheumatoid arthritis, gout arthritis, or osteochondrosis.

Claim 33; Page 116-117; 153pp; English.

The invention relates to new isolated nucleic acid molecule comprising a nucleic acid molecule consisting of a gene differentially expressed in cells undergoing differentiation from mesenchymal cell to a chondroblastic phenotype, or hybridising under stringent conditions to them (or their fragments). Also included are expression vectors, transformed host cells, expressed polypeptides or peptide fragments (which induce differentiation of a mesenchymal cell and may be used as an immunogen), binding partners of the polypeptides, a method for identifying an agent useful in modulating mesenchymal cell differentiation induction activity of a molecule, a method of diagnosing a condition characterized by aberrant expression of a nucleic acid molecule or its expression product; a method for determining regression, progression or onset of cartilaginous tissue degeneration condition, a subject characterised by aberrant expression of a nucleic acid molecule or its expression product, a method for treating a cartilaginous tissue degeneration condition, a method for treating a subject to reduce the risk of cartilaginous tissue degeneration condition developing in the subject, a method for identifying a candidate agent for treating a cartilaginous tissue degeneration condition, and a solid-phase nucleic acid molecule array consisting essentially of a set of nucleic acid molecule as cited above (or known from known genes shown to be differentially expressed in developing mesenchymal cells using the technique of representational difference analysis, RDA), its expression products or fragments fixed to a solid substrate. The nucleic acids, polypeptides and agents are useful for treating cartilaginous tissue degeneration conditions such as osteoarthritis, rheumatoid arthritis, gout arthritis, adjuvant arthritis, arthritis deformans, infectious arthritis or osteochondrosis. The present sequence is a cDNA from a known gene differentially expressed in developing mesenchymal cells

481 GCAGCTACCTGCTGCGAGCCGCGAGCTCCAGAAATGCTAGTGCAGGAGAGAC 540
 Db GCAGCTACCTGCTGCGAGCCGCGAGCTCCAGAAATGCTAGTGCAGGAGAGAC 561
 541 GCAGCGCGCGAGTGTGAGAGCCGCGTCTCCAGAGCAGCAGCGGTGCTGATCCC 600
 Db GCAGCGCGCGAGTGTGAGAGCCGCGTCTCCAGAGCAGCAGCGGTGCTGATCCC 621
 601 AAGTTCCACCCCTCCATTCAGAAATATCATCATCAAGAAAGGCGATGCTAAAGACAGC 660
 Db AAGTTCCACCCCTCCATTCAGAAATATCATCATCAAGAAAGGCGATGCTAAAGACAGC 681
 661 CAGCGCTACAAAGTTGACTACAGTCTCAGAGCAGATACCCAGAACTTCTCCTCCGAG 720
 Db CAGCGCTACAAAGTTGACTACAGTCTCAGAGCAGATACCCAGAACTTCTCCTCCGAG 741
 721 TCCAGCGGAGAGAGAAATATGTCCTGCGGTAGAGAAATGAAAGACACACTGAATCAC 780
 Db TCCAGCGGAGAGAGAAATATGTCCTGCGGTAGAGAAATGAAAGACACACTGAATCAC 801
 781 CTGAAGTTCTCAATGTGCTGAGTCCAGAGGCTGTACACATTCCTCAACTGTGACAGAGAG 840
 Db CTGAAGTTCTCAATGTGCTGAGTCCAGAGGCTGTACACATTCCTCAACTGTGACAGAGAG 861
 841 GGATTTTATAGAAAGACAGTGTGCGCTTCCAAAGGAGAGAGCGGCTTCTGCTGG 900
 Db GGATTTTATAGAAAGACAGTGTGCGCTTCCAAAGGAGAGAGCGGCTTCTGCTGG 921
 901 TGTGTGGATATAGTGGAGCGCTTCCAGAGCTACACACCAAGGAGAGAGAGAGCGTG 960
 Db TGTGTGGATATAGTGGAGCGCTTCCAGAGCTACACACCAAGGAGAGAGAGAGAGCGTG 981
 961 CACTGCTACAGCATGCGAGAGCAATGAGCGCTGCGCAAGGTTAATGTGAGAGCTCAAT 1020
 Db CACTGCTACAGCATGCGAGAGCAATGAGCGCTGCGCAAGGTTAATGTGAGAGCTCAAT 1041
 1021 ATGCGCTATTTTGCACAAAGACTGCCAAGAGATGACAGAGCTGGCTACAGCGCTCGA 1080
 Db ATGCGCTATTTTGCACAAAGACTGCCAAGAGATGACAGAGCTGGCTACAGCGCTCGA 1101
 1081 TTTATATTTCTGTTGGTGAAGTATTTTAAACCAAGTTTAAAGAGGTTT 1140
 Db TTTATATTTCTGTTGGTGAAGTATTTTAAACCAAGTTTAAAGAGGTTT 1160
 1141 TTGAATGCTATGCTTCTTTGAATGGTAACTTGAAGCATCTTTTCACTTTCCAGTAGT 1200
 Db TTGAATGCTATGCTTCTTTGAATGGTAACTTGAAGCATCTTTTCACTTTCCAGTAGT 1220
 1201 CAGCAAGAGAGAGTTGAAATTTTCTGCTGCTTCTTAAATATTTAGAGACTGAGC 1260
 Db CAGCAAGAGAGAGTTGAAATTTTCTGCTGCTTCTTAAATATTTAGAGACTGAGC 1280
 1261 ACAGCACCAGACTTTCATGCGCCGCTGGAATGCTCAGCAGATGCTGGTGAAGCGGCGA 1320
 Db ACAGCACCAGACTTTCATGCGCCGCTGGAATGCTCAGCAGATGCTGGTGAAGCGGCGA 1340
 1321 CACTGACTTTGACTTTAGCGGCTGTGTCCTATGAGAAACACCGCTTCAACCCCA 1380
 Db CACTGACTTTGACTTTAGCGGCTGTGTCCTATGAGAAACACCGCTTCAACCCCA 1400
 1381 CTCCCGGTACAGTGGCAGAGCTTTATCGAGAAATAGAAACCTTTAAACCCCGGTCTAT 1440
 Db CTCCCGGTACAGTGGCAGAGCTTTATCGAGAAATAGAAACCTTTAAACCCCGGTCTAT 1460
 1441 CCGNACATCCCAAGCATGCTCTGAGAGCTCAGAGCTTCTGAGTGTCTATTTCTGAAC 1500
 Db CCGNACATCCCAAGCATGCTCTGAGAGCTCAGAGCTTCTGAGTGTCTATTTCTGAAC 1520
 1501 AAGGCGGTGATCTCCTCAACCAAGAGAAATGTTTATGCTTCAAGTGAAGCTGTACTGCTT 1560
 Db AAGGCGGTGATCTCCTCAACCAAGAGAGTGTGTTATGCTTCAAGTGAAGCTGTACTGCTT 1580
 1561 GGGNACTATTGGAGAAATAGGTGGAGTCTGCTGTTTAAATAATATGATATCAAGAA 1620

1581 GGGGACTATTGAGAAATAAGGTGGAGTCTACTGTTTCAAAATATGATATCAAGAA 1640
 1621 TGTTCTAGGSCACTCTGGGAACCTATAAAGGAGAGTATTTGCGGCCCTCTCTTCAGGAA 1680
 1641 TGTTCTAGGSCACTCTGGGAACCTATAAAGGAGAGTATTTGCGGCCCTCTCTTCAGGAA 1700
 1681 TCTTCTGAAAGACATGCGCCAGTCTGAAAGGCCAGGATGCTTTGTCGGGCCCGGTGG 1740
 1701 TCTTCTGAAAGACATGCGCCAGTCTGAAAGGCCAGGATGCTTTGTCGGGCCCGGTGG 1760
 1741 GTAGAGGGGACAGAGAGACAGGAGAGTCTGAGCTCCACATTCAGAGGCAATCAAAAGTAA 1800
 1761 GTAGAGGGGACAGAGAGACAGGAGAGTCTGAGCTCCACATTCAGAGGCAATCAAAAGTAA 1820
 1801 GGCACAATTTCTCGATGACTGCGAGAAATAGTGTGTTTGTAGTTCAACAACTCAAGAGCA 1860
 1821 GGCACAATTTCTCGATGACTGCGAGAAATAGTGTGTTTGTAGTTCAACAACTCAAGAGCA 1880
 1861 AGCTTATTTCTGAGGATAAGTCTTTTAAAGGCAAGCTTTTATTTTCACTCTCATCTTTT 1920
 1881 AGCTTATTTCTGAGGATAAGTCTTTTAAAGCAAGCTTTTATTTTCACTCTCATCTTTT 1940
 1921 GTCTCTCTTAGCACAATGTAAGAAATAGTAATATCAGAAACAGAGAGGAGAAATGCGT 1980
 1941 GTCTCTCTTAGCACAATGTAAGAAATAGTAATATCAGAAACAGAGAGGAGAAATGCGT 2000
 1981 TGCTGGGGAGCCCATCCAGGACACTGGGAGCAGATAGAGATTCAAGGATTTGTTGAAAC 2040
 2001 TGCTGGGGAGCCCATCCAGGACACTGGGAGCAGATAGAGATTCAAGGATTTGTTGAAAC 2060
 2041 TTAGAGTCAATCTCATGCTTTTCTTTTAAATTCACACATATATGCGAGAGAGATATGTT 2100
 2061 TTAGAGTCAATCTCATGCTTTTCTTTTAAATTCACACATATATGCGAGAGAGATATGTT 2120
 2101 TTGTTAACTTTGATACAACTAGCCCAATATATAGTAAGATCTATAGATAATCTTA 2160
 2121 TTGTTAACTTTGATACAACTAGCCCAATATATAGTAAGATCTATAGATAATCTTA 2180
 2161 GATGAATGTTAGAGATGCTTTTGTATACAACTGTCGCGCATGACTGAGGAAAGAGCTCA 2220
 2181 GATGAATGTTAGAGATGCTTTTGTATACAACTGTCGCGCATGACTGAGGAAAGAGCTCA 2240
 2221 CGCCCAAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCCAAGAGGCTGCGCAAGCTCAGG 2280
 2241 CGCCCAAGAGACTGGGCTGCTCTCCCGAGGCCAAACCCCAAGAGGCTGCGCAAGCTCAGG 2300
 2281 CTGAGGAGACTCTGCGCTGCTGCGAGACCTCGGTGTGGACACACGCTGCTAGAGCTCTC 2340
 2301 CTGAGGAGACTCTGCGCTGCTGCGAGACCTCGGTGTGGACACACGCTGCTAGAGCTCTC 2360
 2341 CTGAGGAGACTCTGCGCTGCTGCGAGACCTCGGTGTGGACACACGCTGCTAGAGCTCTC 2400
 2361 CTGAGGAGACTCTGCGCTGCTGCGAGACCTCGGTGTGGACACACGCTGCTAGAGCTCTC 2420
 2401 AACTTTTGGGGGAAAGTATTTTGAAGTGTCTGCAATGATGATTAATAGT 2460
 2421 AACTTTTGGGGGAAAGTATTTTGAAGTGTCTGCAATGATGATTAATAGT 2480
 2461 AAATAAAGTTTTTACCATT 2479
 2481 AAATAAAGTTTTTACCATT 2499

RESULT 8
 ACF12873
 ID ACF12873 standard; cDNA; 2499 BP.
 XX ACF12873;
 XX AC
 DT 10-SEP-2003 (first entry)
 XX Human cervical cancer cell marker protein SEQ ID NO:90.
 DE

Db 1401 CTCCTGTACAGTGGCAGCAGGCTTTATCGAGAAATAGGAAACCTTTAAACCCCGGTCTCAT 1460
 Qy 1441 CCGGACATCCCAACGCGATGCTCTGGAGCTCACAGCTTCTGGTGTCTATTTCTGAAC 1500
 Db 1461 CCGGACATCCCAACGCGATGCTCTGGAGCTCACAGCTTCTGGTGTCTATTTCTGAAC 1520
 Qy 1501 AAGGCGTGATGCTCTCAACCAAGAGATGTTTATGCTCTCAAGTGAAGCTCTACTGCTT 1560
 Db 1521 AAGGCGTGATGCTCTCAACCAAGAGATGTTTATGCTCTCAAGTGAAGCTCTACTGCTT 1580
 Qy 1561 GGGGACTATTGGAGAAATTAAGTGGAGTCTACTTGTGTTTAAATAATATGATCTAAAGAA 1620
 Db 1581 GGGGACTATTGGAGAAATTAAGTGGAGTCTACTTGTGTTTAAATAATATGATCTAAAGAA 1640
 Qy 1621 TGTTCTAGGCACTCTGGGAACCTATAAGGCAAGTATTTGGGCGCTCTCTCTCAGAA 1680
 Db 1641 TGTTCTAGGCACTCTGGGAACCTATAAGGCAAGTATTTGGGCGCTCTCTCTCAGAA 1700
 Qy 1681 TCTTCTGAAGACATGCGCCAGTCGAAGGCCCAAGGATGGCTTTGCTGGGCGCCGCTGGG 1740
 Db 1701 TCTTCTGAAGACATGCGCCAGTCGAAGGCCCAAGGATGGCTTTGCTGGGCGCCGCTGGG 1760
 Qy 1741 GTAGAGGGACAGAGACAGGAGAGTCAAGCTCCACATTCAGAGGCATCAAGTAAAT 1800
 Db 1761 GTAGAGGGACAGAGACAGGAGAGTCAAGCTCCACATTCAGAGGCATCAAGTAAAT 1820
 Qy 1801 GGCACAAATCTTCGGATGACTCGAGAAAATAGTGTGTTTGTAGTTCACAACTCAAGACGA 1860
 Db 1821 GGCACAAATCTTCGGATGACTCGAGAAAATAGTGTGTTTGTAGTTCACAACTCAAGACGA 1880
 Qy 1861 AGCTTATCTGAGGATAAGCTCTTTAAAGGCAAGCTTTTATTCATCTCATCTTTT 1920
 Db 1881 AGCTTATCTGAGGATAAGCTCTTTAAAGGCAAGCTTTTATTCATCTCATCTTTT 1940
 Qy 1921 GTCTCTCTAGCAATGTAAAAAAGATAGTAATACAGACAGAGAGGAATGGCT 1980
 Db 1941 GTCTCTCTAGCAATGTAAAAAAGATAGTAATACAGACAGAGAGGAATGGCT 2000
 Qy 1981 TGCTGGGAGCCCATCAGACACTGGAGCACATAGATTCACCCATGTTTGTGAAC 2040
 Db 2001 TGCTGGGAGCCCATCAGACACTGGAGCACATAGATTCACCCATGTTTGTGAAC 2060
 Qy 2041 TTAGAGTCATCTCATGCTTTCTTTATATTCACACATATATGAGAGAGATATGTC 2100
 Db 2061 TTAGAGTCATCTCATGCTTTCTTTATATTCACACATATATGAGAGAGATATGTC 2120
 Qy 2101 TTGTTAATGTTATACACATAGCCCAATATAGTAGATCTATAGTAATATCTTA 2160
 Db 2121 TTGTTAATGTTATACACATAGCCCAATATAGTAGATCTATAGTAATATCTTA 2180
 Qy 2161 GATCAATGTTAGAGATGCTTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2220
 Db 2181 GATCAATGTTAGAGATGCTTATATGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCA 2240
 Qy 2221 CGCCAGAGACTGGCTGCTCTCCGAGGCCAAACCCAGAGAGTCTGGCAAGTCAAG 2280
 Db 2241 CGCCAGAGACTGGCTGCTCTCCGAGGCCAAACCCAGAGAGTCTGGCAAGTCAAG 2300
 Qy 2281 CTCAGGAGACTCTGCTCCCTGCTCAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2340
 Db 2301 CTCAGGAGACTCTGCTCCCTGCTCAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2360
 Qy 2341 CTTGAAACAGAGGGTCTCAAGACATCTGCCCTACTATAGCTTTCTTTATTTT 2400
 Db 2361 CTTGAAACAGAGGGTCTCAAGACATCTGCCCTACTATAGCTTTCTTTATTTT 2420
 Qy 2401 AACTTTTGGGGGAAAGTATTTTGAAGAGTTTGTCTTGAAGTATTTTATAAATAGT 2460
 Db 2421 AACTTTTGGGGGAAAGTATTTTGAAGAGTTTGTCTTGAAGTATTTTATAAATAGT 2480
 Qy 2461 AATAAAGTTTACCAT 2479
 Db 2481 AATAAAGTTTACCAT 2499

RESULT 9

ACC51197
 ID ACC51197 standard; cDNA; 2506 BP.

XX ACC51197;

XX 16-JUN-2003 (first entry)

XX Human Plk-1 related cDNA sequence hkmt-1013 SEQ ID NO:82.

XX Human; hepatoblastoma; cancer detection probe; cancer; detection;
 KW hepatocellular carcinoma; hereditary non-polyposis colorectal cancer;
 KW desmoid tumour; anaplastic thyroid carcinoma; Wilms' tumour; tumour;
 KW Plk-1; polo-like kinase-1; gene; ss.

OS Homo sapiens.

XX WO2003018807-A1.

XX 06-MAR-2003.

XX 26-AUG-2002; 2002WO-JP008580.

XX 24-AUG-2001; 2001JP-00255225.

XX (HISM) HISAMITSU PHARM CO LTD.
 XX (CHIB-) CHIBA PREFECTURE.

XX Nakagawara A;

XX WPI; 2003-268424/26.

Nucleic acid sequences differently expressed between hepatoblastoma and normal liver tissue, are useful for cancer detection and diagnosis.

Claim 4; Page 129-131; 180pp; Japanese.

The present invention describes nucleic acid sequences (I) having a different degree of expression in hepatoblastoma from their expression in normal liver tissue. ACC51197 to ACC51219 represents specifically claimed examples of (I). Also described: (1) nucleic acids stringently hybridising to (I); (2) cancer detection probes containing one or more of 104 listed sequences (II); (3) cancer detection probes derived from them; (3) PCR primers for cancer detection based on sequences (II); (4) marker see ACC51116 to ACC51194, or partial sequences encoded by (II); (5) diagnostic reagents for cancer diagnosis, containing (II) or their partial sequences. The nucleic acid sequences are useful in the detection and diagnosis of cancers including liver, colon, breast, kidney, bladder, ovary and thyroid cancer, especially for hepatoblastoma, hepatocellular carcinoma, hereditary non-polyposis colorectal cancer, desmoid tumour, anaplastic thyroid carcinoma and Wilms' tumour. They are also used as markers for predicting the prognosis of these tumours. ACC51220 to ACC51233 represent PCR primers used in the exemplification of the present invention. The nucleic acid sequences given in ACC51116 to ACC51219 are related to human Plk-1 (polo-like kinase-1), which is located on chromosome 16p12

Sequence 2506 BP; 647 A; 634 C; 649 G; 576 T; 0 U; 0 Other;

Query Match 98.1%; Score 2445.8; DB 7; Length 2506;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2459; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 34 CACAGCTTCGCGCGGTGTAATCTGCGCCCATCTCTGCGCGCCCGCCAGCGGT 93

Db 10 CACAGCTTCGCGCGGTGTAATCTGCGCCCATCTCTGCGCGCCCGCCAGCGGT 69

Qy 94 GCCCGCGTTGCGAGGCTCATGCGCGGGCGGCGCCACGCTCTGGCGCGCTGACT 153

Db 70 GCCCGCGTTGCGAGGCTCATGCGCGGGCGGCGCCACGCTCTGGCGCGCTGACT 129

Db 2289 TGTGGACACAGCTGCATAGAGCTCTCCTTGAACACAGAGGGGTCTCAAGACATTCGTGCC 2348
 2y 2374 TACCTATTAGCTTTCTTTATTTTAACTTTTGGGGGGGAAAAGTATTTTGGAGAAGT 2433
 Db 2349 TACCTATTAGCTTTCTTTATTTTAACTTTTGGGGGGGAAAAGTATTTTGGAGAAGT 2408
 2y 2434 TTGCTTTGCAATGATTTTATAATAGTAATAAAGTTTACCATTAATAAAAAA 2493
 Db 2409 TTGCTTTGCAATGATTTTATAATAGTAATAAAGTTTACCATTAATAAAAAA 2468
 2y 2494 A 2494
 Db 2469 A 2469

RESULT 10
 AAN91467
 ID AAN91467 standard; cDNA; 2549 BP.
 XX
 AC AAN91467;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-MAR-1990 (first entry)
 XX
 DE Sequence of human BP53 from cDNA clone ibp.118.
 XX
 KW Insulin-like growth factor binding protein; BP53; clone ibp.118.
 XX
 OS Homo sapiens.
 XX
 XX Location/Qualifiers
 FH CDS 110..190
 FT /*tag= a
 FT /*note= "Encodes signal sequence."
 FT 191..980
 FT /*tag= b
 FT /*note= "Encodes mature peptide."
 XX
 PN WO8909268-A.
 XX
 PD 05-OCT-1989.
 XX
 PF 10-MAR-1989; 89WO-US000983.
 XX
 PR 22-MAR-1989; 88US-00171623.
 XX
 PA (GETH) GENENTECH INC.
 PA (ROYA-) ROYAL PRINCE ALFRED HOSP.
 PA (SYDN-) CENT SYDNEY AREA HEALTH.
 XX
 XX Baxter RC, Wood WI;
 PI
 XX
 DR WFI; 1989-309533/42.
 DR P-PSDB; AAP92300.
 XX
 PT DNA encoding insulin-like growth factor binding protein - used to
 PT increase insulin-like growth factor circulatory half life, and as
 PT metabolic regulator.
 XX
 PS Claim 1; Page 48; 72pp; English.
 XX
 CC The larger internal sequence allows hybridisation probes to be cbtd. to
 CC identify clones with sequences encoding BP53. It is expressed in PRK5-
 CC ibp1.1, and used to transform, eg COS cells or human embryonic kidney
 CC cells transfected with adenovirus EladnE1b (293s). (Updated on 25-MAR-
 CC 2003 to correct PA field.)
 XX
 XX Sequence 2549 BP; 671 A; 640 C; 660 G; 578 T; 0 U; 0 Other;
 SQ

Query Match 97.9%; Score 2441.4; DB 1; Length 2549;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 2470; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 12 CAGCGCTTCTCTGCTGATTCACAGCTTCGCGCGGTGTAATCTGCGCCCATCCCTGGG 71
 Db 10 CAGCGCTTCTCTGCTGAGGCCACAGCTTCGCGCGGTGTAATCTGCGCCCATCCCTGGG 69
 QY 72 CCGCCAGCCTGCGCAAGCAGCGTGCCTCCCGTTGCGAGGCGTCAATGACAGGGGGCGGACCCAC 131
 Db 70 CCGCCAGCCTGCGCAAGCAGCGTGCCTCCCGTTGCGAGGCGTCAATGACAGGGGGCGGACCCAC 129
 QY 132 GCTCTGGGCGCGTGGCTGACTCTGCTGGTGTGCTCTCGCGGGCGCGCGTGGCGCGGGC 191
 Db 130 GCTCTGGGCGCGTGGCTGACTCTGCTGGTGTGCTCTCGCGGGCGCGCGTGGCGCGGGC 189
 QY 192 TGGCGCGAGCTCGGGGGGCTTTGGGTCCGCTGGTGGCTGCGAGCGGTGCGACGCGCGTGC 251
 Db 190 TGGCGCGAGCTCGGGGGGCTTTGGGTCCGCTGGTGGCTGCGAGCGGTGCGACGCGCGTGC 249
 QY 252 ACTGGCCAGTGGCGCGCTCCGCGCGCGTGGCGCGAGCTGGTGGCGAGCGCGGCTG 311
 Db 250 ACTGGCCAGTGGCGCGCTCCGCGCGCGTGGCGCGAGCTGGTGGCGAGCGCGGCTG 309
 QY 312 CGGCTGCTGCTGAGCTGCGCACTGAGCGAGGGCGAGCGCTGCGGCGATCTACACCGAGCG 371
 Db 310 CGGCTGCTGCTGAGCTGCGCACTGAGCGAGGGCGAGCGCTGCGGCGATCTACACCGAGCG 369
 QY 372 CTGTGCTCCGCGCTTCCGCTGCGAGCGCTGCCGAGCGAGCGCGAGCGCTGCGAGCGCT 431
 Db 370 CTGTGCTCCGCGCTTCCGCTGCGAGCGCTGCCGAGCGAGCGCGAGCGCTGCGAGCGCT 429
 QY 432 GCTGAGCGCGCGCGGCTTCTGCTCAACGCTAGTGGCTGAGCGCGCTGCGCGCTACCT 491
 Db 430 GCTGAGCGCGCGCGGCTTCTGCTCAACGCTAGTGGCTGAGCGCGCTTGGCGCGCTACCT 489
 QY 492 GCTGCGAGCGCGCGAGCTCCAGGAAATGCTAGTAGTGGAGGAGGAGGAGCGCGCGG 551
 Db 490 GCTGCGAGCGCGCGAGCTCCAGGAAATGCTAGTAGTGGAGGAGGAGGAGCGCGCGG 549
 QY 552 CAGTGTGAGAGCGCGCTCCGCTCCAGCAACGCGCGGTGCTGATCCCAAGTTCCACCC 611
 Db 550 CAGTGTGAGAGCGCGCTCCGCTCCAGCAACGCGCGGTGCTGATCCCAAGTTCCACCC 609
 QY 612 CCTCCATTCAAAGATAATCATCATCAGAAAGGCGATGCTAAAGACAGCCAGCGCTACAA 671
 Db 610 CCTCCATTCAAAGATAATCATCATCAGAAAGGCGATGCTAAAGACAGCCAGCGCTACAA 669
 QY 672 AGTTGACTACGAGTCTCAGAGCAGATACCCAGAACTTCTCTCCGAGTCCAAAGCGGA 731
 Db 670 AGTTGACTACGAGTCTCAGAGCAGATACCCAGAACTTCTCTCCGAGTCCAAAGCGGA 729
 QY 732 GACAGAAATATGTCCTCCGCTAGAGAAATGGAAGACACACTGAATCAGCTGAAGTTCT 791
 Db 730 GACAGAAATATGTCCTCCGCTAGAGAAATGGAAGACACACTGAATCAGCTGAAGTTCT 789
 QY 792 CAATGTGCTGAGTCCAGGGGTGTACATTCCTCAATGCTGACAAAGAGGATTTTATAA 851
 Db 790 CAATGTGCTGAGTCCAGGGGTGTACATTCCTCAATGCTGACAAAGAGGATTTTATAA 849
 QY 852 GAAAAGCAGTGTGCGCCCTTCCAAAGGAGGAGGCGGCTTCTGCTGCTGCTGGGATAA 911
 Db 850 GAAAAGCAGTGTGCGCCCTTCCAAAGGAGGAGGCGGCTTCTGCTGCTGCTGGGATAA 909
 QY 912 GTATGGCAGCTCTCCAGGCTACACCAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 971
 Db 910 GTATGGCAGCTCTCCAGGCTACACCAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 969
 QY 972 CATGCAGAGCAAGTAGAGCGCTGCGCAAGGTTAATGTGGAGCTCAATATGCTTATTT 1031
 Db 970 CATGCAGAGCAAGTAGAGCGCTGCGCAAGGTTAATGTGGAGCTCAATATGCTTATTT 1029
 QY 1032 TGCAAAAGAGCTGCCAAGGACATGACAGCAGCTGGCTACAGCTCGATTTATTTCT 1091
 Db 1030 TGCAAAAGAGCTGCCAAGGACATGACAGCAGCTGGCTACAGCTCGATTTATTTCT 1089
 QY 1092 GTTTGTGTGAAGTGAATTTTAAAAACCAAGTTTAAAGAGAGGTTTAAAGAGGCTCT 1151

1090 GTTGTGGTGAACCTGA-TTTTTTTTAAACCAAGT-TAGAAAGAGGTTTTTGAATGCGCT 1148
1152 ATGGTCTCTTTGAATGGTAACTTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAGAGC 1211
1149 ATGGTCTCTTTGAATGGTAACTTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAGAGC 1208
1212 AGTTGAATTTTCTGTGCGTCTCCTATCAAAATATTAGAGACTCGAGCACAGCAGCCAG 1271
1209 AGTTGAATTTTCTGTGCGTCTCCTATCAAAATATTAGAGACTCGAGCACAGCAGCCAG 1268
1272 ACTTCATGCGCGGTGAATGCTTCAACACATGTTGTCGAAGCGCGCCAGCCACTGACTTT 1331
1269 ACTTCATGCGCGGTGAATGCTTCAACACATGTTGTCGAAGCGCGCCAGCCACTGACTTT 1328
1332 GTGACTTTAGCGCGGTGTGTTGCGCTATGTAGAGAACAGCTTACCCCGCTCCCGGTACA 1391
1329 GTGACTTTAGCGCGGTGTGTTGCGCTATGTAGAGAACAGCTTACCCCGCTCCCGGTACA 1388
1392 GTGCGCACAGCGTTTATCGAGATAGAGAAACCTTTAAACCCCGGTTCATCCGACATCCC 1451
1389 GTGCGCACAGCGTTTATCGAGATAGAGAAACCTTTAAACCCCGGTTCATCCGACATCCC 1448
1452 AACCATGCTCTCGAGCTCACAGCCTTCTGTGTGTCAITTTCTGAAACAAAGGCGGTGA 1511
1449 AACCATGCTCTCGAGCTCACAGCCTTCTGTGTGTCAITTTCTGAAACAAAGGCGGTGA 1508
1512 TCCCTCAACCAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTGGGACTATTG 1571
1509 TCCCTCAACCAAGAAATGTTTATGTCTTCAAGTGACCTGTACTGCTGGGACTATTG 1568
1572 GAGAAATATAGTGGTCTCTACTGTTTAAATAATATGTATCAAGATGTTCTAGGGC 1631
1569 GAGAAATATAGTGGTCTCTACTGTTTAAATAATATGTATCAAGATGTTCTAGGGC 1628
1632 ACTCTGGGAACCTATAAGGAGAGTATTTGGGCGCTCTCTTCAAGAAATCTCTGGAAG 1691
1629 ACTCTGGGAACCTATAAGGAGAGTATTTGGGCGCTCTCTTCAAGAAATCTCTGGAAG 1688
1692 ACATGGCCAGTCCAGAGCCAGAGTGGTCTTCTGCGCGCGGTGGGTAGAGGGAC 1751
1689 ACATGGCCAGTCCAGAGCCAGAGTGGTCTTCTGCGCGCGGTGGGTAGAGGGAC 1748
1752 AGAGAGACAGGAGAGTCCAGCTCCACATTCAGAGGATCAAGTAATGGCAATCTT 1811
1749 AGAGAGAC-GGGAGAGTCCAGCTCCACATTCAGAGGATCAAGTAATGGCAATCTT 1807
1812 TCGATGATCGAGAAATAGTGTGTAGTTCAGACTCAAGTCAAGAGGAGTATTTCT 1871
1808 TCGATGATCGAGAAATAGTGTGTAGTTCAGACTCAAGTCAAGAGGAGTATTTCT 1867
1872 GAGGATAAGCTCTTAAAGGCAAGCTTTATTTTCATCTCTCATCTTTTGTCTCTCTAG 1931
1868 GAGGATAAGCTCTTAAAGGCAAGCTTTATTTTCATCTCTCATCTTTTGTCTCTCTAG 1927
1932 CACAATGTAAAGAAATAGTAAATTCAGACAGGAGGAGGATGCTTCTGGGAGC 1991
1928 CACAATGTAAAGAAATAGTAAATTCAGACAGGAGGAGGATGCTTCTGGGAGC 1987
1992 CCATCCAGGACACTCGGAGCACATAGATTCACCCATGTTTGTGAATCTAGAGTCAAT 2051
1988 CCATCCAGGACACTCGGAGCACATAGATTCACCCATGTTTGTGAATCTAGAGTCAAT 2047
2052 CTCATGCTTTCTTTTATTAATTCACATATATTCAGAGAGATATGTTCTGTTAACTT 2111
2048 CTCATGCTTTCTTTTATTAATTCACATATATTCAGAGAGATATGTTCTGTTAACTT 2107
2112 GTATACATAGCCCCCAATATAGTAACTTATCTAGATATCTCTAGATGAATGTT 2171
2108 GTATACATAGCCCCCAATATAGTAACTTATCTAGATATCTCTAGATGAATGTT 2167
2172 AGAGATGCTTATTGTATACAACTGTGCGCATGCTGAGGAAAGGAGCTCACGCCAGAGAC 2231

Db 2168 AGAGATGCTTATGATACAACTGTGGCCATGCTGAGAAAGGAGCTCACGCCAGAGAC 2227
Qy 2232 TGGGCTGCTCTCCCGAGGCGCAAAACCAAGAGTCTGGCAAGTCAAGTCTAGGGAGAC 2291
Db 2228 TGGGCTGCTCTCCCGAGGCGCAAAACCAAGAGTCTGGCAAGTCAAGTCTAGGGAGAC 2287
Qy 2292 TCTGCCCTGCTGAGACTCGGTGTGGACACACGCTGCATAGAGCTCTCCTTGAAACAG 2351
Db 2288 TCTGCCCTGCTGAGACTCGGTGTGGACACACGCTGCATAGAGCTCTCCTTGAAACAG 2347
Qy 2352 AGGGGTCTCAAGACATTTCTGCCTACCTATTAGCTTTTCTTTTATTATTATTATTATT 2411
Db 2348 AGGGGTCTCAAGACATTTCTGCCTACCTATTAGCTTTTCTTTTATTATTATTATTATT 2407
Qy 2412 GGGAAAAGTATTTTGAGAAGTCTTCTGCAAGTATTATTAATAGTAATAAAGTTT 2471
Db 2408 GGGAAAAGTATTTTGAGAAGTCTTCTGCAAGTATTATTAATAGTAATAAAGTTT 2467
Qy 2472 TTACCATTTAAAAAATAAAAAA 2494
Db 2468 TTACCATTTAAAAAATAAAAAA 2490

RESULT 11
AAQ9244
ID AAQ9244 standard; DNA; 2474 BP.
XX
AC AAQ9244;
XX
DT 27-JAN-1997 (first entry)
XX
DE Insulin like growth factor binding protein-3 coding sequence.
XX
KW Insulin like growth factor; binding protein; IGF; IGFBP; inflammation;
KW proliferation; cell; skin; keratinocyte growth factor; antisense; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 110..985
FT /*tag= a
FT /product= "IGFBP-3"
XX
PN WO9601636-Al.
XX
PD 25-JAN-1996.
XX
PF 06-JUL-1995; 95WO-AU000410.
XX
PR 08-JUL-1994; 94AU-00006725.
XX
PA (ROYA-) ROYAL CHILDRENS HOSPITAL RES FOUND.
XX
PI Werther GA, Wright CJ;
XX
XX WPI; 1996-097445/10.
XX P-PSDB; AAR89273.
XX
PT Ameliorating effects of proliferative or inflammatory skin disorder -
PT e.g. ichthyosis, pityriasis and psoriasis, using nucleic acid
PT which modulates growth factor interaction with its receptor.
XX
PS Claim 14; page 78-79; 116pp; English.
XX
XX Cell proliferation and/or inflammation is mediated by at least one of
XX insulin like growth factor (IGF-I); keratinocyte growth factor; TGF-alpha
XX ; TNF-alpha; interleukin-1 (IL-1); IL-4, IL-6, IL-8 and bFGF. The effects
XX of a proliferative and/or inflammatory skin disorder in a mammal can be
XX ameliorated by administering a nucleic acid or its chemical analogue to
XX inhibit or reduce cell proliferation/inflammation. The nucleic acid
XX inhibits, reduces or otherwise interferes with IGF-I's interaction with
XX its receptor. It is preferably an antisense molecule which reduces
XX expression of the gene encoding IGF-I, an IGF-I receptor or an IGF

Db 730 GACAGAAATATGGTCCCTCGCGTATGAGAAATGGAGACACACTGAATCACCTGAAGTTCTT 789
 Qy 792 CAATGTGCTGAGTCCCAAGGGGTGACACATTTCCCAACTGTGACAAAGAGGATTTTATAA 851
 Db 790 CAATGTGCTGAGTCCCAAGGGGTGACACATTTCCCAACTGTGACAAAGAGGATTTTATAA 849
 Qy 852 GAAAAAGAGTGTGCGCTTCCAAAGGAGGAGGAGCGGGGCTTCTGCTGCTGTGCTGATAA 911
 Db 850 GAAAAAGCAGTGTGCGCTTCCAAAGGAGGAGGAGCGGGGCTTCTGCTGCTGTGCTGATAA 909
 Qy 912 GTATGGGAGGCTCTCCAGGCTACACCAAGGAGGAGGAGCGGCTGACCTGCTACAG 971
 Db 910 GTATGGGAGGCTCTCCAGGCTACACCAAGGAGGAGGAGCGGCTGACCTGCTACAG 969
 Qy 972 CATGACAGCAAGTAGAGCGCTCGCGGAGGAGTGAATGTGAGCTCAATATGCTTATTT 1031
 Db 970 CATGACAGCAAGTAGAGCGCTCGCGGAGGAGTGAATGTGAGCTCAATATGCTTATTT 1028
 Qy 1032 TGCAAAAGAGCTGCAAGGACATGACAGGAGCTGGCTACAGGCTCGAATTTATATTTCT 1091
 Db 1029 TGCAAAAGAGCTGCAAGGACATGACAGGAGCTGGCTACAGGCTCGAATTTATTTCT 1088
 Qy 1092 GTTGTGTGAGTGAATTTTAAACCAAGTTTGAAGAGGTTTGAATGCTT 1151
 Db 1089 GTTGTGTGAGTGAATTTTAAACCAAGTTTGAAGAGGTTTGAATGCTT 1147
 Qy 1152 ATGGTTCTTGAATGTGAGTGAATTTTAAACCAAGTTTGAAGAGGTTTGAATGCTT 1211
 Db 1148 ATGGTTCTTGAATGTGAGTGAATTTTAAACCAAGTTTGAAGAGGTTTGAATGCTT 1207
 Qy 1212 AGTTTGAATTTTCTGCTGCTTCTTATCAAAATATTCAGAGCTCGAGCAGCAGCCAG 1271
 Db 1208 AGTTTGAATTTTCTGCTGCTTCTTATCAAAATATTCAGAGCTCGAGCAGCAGCCAG 1267
 Qy 1272 ACTTCATGCGCCGCTGAGTCTCAGGATGCTCAGGAGGCTGAGGAGGCTGAGGAGGCT 1331
 Db 1268 ACTTCATGCGCCGCTGAGTCTCAGGATGCTCAGGAGGCTGAGGAGGCTGAGGAGGCT 1327
 Qy 1332 GTGACTTGGGCGCTGCTGCTGCTATGTAGAGACAGCTTCAACCCGCTGAGGAGGCTGGA 1391
 Db 1328 GTGACTTGGGCGCTGCTGCTGCTATGTAGAGACAGCTTCAACCCGCTGAGGAGGCTGGA 1387
 Qy 1392 GTGCGCAGGCTTTATCGAGATAGGAAACCTTTAAACCCGCTGAGGAGGCTGAGGAGGCT 1451
 Db 1388 GTGCGCAGGCTTTATCGAGATAGGAAACCTTTAAACCCGCTGAGGAGGCTGAGGAGGCT 1447
 Qy 1452 AACGATGCTCTGAGGCTCAGAGCTTCTGTGTGTCTATTTCTGAAACAGAGGCGTGA 1511
 Db 1448 AACGATGCTCTGAGGCTCAGAGCTTCTGTGTGTCTATTTCTGAAACAGAGGCGTGA 1507
 Qy 1512 TCCCTCAACCAAGAGATGTTTATGCTTCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1571
 Db 1508 TCCCTCAACCAAGAGATGTTTATGCTTCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1567
 Qy 1572 GAGAAATAGGTGGAGTCTACTTGTGTTTAAATAATATGCTATCAAGATGCTTCTAGGCT 1631
 Db 1568 GAGAAATAGGTGGAGTCTACTTGTGTTTAAATAATATGCTATCAAGATGCTTCTAGGCT 1627
 Qy 1632 ACTCTGGGAACCTATAAGGAGGATTTTGGGCGCTCTCTTCTGAGGATCTTCTGAGG 1691
 Db 1628 ACTCTGGGAACCTATAAGGAGGATTTTGGGCGCTCTCTTCTGAGGATCTTCTGAGG 1687
 Qy 1692 ACATGCGCCAGTTCGAGGCGCCAGGATGCTTGTGCGGCGCCGCTGCGGCTGAGGAGGAC 1751
 Db 1688 ACATGCGCCAGTTCGAGGCGCCAGGATGCTTGTGCGGCGCCGCTGCGGCTGAGGAGGAC 1747
 Qy 1752 AGAGACAGGAGGAGTACGCTTCCACATTCAGAGGCTATCAAGTATGCGACATTTCT 1811
 Db 1748 AGAGAGAC-GGAGAGTACGCTTCCACATTCAGAGGCTATCAAGTATGCGACATTTCT 1806
 Qy 1812 TCGATGCTGAGAAATAGTGTGTTGAGTTCAACACTCAAGCAGGCTTATTTCT 1871

Db 1807 TCGGATGACTCGAGAAATAGTGTGTTTGTAGTTCAACAACTCAAGACGAAGCTTATTTCT 1866
 Qy 1872 GAGGATAAGCTCTTTAAAGGCAAAAGCTTTATTTTCTCTCTCATCTTTTGTCTCTCTTAG 1931
 Db 1867 GAGGATAAGCTCTTTAAAGGCAAAAGCTTTATTTTCTCTCTCATCTTTTGTCTCTCTTAG 1926
 Qy 1932 CACATGTAAAAAAGAAATAGTAATATCAGAACAGGAAGGAGGATGCTTCTGGGAGC 1991
 Db 1927 CACATGTAAAAAAGAAATAGTAATATCAGAACAGGAAGGAGGATGCTTCTGGGAGC 1986
 Qy 1992 CCATCCAGACACTCGGAGCAGCATAGAGATTCAACCATGTTTGTGTAAGTCTAGTCAATT 2051
 Db 1987 CCATCCAGACACTCGGAGCAGCATAGAGATTCAACCATGTTTGTGTAAGTCTAGTCAATT 2046
 Qy 2052 CTCATGCTTTTCTTTATTAATTCACACATATATGACAGAGATATGTTTCTTTAAACATT 2111
 Db 2047 CTCATGCTTTTCTTTATTAATTCACACATATATGACAGAGATATGTTTCTTTAAACATT 2106
 Qy 2112 GTATACACATAGCCCCCAATATAGTAAGATCTATCTAGATATCTTAGATGAATGTT 2171
 Db 2107 GTATACACATAGCCCCCAATATAGTAAGATCTATCTAGATATCTTAGATGAATGTT 2166
 Qy 2172 AGAGATGCTTATTTGATACAACTGTGCGCATGACTGAGGAAAGGAGCTCACGCCACAGAGAC 2231
 Db 2167 AGAGATGCTTATGATACAACTGTGCGCATGACTGAGGAAAGGAGCTCACGCCACAGAGAC 2226
 Qy 2232 TGGGCTGCTCTCCCGAGGCGCCAAACCAAGAGGCTGCGCAAGTCAGGCTCAGGAGAC 2291
 Db 2227 TGGGCTGCTCTCCCGAGGCGCCAAACCAAGAGGCTGCGCAAGTCAGGCTCAGGAGAC 2286
 Qy 2292 TCTGCCCTGCTCAGACCTCGGCTGCGGACACACGCTGCATAGAGCTCTCTTTGAAACAG 2351
 Db 2287 TCTGCCCTGCTCAGACCTCGGCTGCGGACACACGCTGCATAGAGCTCTCTTTGAAACAG 2346
 Qy 2352 AGGGTCTCAAGACATTCGCTACTATAGCTTTCTTTTATTTTAACTTTTGGG 2411
 Db 2347 AGGGTCTCAAGACATTCGCTACTATAGCTTTCTTTTATTTTAACTTTTGGG 2406
 Qy 2412 GGGAAAGTATTTTGGAGAGTTTCTTGCATGCTTATTAATAGTAATAAAGTTT 2471
 Db 2407 GGGAAAGTATTTTGGAGAGTTTCTTGCATGCTTATTAATAGTAATAAAGTTT 2466
 Qy 2472 TTACCATT 2479
 Db 2467 TTACCATT 2474

RESULT 13
 ADAS2925
 ID ADAS2925 standard; cDNA; 2448 BP.
 XX
 AC ADAS2925;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human coding sequence, SEQ ID 493.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002BP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.

(REAS-) RES ASSOC BIOTECHNOLOGY.

I Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
R WPI: 2003-395539/39.
R P-PSDB; ADA54564.

New polynucleotides encoding full-length polypeptides, e.g. secretory
and/or membrane proteins, useful for developing medicines for diseases in
which the gene is involved, or as target molecules for gene therapy.

Claim 1; SEQ ID NO 493; 205pp; English.

The present invention relates to novel human secretory or membrane
proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
ADA54071). The coding sequences are useful in the gene therapy of
diseases caused by abnormalities of the proteins, e.g. cancer,
inflammatory diseases, osteoporosis or neurological disease.

Sequence 2448 BP; 599 A; 627 C; 642 G; 580 T; 0 U; 0 Other;

Query Match 94.7%; Score 2361.8; DB 7; Length 2448;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 2425; Conservative 0; Mismatches 2; Indels 52; Gaps 1;

2y 1 GCGGTGAGGATCAGCGCTTCTCCCTGCTGGATTCCACAGCTTCGCGCGTGTACTGTCGCC 60
2b 22 GCGGTGAGGATCAGCGCTTCTCCCTGCTGGATTCCACAGCTTCGCGCGTGTACTGTCGCC 81
2y 61 CCATCCCTGCGCGGCCAGCTGTCGCAAGCAGCGTGCCTCCCGTTCAGCGGTTCATGACGCG 120
2b 82 CCATCCCTGCGCGGCCAGCTGTCGCAAGCAGCGTGCCTCCCGTTCAGCGGTTCATGACGCG 141
2y 121 GCGGACCCAGCTTCGGCGGCTGCGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
2b 142 GCGGACCCAGCTTCGGCGGCTGCGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201
2y 181 GTGCGCGGGGTGCGCGGAGCTGCGGGGGTTCGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
2b 202 GTGCGCGGGGTGCGCGGAGCTGCGGGGTTCGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 257
2y 241 GACCGGTGCACTGGCCAGTGGCGGCTCCGCCCTCGCGCGGAGTGTGCGC 300
2b 258 -----GAGCTGGTGGCG 269
2y 301 GAGCGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
2b 270 GAGCGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 329
2y 361 TACACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
2b 330 TACACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 399
2y 421 CTGAGGCGCTGCTGAGCGCGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
2b 390 CTGAGGCGCTGCTGAGCGCGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
2y 481 CGCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
2b 450 CGCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509
2y 541 CGCAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
2b 510 CGCAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 569
2y 601 AAGTTCCACCCCTCCATTCATAAGATAATCATCATCATCATCATCATCATCATCATCATCATCAT 660
2b 570 AAGTTCCACCCCTCCATTCATAAGATAATCATCATCATCATCATCATCATCATCATCATCATCAT 629
2y 661 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCAGATACCCAGAACTTCTCTCTCCGAG 720

QY 1801 GGCACAAATCTTCGGATGACCTGCAGAAAAATAGTGTCTTTTGTAGTTCAACAACTCAAGACGA 1860
Db 1770 GGCACAAATCTTCGGATGACCTGCAGAAAAATAGTGTCTTTTGTAGTTCAACAACTCAAGACGA 1829
QY 1861 AGCTTAATCTTCGAGGATAAGCTCTTTAAAGGCAAAAGCTTTTATTTTTCATCTCTCATCTTTT 1920
Db 1830 AGCTTAATCTTCGAGGATAAGCTCTTTAAAGGCAAAAGCTTTTATTTTTCATCTCTCATCTTTT 1889
QY 1921 GTCTCTCTTAGACAAATGTAAAAAAGAAATAGTAATATCAGAACAGGAGGAGATGGCT 1980
Db 1890 GTCTCTCTTAGACAAATGTAAAAAAGAAATAGTAATATCAGAACAGGAGGAGATGGCT 1949
QY 1981 TGCTGGGAGCCATCCAGGACACTGGAGACACATAGAGATTCACCCATGTTTGTTCGAAC 2040
Db 1950 TGCTGGGAGCCATCCAGGACACTGGAGACACATAGAGATTCACCCATGTTTGTTCGAAC 2009
QY 2041 TTAGAGTCAATCTCATGCTTTCTTTTATAATATCACATATATCAGAGAGATATGTTT 2100
Db 2010 TTAGAGTCAATCTCATGCTTTCTTTTATAATATCACATATATCAGAGAGATATGTTT 2069
QY 2101 TTGTTAAATGTATACAAATAGCCCAATATAGTAAGATCTATATAGATAATCTTA 2160
Db 2070 TTGTTAAATGTATACAAATAGCCCAATATAGTAAGATCTATATAGATAATCTTA 2129
QY 2161 GATGAAATGTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGAGTCA 2220
Db 2130 GATGAAATGTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGAGTCA 2189
QY 2221 CGCCAGAGACTGGGCTGCTCTCCGGAGGCAACCCCAAGAGTCTGCAAAAGTCAGG 2280
Db 2190 CGCCAGAGACTGGGCTGCTCTCCGGAGGCAACCCCAAGAGTCTGCAAAAGTCAGG 2249
QY 2281 CTCAGGAGACTCTGCCCTGTGTCAGACTCGGTGTGAGACACAGCTGTCATAGAGCTCTC 2340
Db 2250 CTCAGGAGACTCTGCCCTGTGTCAGACTCGGTGTGAGACACAGCTGTCATAGAGCTCTC 2309
QY 2341 CTTGAAACAGAGGGGTCTCAGACATCTGCTACCTATTAGCTTTTCTTTATTTTTT 2400
Db 2310 CTTGAAACAGAGGGGTCTCAGACATCTGCTACCTATTAGCTTTTCTTTATTTTTT 2369
QY 2401 AACTTTTTGGGGGAAAAAGTATTTTTGAGAGTGTGCTTGCATGTATTTATAAATAGT 2460
Db 2370 AACTTTTTGGGGGAAAAAGTATTTTTGAGAGTGTGCTTGCATGTATTTATAAATAGT 2429
QY 2461 AATAAAGTTTTTACCATT 2479
Db 2430 AATAAAGTTTTTACCATT 2448

RESULT 14
ID AA241960 standard; cDNA; 2191 BP.
XX AA241960;
AC AC
XX 28-JAN-2000 (first entry)
DT DT
XX Human myometrium tumour cDNA derived EST 11.
DE DE
XX Myometrium; tumour; human; expressed sequence tag; EST; uterine myoma;
KW treatment; carcinoma; cancer; gene therapy; ss.
XX Homo sapiens.
OS OS
XX DE19817947-A1.
PN PN
XX 28-OCT-1999.
PD PD
XX 17-APR-1998; 98DE-01017947.
XX 17-APR-1998; 98DE-01017947.
XX 17-APR-1998; 98DE-01017947.
XX

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
PI WPI; 1999-602380/52.
XX
XX New nucleic acid sequences expressed in uterine myoma, and derived
PT polypeptides, for treatment of uterine carcinoma and identification of
PT therapeutic agents.
XX
XX Claim 3; Page 50; 86pp; German.
PS
CC This invention describes novel polypeptide sequences (I), fragments of
CC (I) fragments and their encoding nucleic acids (II) which are highly
CC expressed in human uterine myoma. (II) are used for recombinant
CC expression of (I) and to isolate complete genes. (I) are used to identify
CC agents suitable for treatment of uterine carcinoma, to directly treat
CC this form of cancer (including expression from gene therapy vectors) and
CC are used in a preparation for cancer treatment (I) is also used for the
CC (generation of specific antibodies. (II) are identified by assembling ESTs
CC of expression patterns. This allows a significantly longer fragment of
CC the gene to be revealed and therefore reduces the number of failures
CC associated with the fact that ESTs from different libraries may represent
CC different parts of the same unknown gene, distorting the estimated
CC frequency of occurrence in a particular tissue. AA241950-241980 represent
CC EST fragments derived from a human myometrium tumour cDNA library which
CC encode the protein sequences represented in AA159921-159940
XX
SQ Sequence 2191 BP; 599 A; 525 C; 539 G; 528 T; 0 U; 0 Other;

Query Match 85.9%; Score 2143.4; DB 2; Length 2191;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2155; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 333 ACTGACGAGGCGACCGCTGCGGCATCTACACGAGCGCTGTGGCTCGGGCTTCGCTG 392
Db 1 ACTGACGAGGCGACCGCTGCGGCATCTACACGAGCGCTGTGGCTCGGGCTTCGCTG 60
QY 393 CGAGCGCTGCGCGAGCGCGACCGCTGCGAGCGCTGTGGACGGCGCGGGCTCTG 452
Db 61 CGAGCGCTGCGCGAGCGCGACCGCTGCGAGCGCTGTGGACGGCGCGGGCTCTG 120
QY 453 CGTCAACGCTAGTGTGCGCTGAGCGCGCTGCGCGCTACCTGTGCGAGCGCGCGCTCC 512
Db 121 CGTCAACGCTAGTGTGCGCTGAGCGCGCTGCGCGCTACCTGTGCGAGCGCGCGCTCC 180
QY 513 AGGAATGTAGTGTGCGAGGAGACCGCGCGCGCTGCGAGCGCGCGCTCCGCT 572
Db 181 AGGAATGTAGTGTGCGAGGAGACCGCGCGCGCTGCGAGCGCGCGCTCCGCT 240
QY 573 CTCACGACGACCGGGGTGTCTGATCCCAAGTTTCCACCCCTCCATTTCAAGATAATCAT 632
Db 241 CTCACGACGACCGGGGTGTCTGATCCCAAGTTTCCACCCCTCCATTTCAAGATAATCAT 300
QY 633 CATCAAGAAAGGCGATGCTTAAGACAGCGCGCTACAAAGTTGACTAGAGTCTCAGAG 692
Db 301 CATCAAGAAAGGCGATGCTTAAGACAGCGCGCTACAAAGTTGACTAGAGTCTCAGAG 360
QY 693 CACAGATACCCGAACTTCTCTCCAGTCCAAAGCGGAGACAGAAATATGTCCTCCCG 752
Db 361 CACAGATACCCGAACTTCTCTCCAGTCCAAAGCGGAGACAGAAATATGTCCTCCCG 420
QY 753 TAGAGAAATGGAAGACACACTGAATCACCTGAAGTTTCTCAATGTGCTGAGTCCCAAGGG 812
Db 421 TAGAGAAATGGAAGACACACTGAATCACCTGAAGTTTCTCAATGTGCTGAGTCCCAAGGG 480
QY 813 TGTACACATTCCCAACTGTGACAAAGAGGATTTTATAAGAAAAAGCAGTGTGCGCTTC 872
Db 481 TGTACACATTCCCAACTGTGACAAAGAGGATTTTATAAGAAAAAGCAGTGTGCGCTTC 540
QY 873 CAAAGGAGGAAAGCGGGCTTCTGCTGTGTGGATAGTATGCGCAGCTTCCAGG 932

541	CA	AAAGCAGGAAGCGGGGCTTCTGCTGGTGTGCGATAAGTATGGCGACGCTTCCACGG	600
933	CT	ACACCAAGGGGAAGAGGACGTGCACTGCTACAGCATGCAAGCAAGTAGACGCC	992
601	CT	ACACCAAGGGGAAGAGGACGTGCACTGCTACAGCATGCAAGCAAGTAGACGCC	660
993	TG	CCGCAAGGTTAAATGTGGAGCTCAAAATATGCCTATTTTGTGCGTGAACGACATG	1052
661	TG	CCGCAAGGTTAAATGTGGAGCTCAAAATATGCCTATTTTGTGCGTGAACGACATG	720
1053	CA	TGACACGAGCTGGCTACAGCCTCGAATTAATTTCTGTTTGTGGTGAACGATTTT	1112
721	CA	TGACACGAGCTGGCTACAGCCTCGAATTAATTTCTGTTTGTGGTGAACGACATG	779
1113	TT	TTAAACCAAGCTTAGAAAGAGGTTTTGAAATGCCTATGCTTTCTTGAATGTAATA	1172
780	TT	TTAAACCAAGCTTAGAAAGAGGTTTTGAAATGCCTATGCTTTCTTGAATGTAATA	839
1173	CT	TGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAAGAGAGTTTGAATTTCTTGTG	1232
840	CT	TGAGCATCTTTTCACTTTCCAGTAGTCAGCAAAAGAGAGTTTGAATTTCTTGTG	899
1233	TC	CTACAAATATTCAGAGACTCGAGCAGACACCCAGACTTCATGCGCCCGTGAATG	1292
900	TC	CTACAAATATTCAGAGACTCGAGCAGACACCCAGACTTCATGCGCCCGTGAATG	959
1293	CT	CACACATGTTGGTGCAGAGCGGCGACACGTGACTTTGTGACTTAGCGGCTGTG	1352
960	CT	CACACATGTTGGTGCAGAGCGGCGACACGTGACTTTGTGACTTAGCGGCTGTG	1019
1353	CT	ATGTAGAGAACACGCTTCAACCCACCTCCCGGTACAGTGCAGCAGGCTTTATCG	1412
1020	CT	ATGTAGAGAACACGCTTCAACCCACCTCCCGGTACAGTGCAGCAGGCTTTATCG	1079
1413	AA	TAGAAAACCTTTAAACCCGGTCAATCCGAGATCCCAACGATGCTCTCTGGAGTCA	1472
1080	AA	TAGAAAACCTTTAAACCCGGTCAATCCGAGATCCCAACGATGCTCTCTGGAGTCA	1139
1473	CAG	CTCTGTGTGTCATTCTTGAACAAGGCGTGGATCCCTCAACCAAGAAGAAATGT	1532
1140	CAG	CTCTGTGTGTCATTCTTGAACAAGGCGTGGATCCCTCAACCAAGAAGAAATGT	1199
1533	TT	ATGCTTCAAGTGACCTGACTGTGTTGGGACTATTGAGAAATAAGTGGAGTCTCT	1592
1200	TT	ATGCTTCAAGTGACCTGACTGTGTTGGGACTATTGAGAAATAAGTGGAGTCTCT	1259
1593	AC	TGTTTTAAAAATATGTATCTAAGAAATGTTCTAGGGCACTCTGGGAACCTATAAG	1652
1260	AC	TGTTTTAAAAATATGTATCTAAGAAATGTTCTAGGGCACTCTGGGAACCTATAAG	1319
1653	AG	GTATTTGGGCCCTCTCTTCAGGAATCTTCTGAAAGCATGGCCAGTCCGAGCC	1712
1320	AG	GTATTTGGGCCCTCTCTTCAGGAATCTTCTGAAAGCATGGCCAGTCCGAGCC	1379
1713	AG	GATGGCTTTTGTGCGGGCCCCGTGGGTAGGAGGACAGAGACAGGAGAGTCCAG	1772
1380	AG	GATGGCTTTTGTGCGGGCCCCGTGGGTAGGAGGACAGAGACAGGAGAGTCCAG	1439
1773	CT	CACATTCAGAGCATCAAGTAAATGSCACAAATTTCTGGATGACTCCGAAATAG	1832
1440	CT	CACATTCAGAGCATCAAGTAAATGSCACAAATTTCTGGATGACTCCGAAATAG	1499
1833	TG	TTTTGTAGTTCACCAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTTTTAAAG	1892
1500	TG	TTTTGTAGTTCACCAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTTTTAAAG	1559
1893	AA	AGCTTTATTTTCATCTCATCTTTTGTCTCTTGTAGCAGCATGTAAAGAAATAG	1952
1560	AA	AGCTTTATTTTCATCTCATCTTTTGTCTCTTGTAGCAGCATGTAAAGAAATAG	1619
1953	AA	TATCAGAAACAGGAAGAGGAATGGCTTGTCTGGGAGCCCATCCAGCACTGGGAC	2012
1620	AA	TATCAGAAACAGGAAGAGGAATGGCTTGTCTGGGAGCCCATCCAGCACTGGGAC	1679

QY	2013	CATAGAGATTCA	CCCATCTTTGTTGAACTTAGAGTCATTTCTCATGCTTTCTTTATAATT	207
Db	1680	CA*TAGAGATTCA	CCCATCTTTGTTGAACTTAGAGTCATTTCTCATGCTTTCTTTATAATT	1739
QY	2073	CACACATATATG	CAGAGAAGATATGTTCTTTGTTAA	2132
Db	1740	CACACATATATG	CAGAGAAGATATGTTCTTTGTTAA	1799
QY	2133	ATAGTAGAATCT	TATCTAGATATCTCTAGATGAAATGTTAGAGATGCTATTTGATACAAC	2192
Db	1800	ATAGTAGAATCT	TATCTAGATATCTCTAGATGAAATGTTAGAGATGCTATTTGATACAAC	1859
QY	2193	TGTGGCCATGACT	GTAGAGAAAGAGACTCAGCCCCAGAGACTGGCTCTCTCCCGAGGCC	2252
Db	1860	TGTGGCCATGACT	GTAGAGAAAGAGACTCAGCCCCAGAGACTGGCTCTCTCCCGAGGCC	1919
QY	2253	AAACCCAAAGAGT	CTGGCMAAGTCAAGCTCAGGCTCAGGAGAGCTCTGCCCTGCTGCAGAGCCTCG	2312
Db	1920	AAACCCAAAGAGT	CTGGCMAAGTCAAGCTCAGGCTCAGGAGAGCTCTGCCCTGCTGCAGAGCCTCG	1979
QY	2313	GTGTGGACACAC	CGCTGCATAGAGCTCTCCTTTGAAACACAGAGGGGTCTCAAGACATTTCTGC	2372
Db	1980	GTGTGGACACAC	CGCTGCATAGAGCTCTCCTTTGAAACACAGAGGGGTCTCAAGACATTTCTGC	2039
QY	2373	CTACCTATTAGCT	TTTTCTTTTATTTTAACTTTTGGGGGGGAAAAGTATTTTGTGAGAAG	2432
Db	2040	CTACCTATTAGCT	TTTTCTTTTATTTTAACTTTTGGGGGGGAAAAGTATTTTGTGAGAAG	2099
QY	2433	TTTGCTCTTGCA	ATGTTATTAATAATAGTAATAAAGTTTTTACCATTAATAAAAAAAA	2489
Db	2100	TTTGCTCTTGCA	ATGTTATTAATAATAGTAATAAAGTTTTTACCATTAATAAAAAAAA	2156
RESULT 15				
ADB62922				
ID	ADB62922 standard; cDNA; 2327 BP.			
XX				
AC	ADB62922;			
XX				
XX	04-DEC-2003 (first entry)			
XX	Human cDNA encoding clone PLACE60087680.			
XX	Human; ss; gene; pharmaceutical; diagnostic; gene therapy;			
KW	tissue regeneration; cell regeneration; membrane protein;			
KW	signal transduction-related protein; transcription-related protein;			
KW	osteoporosis; neurological disease; cancer; tumour.			
XX				
XX	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	3'-836		
FT	FT	/*tag= a		
XX	FT	/product= "Clone PLACE60087680 protein"		
XX	FN	EP1308459-A2.		
XX	XX	07-MAY-2003.		
XX	PD	28-MAR-2002; 2002EP-00007401.		
XX	PF	05-NOV-2001; 2001JP-00379298.		
XX	PR	25-JAN-2002; 2002US-00350978.		
XX	PR	(HELI-) HELIX RES INST.		
XX	PA	(REAS-) RES ASSOC BIOTECHNOLOGY.		
XX	XX	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;		
XX	PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;		
XX	PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;		
XX	XX	WPI; 2003-450961/43.		

2y	1621	TGTTCTAGGCACTCTGGGAACCTATATAAGGCAGGTATTTTCGGGCCCTCTCTTCAGGAA	1680
2b	1469	TGTTCTAGGCACTCTGGGAACCTATATAAGGCAGGTATTTTCGGGCCCTCTCTTCAGGAA	1528
2y	1681	TCCTTCCTGAAGACATGCGCCAGTCGAAAGGCCCGAGATGGCTTTTGTGCGGCCCGCTGGG	1740
2b	1529	TCCTTCCTGAAGACATGCGCCAGTCGAAAGGCCCGAGATGGCTTTTGTGCGGCCCGCTGGG	1588
2y	1741	GTAGAGGACAGAGACAGGAGAGTCCACATTCAGAGGCATCAAGTAAT	1800
2b	1589	GTAGAGGACAGAGACAGGAGAGTCCACATTCAGAGGCATCAAGTAAT	1648
2y	1801	GGCAACAATTCCTCGGATGACATGCAGAGAAATAGTGTGTTGTAGTTCACAACTCAAGACGA	1860
2b	1649	GGCAACAATTCCTCGGATGACATGCAGAGAAATAGTGTGTTGTAGTTCACAACTCAAGACGA	1708
Qy	1861	AGCTTATTCGAGAGTAAGCTCTTTAAAGCAAGCTTTTATTTTCATCTCTCATCTTTT	1920
Db	1709	AGCTTATTCGAGAGTAAGCTCTTTAAAGCAAGCTTTTATTTTCATCTCTCATCTTTT	1768
Qy	1921	GTCTCTCTTAGCAACAATGTAAAGAAATAGTAATATCAGAACAGGAGGAAATGGCT	1980
Db	1769	GTCTCTCTTAGCAACAATGTAAAGAAATAGTAATATCAGAACAGGAGGAAATGGCT	1828
Qy	1981	TGCTGGGAGGCCATCCAGGACATCGGAGACATAGAGATTCCACCATGTTTGTGTAAC	2040
Db	1829	TGCTGGGAGGCCATCCAGGACATCGGAGACATAGAGATTCCACCATGTTTGTGTAAC	1888
Qy	2041	TTAGAGCATTCCTCATGCTTTCTTTTATATTTACACATATATGCAGAGAGATATGTTT	2100
Db	1889	TTAGAGCATTCCTCATGCTTTCTTTTATATTTACACATATATGCAGAGAGATATGTTT	1948
2y	2101	TTGTTAACAATGTATACAAATAGCCCCAAATATAGTAAGATCTATATCTAGATAATCCTA	2160
2b	1949	TTGTTAACAATGTATACAAATAGCCCCAAATATAGTAAGATCTATATCTAGATAATCCTA	2008
Qy	2161	GATGAATGTTAGAGATGCTATTTGATACAACTCTGGCCATGCTGAGGAAAGGAGCTCA	2220
Db	2009	GATGAATGTTAGAGATGCTATATGATACAACTCTGGCCATGCTGAGGAAAGGAGCTCA	2068
Qy	2221	CGCCAGAGACTGGGCTGCTCTCCCGAGGCGCAACCCCAAGAGGTCTGGCAAAGTCAGG	2280
Db	2069	CGCCAGAGACTGGGCTGCTCTCCCGAGGCGCAACCCCAAGAGGTCTGGCAAAGTCAGG	2128
Qy	2281	CTCAGGAGACTCTGCCCTGCTGAGACCTCGGTGTGGACACAGCTGCAATAGAGCTCTC	2340
Db	2129	CTCAGGAGACTCTGCCCTGCTGAGACCTCGGTGTGGACACAGCTGCAATAGAGCTCTC	2188
Qy	2341	CTTGAAAACAGAGGGGTCTCAAGACATTCGCTACCTATTAGCTTTTCTTTATTTTTT	2400
Db	2189	CTTGAAAACAGAGGGGTCTCAAGACATTCGCTACCTATTAGCTTTTCTTTATTTTTT	2248
Qy	2401	AACTTTTGGGGGAAAAGTATTTTGAAGAAGTTTGCTTCCAATGATATTTATAATAGT	2460
Db	2249	AACTTTTGGGGGAAAAGTATTTTGAAGAAGTTTGCTTCCAATGATATTTATAATAGT	2308
Qy	2461	AAATAAGTTTTTACCATT	2479
Db	2309	AAATAAGTTTTTACCATT	2327

Search completed: March 10, 2004, 10:59:17
 Job time : 617.991 secs

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	2446.2	98.1	2550	6	Patent No. 5258287
2	2430.4	97.4	2474	2	Sequence 2, Appli
3	2430.4	97.4	2474	3	Sequence 2, Appli
4	914.4	36.7	916	4	Sequence 73, Appli
5	914.4	36.7	916	4	Sequence 73, Appli
6	914.4	36.7	916	4	Sequence 73, Appli
7	914.4	36.7	916	4	Sequence 73, Appli
8	914.4	36.7	916	4	Sequence 73, Appli
9	874.4	35.1	876	1	Sequence 6, Appli
10	874.4	35.1	876	5	Sequence 6, Appli
11	874.4	35.1	876	5	Sequence 6, Appli
12	648.4	25.7	798	1	Sequence 5, Appli
13	639.8	25.7	795	3	Sequence 3, Appli
14	639.8	25.7	795	5	Sequence 3, Appli
15	472.8	19.0	1141	4	Sequence 877, App
16	395	15.8	396	4	Sequence 12, Appl
17	395	15.8	396	4	Sequence 12, Appl
18	382.4	15.3	396	4	Sequence 58, Appl
19	382.4	15.3	396	4	Sequence 58, Appl
20	347	13.9	358	2	Sequence 1, Appli
21	262.8	10.5	795	2	Sequence 46, Appl
22	262.8	10.5	811	1	Sequence 6, Appli
23	262.8	10.5	811	3	Sequence 5, Appli
24	262.8	10.5	811	5	Sequence 5, Appli
25	258	10.3	258	3	Sequence 8, Appli
26	237	9.5	241	4	Sequence 358, App
27	237	9.5	241	4	Sequence 358, App

QY 492 GCTGCCAGCGCGCGCTCAGGAATGCTAGTCCGAGGAAAGACCGCAGCGCGG 551
Db 490 GCTGCCAGCGCGCGCTCAGGAATGCTAGTCCGAGGAAAGACCGCAGCGCGG 549
QY 552 CAGTGTGAGAGCGCGCTCCGCTCCAGCAGCAGCGCGGTCTCATCCCAAGTTCCACCC 611
Db 550 CAGTGTGAGAGCGCGCTCCGCTCCAGCAGCAGCGCGGTCTCATCCCAAGTTCCACCC 609
QY 612 CTTCAATCAAGATATATCATCATCAAGAAAGGCGATCTAAGACACAGCGCTACAA 671
Db 610 CTTCAATCAAGATATATCATCATCAAGAAAGGCGATCTAAGACACAGCGCTACAA 669
QY 672 AGTTCACTACAGTCTCAGAGCAGATATCCAGAACTTTCTCCGAGTCCCAAGCGGGA 731
Db 670 AGTTCACTACAGTCTCAGAGCAGATATCCAGAACTTTCTCCGAGTCCCAAGCGGGA 729
QY 732 GACAGAAATATGCTCCCTCCGCTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCT 791
Db 730 GACAGAAATATGCTCCCTCCGCTAGAGAAATGGAAGACACACTGAATCACCTGAAGTTCT 789
QY 792 CAATGTGTGAGTCCAGCGGTGTACATATCCCAACTGTGACAAAGAGGATTTATAA 851
Db 790 CAATGTGTGAGTCCAGCGGTGTACATATCCCAACTGTGACAAAGAGGATTTATAA 849
QY 852 GAAAAAGCAGTGTCCCTTCCAAAGCAGGAAGCGGGCTTTCTGCTGTGTGGATAA 911
Db 850 GAAAAAGCAGTGTCCCTTCCAAAGCAGGAAGCGGGCTTTCTGCTGTGTGGATAA 909
QY 912 GTATGGGAGCGCTTCCAGGCTTACACACAGGGAAGGAGGAGCTGCACTGCTACAG 971
Db 910 GTATGGGAGCGCTTCCAGGCTTACACACAGGGAAGGAGGAGCTGCACTGCTACAG 969
QY 972 CATGACAGCAAGTAGAGCGCTTCCGCAAGTAAATGTGAGCTCAATATGCTTTATTT 1031
Db 970 CATGACAGCAAGTAGAGCGCTTCCGCAAGTAAATGTGAGCTCAATATGCTTTATTT 1029
QY 1032 TGCACAAAGACTGCAAGGACATGACAGAGCTGCTTACAGCTTCACTTCCAGTACGAAAGG 1091
Db 1030 TGCACAAAGACTGCAAGGACATGACAGAGCTGCTTACAGCTTCACTTCACTTCACTT 1089
QY 1092 GTTGTGTGAACTGATTTTTTTTTTAAACCAAGTTTAAAGAGGTTTTTGAATGCTT 1151
Db 1090 GTTGTGTGAACTGATTTTTTTTTTAAACCAAGTTTAAAGAGGTTTTTGAATGCTT 1148
QY 1152 ATGTTTCTTTGAATGTTAACTGAGCTTCTTTTCACTTTCCAGTACGAAAGG 1211
Db 1149 ATGTTTCTTTGAATGTTAACTGAGCTTCTTTTCACTTTCCAGTACGAAAGG 1208
QY 1212 AGTTTGAATTTTCTTGTGCTTCTTCAATCAATATTCAGAGACTCGAGCAGCACCAG 1271
Db 1209 AGTTTGAATTTTCTTGTGCTTCTTCAATCAATATTCAGAGACTCGAGCAGCACCAG 1268
QY 1272 ACTTCATGCGCGGTGAATGCTACACCATGTTGTTGAGCGGCGGACCACTGACTTT 1331
Db 1269 ACTTCATGCGCGGTGAATGCTACACCATGTTGTTGAGCGGCGGACCACTGACTTT 1328
QY 1332 GTGACTTACGCGCTGTTGCTATGTAGAGAAACAGCTTCCACCCCACTCCCCGTACA 1391
Db 1329 GTGACTTACGCGCTGTTGCTATGTAGAGAAACAGCTTCCACCCCACTCCCCGTACA 1388
QY 1392 GTGCGCACAGGCTTTATCGAGAAATAGGAAAACTTTTAAACCCCGGTATCGGACATCCC 1451
Db 1389 GTGCGCACAGGCTTTATCGAGAAATAGGAAAACTTTTAAACCCCGGTATCGGACATCCC 1448
QY 1452 AACGCATGCTCCGAGCTCAGAGCTTCTGTTGTTGCTATTTCTGAAACAGGCGGTGGA 1511
Db 1449 AACGCATGCTCCGAGCTCAGAGCTTCTGTTGTTGCTATTTCTGAAACAGGCGGTGGA 1508
QY 1512 TCCCTCAACCAAGAAATGTTTATGCTTCAAGTGAACCTGCTGCTGCGGACTATTG 1571
Db 1509 TCCCTCAACCAAGAAATGTTTATGCTTCAAGTGAACCTGCTGCTGCGGACTATTG 1568
QY 1572 GAGAAATAGGTGGAGTCTCTACTTGTGTTTAAAAAATATGCTATAGAAATGTTCTAGGCG 1631

Db 1569 GAGAAATAGGTGGAGTCTCTACTTGTGTTTAAAAAATATGTTATAGAAATGTTCTAGGCG 1628
QY 1632 ACTTGGGAAACCTATAAAGGAGGAGTATTTTCGGCCCTCTCTTTCAGGAACTTCTCTGAG 1691
Db 1629 ACTTGGGAAACCTATAAAGGAGGAGTATTTTCGGCCCTCTCTTTCAGGAACTTCTCTGAG 1688
QY 1692 ACATGGCCCGCAGTCGAAGCCCGCAGGATGCTTTTGTGCGGCCCGCTGGGTAGGAGGAC 1751
Db 1689 ACATGGCCCGCAGTCGAAGCCCGCAGGATGCTTTTGTGCGGCCCGCTGGGTAGGAGGAC 1748
QY 1752 AGAGAGACAGGAGAGTCTGCTCCACATTCAGAGGATCAAGTAATGCGACAAATCT 1811
Db 1749 AGAGAGAC -GGAGAGTCCAGCTCCACATTCAGAGGATCAAGTAATGCGACAAATCT 1807
QY 1812 TCGGATGACTGCAGAAAAATAGTGTGTTTGTAGTTCAACAACTCAAGACGAAAGCTTTTCT 1871
Db 1808 TCGGATGACTGCAGAAAAATAGTGTGTTTGTAGTTCAACAACTCAAGACGAAAGCTTTTCT 1867
QY 1872 GAGGATAAGCTCTTTAAAGGCAAGCTTTTATTTTCATCTCTCATCTTTTGTCTCTCTTAG 1931
Db 1868 GAGGATAAGCTCTTTAAAGGCAAGCTTTTATTTTCATCTCTCATCTTTTGTCTCTCTTAG 1927
QY 1932 CACAATGTAAGAAAGAAATAGTAAATATCAGAACAGGAAGGAAATGGCTTGTGGGAGC 1991
Db 1928 CACAATGTAAGAAAGAAATAGTAAATATCAGAACAGGAAGGAAATGGCTTGTGGGAGC 1987
QY 1992 CCATCCAGACACTGGGACCATAGAGATTCACCCATGTTTGTGAACTTAGAGTCATT 2051
Db 1988 CCATCCAGACACTGGGACCATAGAGATTCACCCATGTTTGTGAACTTAGAGTCATT 2047
QY 2052 CTCTGCTTTCTTTTATATATTCACATATATGAGAGAAATATGTTCTTCTGTTAACTTT 2111
Db 2048 CTCTGCTTTCTTTTATATATTCACATATATGAGAGAAATATGTTCTTCTGTTAACTTT 2107
QY 2112 GTATACAAATAGCCCAATATAGTAACTATATCTAGATAATCTCTAGATGAAATGTT 2171
Db 2108 GTATACAAATAGCCCAATATAGTAACTATATCTAGATAATCTCTAGATGAAATGTT 2167
QY 2172 AGAGATGCTTTTGTATACAACTGTGCGCATGCTAGGAAAGAGCTCACGCCAGAGAC 2231
Db 2168 AGAGATGCTTTTGTATACAACTGTGCGCATGCTAGGAAAGAGCTCACGCCAGAGAC 2227
QY 2232 TGGGCTGCTCTCCGCGAGGCCAAACCCAAAGAGGTTGCAAGAGTCCAGGCTCAGGAGAC 2291
Db 2228 TGGGCTGCTCTCCGCGAGGCCAAACCCAAAGAGGTTGCAAGAGTCCAGGCTCAGGAGAC 2287
QY 2292 TCTGCCCTGCTCAGACCTCGGTGTGACACAGCTGCTAGAGCTCTCTCTGAAACAG 2351
Db 2288 TCTGCCCTGCTCAGACCTCGGTGTGACACAGCTGCTAGAGCTCTCTCTGAAACAG 2347
QY 2352 AGGGGTCTCAAGACATTCGCTTACCTATTTAGCTTTTCTTTTAACTTTTGGG 2411
Db 2348 AGGGGTCTCAAGACATTCGCTTACCTATTTAGCTTTTCTTTTAACTTTTGGG 2407
QY 2412 GGGAAAGTATTTTGTAGAAAGTGTGCTGCAATGTTTATTAATAGTAATAAGTTT 2471
Db 2408 GGGAAAGTATTTTGTAGAAAGTGTGCTGCAATGTTTATTAATAGTAATAAGTTT 2467
QY 2472 TTACATTAAGAAAAA 2494
Db 2468 TTACATTAAGAAAAA 2490

RESULT 2
US-08-666-392A-2
; Sequence 2, Application US/08666392A
; Patent No. 5929040
; GENERAL INFORMATION:
; APPLICANT: (countries other than U.S.): Royal Children's Hospital
; APPLICANT: Research Foundation
; APPLICANT: (U.S. only): George A. WERTHER and
; APPLICANT: Christopher J. WRAIGHT

Db 1328 GTGACTTAGCGGCTGTGTTCCTATGTAGAGAACACGCTTCAACCCCACTCCCGTACA 1387
 Qy 1392 GTGCGCACAGGCTTTATCGAAGATAGGAAACCTTTAAACCCCGGTCAATCGGACATCCC 1451
 Db 1388 GTGCGCACAGGCTTTATCGAAGATAGGAAACCTTTAAACCCCGGTCAATCGGACATCCC 1447
 Qy 1452 AACGATGCTCTCGAGGCTCACAGGCTTCTGTGGTGTCAATTTCTGAAACCAAGGCGGTGGA 1511
 Db 1448 AACGATGCTCTCGAGGCTCACAGGCTTCTGTGGTGTCAATTTCTGAAACCAAGGCGGTGGA 1507
 Qy 1512 TCCCTCAACCAAGAGAAATGTTATGTCTCAAGTGACCTGTACTGTGGGACTATTG 1571
 Db 1508 TCCCTCAACCAAGAGAAATGTTATGTCTCAAGTGACCTGTACTGTGGGACTATTG 1567
 Qy 1572 GAGAAATAAGGTGAGTCTCTACTGTTTAAATAATATGATCTAAAGATGTTCTAGGGC 1631
 Db 1568 GAGAAATAAGGTGAGTCTCTACTGTTTAAATAATATGATCTAAAGATGTTCTAGGGC 1627
 Qy 1632 ACTCTGGAACTCTAAAGGAGGATTTCTGGGCGCTCTCTTCTAGGAATCTTCTGAAG 1691
 Db 1628 ACTCTGGAACTCTAAAGGAGGATTTCTGGGCGCTCTCTTCTAGGAATCTTCTGAAG 1687
 Qy 1692 ACATGCGCCAGTCGAGGCCAGGATGCTTTTGTGGCGCCCGTGGGTAGGAGGAC 1751
 Db 1688 ACATGCGCCAGTCGAGGCCAGGATGCTTTTGTGGCGCCCGTGGGTAGGAGGAC 1747
 Qy 1752 AGAGACAGGAGAGTCAAGCTCCACATTCAGAGGCATCAAGTAATGGCAATCT 1811
 Db 1748 AGAGAGAC -GGAGAGTCAAGCTCCACATTCAGAGGCATCAAGTAATGGCAATCT 1806
 Qy 1812 TCGGATGCTGAGAAATAGTGTCTTCTAGTCAACAACTCAAGCAAGCTTATTCT 1871
 Db 1807 TCGGATGCTGAGAAATAGTGTCTTCTAGTCAACAACTCAAGCAAGCTTATTCT 1866
 Qy 1872 GAGGATAAGCTCTTTAAAGGCAGGCTTTATTTTCACTCTCATCTTTTGTCTCTCTAG 1931
 Db 1867 GAGGATAAGCTCTTTAAAGGCAGGCTTTATTTTCACTCTCATCTTTTGTCTCTCTAG 1926
 Qy 1932 CACATGTAAAGAAATAGTAATTCAGAGAGGAGGATGCTTCTGGGAGC 1991
 Db 1927 CACATGTAAAGAAATAGTAATTCAGAGAGGAGGATGCTTCTGGGAGC 1986
 Qy 1992 CCATCCAGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCATT 2051
 Db 1987 CCATCCAGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCATT 2046
 Qy 2052 CTCATGCTTTCTTTATAATTCACATATATGAGAGAGATATGTTCTTGTAACTT 2111
 Db 2047 CTCATGCTTTCTTTATAATTCACATATATGAGAGAGATATGTTCTTGTAACTT 2106
 Qy 2112 GTATACACATAGCCCCCAATATAGTAATCTTACTAGATAATCTTAGATGAATGTT 2171
 Db 2107 GTATACACATAGCCCCCAATATAGTAATCTTACTAGATAATCTTAGATGAATGTT 2166
 Qy 2172 AGAGATGCTATTGTATACAACTGTGGCCATGATGAGGAAAGAGCTCAGGCCAGAGAC 2231
 Db 2167 AGAGATGCTATTGTATACAACTGTGGCCATGATGAGGAAAGAGCTCAGGCCAGAGAC 2226
 Qy 2232 TGGGCTGCTCTCCGAGGCGCAACCCBAGAGAGGCTGSCAAAGTCAGCTCAGGAGAC 2291
 Db 2227 TGGGCTGCTCTCCGAGGCGCAACCCBAGAGAGGCTGSCAAAGTCAGCTCAGGAGAC 2286
 Qy 2292 TCTGCCCTGCTGAGACCTCGGTGTGGACACACGCTGCATAGAGTCTCTTGAAGAACAG 2351
 Db 2287 TCTGCCCTGCTGAGACCTCGGTGTGGACACACGCTGCATAGAGTCTCTTGAAGAACAG 2346
 Qy 2352 AGGGTCTCAGACATCTGCTTACTATAGCTTTCTTTTATTTTAACTTTTGGG 2411
 Db 2347 AGGGTCTCAGACATCTGCTTACTATAGCTTTCTTTTATTTTAACTTTTGGG 2406
 Qy 2412 GGGAAAGATTTTGGAGAGTTTGTCTGCAATGATTTATAAATAGTAATAAAGTTT 2471
 Db 2407 GGGAAAGATTTTGGAGAGTTTGTCTGCAATGATTTATAAATAGTAATAAAGTTT 2466

Qy 2472 TTACCATT 2479
 Db 2467 TTACCATT 2474

RESULT 3

US-09-199-926-2
 ; Sequence 2, Application US/09199926
 ; Patent No. 6284741
 ; GENERAL INFORMATION:
 ; APPLICANT: (Countries other than U.S.): Royal Children's Hospital
 ; APPLICANT: Research Foundation
 ; APPLICANT: (U.S. only): George A. WERTHER and
 ; APPLICANT: Christopher J. WRIGHT
 ; TITLE OF INVENTION: A METHOD FOR THE PROPHYLAXIS AND/OR
 ; TITLE OF INVENTION: TREATMENT OF PROLIFERATIVE AND/OR
 ; TITLE OF INVENTION: INFLAMMATORY SKIN DISORDERS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: U.S.A.
 ; ZIP: 10112-0228
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/199,926
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/666,392
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MacLeod, Janet M.
 ; REGISTRATION NUMBER: 35,263
 ; REFERENCE/DOCKET NUMBER: A30626-PCT-USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-408-2500
 ; TELEFAX: 212-765-2519
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2474 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 110...982
 ; OTHER INFORMATION:
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Wood, W.I., et al.
 ; TITLE: Cloning and expression of the growth...
 ; JOURNAL: Mol. Endocrinol.
 ; VOLUME: 2
 ; ISSUE: 1988
 ; PAGES: 1176-1185
 ; DATE:
 ; US-09-199-926-2

Query Match 97.4%; Score 2430.4; DB 3; Length 2474;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2464; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

Qy 12 CAGCCGCTTCTCGCTGGATTCCACAGCTTCGCGCGCTGCTACTGTGCCCCATCCCTGGG 71

QY 2232 TGGGCTGCTCTCCGGAGGCGCAAAACCCAAAGAGTCTGGGCAAAATCAGGCTCAGGGAGAC 2291
 DB 2227 TGGGCTGCTCTCCGGAGGCGCAAAACCCAAAGAGTCTGGGCAAAATCAGGCTCAGGGAGAC 2286
 QY 2292 TCTGCTGCTGCTGAGACCTCGGTGGGACACACGCTGCATAGAGCTCTCCTTGAAAACAG 2351
 DB 2287 TCTGCTGCTGCTGAGACCTCGGTGGGACACACGCTGCATAGAGCTCTCCTTGAAAACAG 2346
 QY 2352 AGGGTCTCAAGACANTCTGCTACCTAATTAGCTTTCTTTTATTTTAACTTTTGGG 2411
 DB 2347 AGGGTCTCAAGACANTCTGCTACCTAATTAGCTTTCTTTTATTTTAACTTTTGGG 2406
 QY 2412 GGGAAAGATTTTGGAGAGTTTGTCTTGCATGTAATTTATAAATAGTAATAAGTTT 2471
 DB 2407 GGGAAAGATTTTGGAGAGTTTGTCTTGCATGTAATTTATAAATAGTAATAAGTTT 2466
 QY 2472 TTACCATT 2479
 DB 2467 TTACCATT 2474

RESULT 4
 US-09-702-705-73
 ; Sequence 73, Application US/09702705
 ; Patent No. 6504010
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedvick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C14
 ; CURRENT APPLICATION NUMBER: US/09/702,705
 ; CURRENT FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 1833
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 73
 ; LENGTH: 916
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-702-705-73

Query Match 36.7%; Score 914.4; DB 4; Length 916;
 Best Local Similarity 99.9%; Pred No. 6.2e-209;
 Matches 915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1571 GGAGAAAATAGGTGGAGTCTCTACTTTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGG 1630
 DB 1 GGAGAAAATAGGTGGAGTCTCTACTTTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGG 60
 QY 1631 CACTCTGGGAACCTATAAAGGAGGATTTTCGGGCCCTCTCTCAGGAATCTCTCTGAA 1690
 DB 61 CACTCTGGGAACCTATAAAGGAGGATTTTCGGGCCCTCTCTCAGGAATCTCTCTGAA 120
 QY 1691 GACATGGCCCACTCGAAGGCCCGCAGGATGCTTTTGTGGGCCCGCTGGGGTAGGAGGA 1750
 DB 121 GACATGGCCCACTCGAAGGCCCGCAGGATGCTTTTGTGGGCCCGCTGGGGTAGGAGGA 180
 QY 1751 CAGAGACAGGGAGAGTCAAGCTCCACATTCAGAGGCATCAAGTAAATGCAATTC 1810
 DB 181 CAGAGACAGGGAGAGTCAAGCTCCACATTCAGAGGCATCAAGTAAATGCAATTC 240
 QY 1811 TTCGGATGACTGCAGAAAATAGTGTGTTTGTAGTTTCAACAACTCAAGACGAAGCTTTATTC 1870
 DB 241 TTCGGATGACTGCAGAAAATAGTGTGTTTGTAGTTTCAACAACTCAAGACGAAGCTTTATTC 300
 QY 1871 TGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTCACTCTCACTCTTCTCTCCTTA 1930

DB 301 TGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCACTCTCTCATCTTTTGTCTCCTTA 360
 QY 1931 GCACAAATGTAAAAAAGAAATAGTAATATCAGAACAGAAAGGAGGAATGCTTGTCTGGGAG 1990
 DB 361 GCACAAATGTAAAAAAGAAATAGTAATATCAGAACAGAAAGGAGGAATGCTTGTCTGGGAG 420
 QY 1991 CCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCAAT 2050
 DB 421 CCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCAAT 480
 QY 2051 TCTCATGCTTTTCTTTTATAAATTCACACATATATGACAGAAAGATATGTTTGTGAACT 2110
 DB 481 TCTCATGCTTTTCTTTTATAAATTCACACATATATGACAGAAAGATATGTTTGTGAACT 540
 QY 2111 TGTATACACATAGCCCCCAATATATAGTAAGATCTATCTAGATAATCTAGATAAATGTT 2170
 DB 541 TGTATACACATAGCCCCCAATATATAGTAAGATCTATCTAGATAATCTAGATAAATGTT 600
 QY 2171 TAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGAAAGGAGCTCACGCCAGAGA 2230
 DB 601 TAGAGATGCTATATGATACAACTGTGGCCATGACTGAGAAAGGAGCTCACGCCAGAGA 660
 QY 2231 CTGGGCTGCTCTCCGGAGGCGCAAAACCCAAAGAGTCTGGGCAAAATCAGGCTCAGGGAG 2290
 DB 661 CTGGGCTGCTCTCCGGAGGCGCAAAACCCAAAGAGTCTGGGCAAAATCAGGCTCAGGGAG 720
 QY 2291 CTCTGCCCTGCTGCAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTCTCTGAAAACA 2350
 DB 721 CTCTGCCCTGCTGCAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTCTCTGAAAACA 780
 QY 2351 GAGGGTCTCAAGACANTCTGCTACCTATTAGCTTTCTTTTATTTTAACTTTTGG 2410
 DB 781 GAGGGTCTCAAGACANTCTGCTACCTATTAGCTTTCTTTTATTTTAACTTTTGG 840
 QY 2411 GGGGAAAGTATTTTGGAGAGTTTGTCTTGCATGTAATTTATAAATAGTAATAAGTT 2470
 DB 841 GGGGAAAGTATTTTGGAGAGTTTGTCTTGCATGTAATTTATAAATAGTAATAAGTT 900
 QY 2471 TTTACCATTAAAAAA 2486
 DB 901 TTTACCATTAAAAAA 916

RESULT 5
 US-09-736-457-73
 ; Sequence 73, Application US/09736457
 ; Patent No. 6509448
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedvick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Wang, Aijun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C15
 ; CURRENT APPLICATION NUMBER: US/09/736,457
 ; CURRENT FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 1864
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 73
 ; LENGTH: 916
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-736-457-73

Query Match 36.7%; Score 914.4; DB 4; Length 916;

Best Local Similarity 99.9%; Pred. No. 6.2e-209;
Matches 915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1571 GGAGAAAAAAGGTGGAGTCTTACTTGTGTTTAAATAATATGATCTAAGAAATCTTCTAGGG 1630
b 1 GGAGAAAAAAGGTGGAGTCTTACTTGTGTTTAAATAATATGATCTAAGAAATCTTCTAGGG 60

1631 CACTCTGGGAACCTATAAGGAGGATTTTCGGGCCCTCTCTTCAGGAATCTTCTCTGAA 1690
b 61 CACTCTGGGAACCTATAAGGAGGATTTTCGGGCCCTCTCTTCAGGAATCTTCTCTGAA 120

1691 GACATGCCCGACGTCGAAGCCCGAGGATGCTTTTGTGCGGCCCGTGGGTAGAGGGA 1750
b 121 GACATGCCCGACGTCGAAGCCCGAGGATGCTTTTGTGCGGCCCGTGGGTAGAGGGA 180

1751 CAGAGAGACGAGGAGTCTCAGCTCCACATTCAGAGGCATCACAAGTATGCAAAATTC 1810
b 181 CAGAGAGACGAGGAGTCTCAGCTCCACATTCAGAGGCATCACAAGTATGCAAAATTC 240

1811 TTCGGATGACTGCAGAAAAATAGTGTGTTTGTAGTTCAAACAATCAAGACGAAGCTTATTTC 1870
b 241 TTCGGATGACTGCAGAAAAATAGTGTGTTTGTAGTTCAAACAATCAAGACGAAGCTTATTTC 300

1871 TGAGGATAGCTCTTTAAAGGCAAGCTTATTTTTCATCTCTCATCTTTTGTCTCCCTTA 1930
b 301 TGAGGATAGCTCTTTAAAGGCAAGCTTATTTTTCATCTCTCATCTTTTGTCTCCCTTA 360

1931 GCACAAATGTAAAAAGAAATAGTAAATACAGAACGAGGAGGATGCTTCTGGGAG 1990
b 361 GCACAAATGTAAAAAGAAATAGTAAATACAGAACGAGGAGGATGCTTCTGGGAG 420

1991 CCATCCAGGACACTGGGAGCACAATAGATTCACCCATGTTTGTGAATCTAGATCAT 2050
b 421 CCATCCAGGACACTGGGAGCACAATAGATTCACCCATGTTTGTGAATCTAGATCAT 480

2051 TCTCATGCTTTCTTTATATTCACACATATGACAGAGAGATGTTCTTGTAAACAT 2110
b 481 TCTCATGCTTTCTTTATATTCACACATATGACAGAGAGATGTTCTTGTAAACAT 540

2111 TGATACACATAGCCCAATATAGTAAATCTATCTAGATATCTTCTAGATGAAATGT 2170
b 541 TGATACACATAGCCCAATATAGTAAATCTATCTAGATATCTTCTAGATGAAATGT 600

2171 TAGAGATGCTATTGTATACAACTGTGCCATGACTCAGGAAGGAGCTCAGCCACAGAGA 2230
b 601 TAGAGATGCTATTGTATACAACTGTGCCATGACTCAGGAAGGAGCTCAGCCACAGAGA 660

2231 CTGGGCTGCTCTCCGAGGCCAAACCCAAAGAGTCTGGCAAGTCTAGGCTCAGGAGGA 2290
b 661 CTGGGCTGCTCTCCGAGGCCAAACCCAAAGAGTCTGGCAAGTCTAGGCTCAGGAGGA 720

2291 CTCTGCCCTGCTGCAGACCTCGGTGGACACAGCTGCATAGAGCTCTCCTTGAACACA 2350
b 721 CTCTGCCCTGCTGCAGACCTCGGTGGACACAGCTGCATAGAGCTCTCCTTGAACACA 780

2351 GAGGGGCTCAAGACATCTGCTTACCTATTAGCTTTTCTTTATTTTTTAACTTTTGG 2410
b 781 GAGGGGCTCAAGACATCTGCTTACCTATTAGCTTTTCTTTATTTTTTAACTTTTGG 840

2411 GGGGAAAGTATTTTGAAGTTTCTTGAAGTTTCTTGAAGTTTATTAATAGTAAATAGTT 2470
b 841 GGGGAAAGTATTTTGAAGTTTCTTGAAGTTTCTTGAAGTTTATTAATAGTAAATAGTT 900

2471 TTTTACCATTAAAAAAA 2486
b 901 TTTTACCATTAAAAAAA 916

RESULT 6
US-09-614-124B-73
; Sequence 73, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:

APPLICANT: Wang, Tongrong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614.124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-614-124B-73

Query Match 36.7%; Score 914.4; DB 4; Length 916;
Best Local Similarity 99.9%; Pred. No. 6.2e-209;
Matches 915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1571 GGAGAAAAAAGGTGGAGTCTTACTTGTGTTTAAATAATATGATCTAAGAAATCTTCTAGGG 1630
Db 1 GGAGAAAAAAGGTGGAGTCTTACTTGTGTTTAAATAATATGATCTAAGAAATCTTCTAGGG 60

QY 1631 CACTCTGGGAACCTATAAGGAGGATTTTCGGGCCCTCTCTTCAGGAATCTTCTCTGAA 1690
Db 61 CACTCTGGGAACCTATAAGGAGGATTTTCGGGCCCTCTCTTCAGGAATCTTCTCTGAA 120

QY 1691 GACATGCCCGACGTCGAAGCCCGAGGATGCTTTTGTGCGGCCCGTGGGTAGAGGGA 1750
Db 121 GACATGCCCGACGTCGAAGCCCGAGGATGCTTTTGTGCGGCCCGTGGGTAGAGGGA 180

QY 1751 CAGAGAGACGAGGAGTCTCAGCTCCACATTCAGAGGCATCACAAGTATGCGCAAAATTC 1810
Db 181 CAGAGAGACGAGGAGTCTCAGCTCCACATTCAGAGGCATCACAAGTATGCGCAAAATTC 240

QY 1811 TTCGGATGACTGCAGAAAAATAGTGTGTTTGTAGTTCAAACAATCAAGACGAAGCTTATTTC 1870
Db 241 TTCGGATGACTGCAGAAAAATAGTGTGTTTGTAGTTCAAACAATCAAGACGAAGCTTATTTC 300

QY 1871 TGAGGATAGCTCTTTAAAGGCAAGCTTTTATTTTTCATCTCTCATCTTTTGTCTCCCTTA 1930
Db 301 TGAGGATAGCTCTTTAAAGGCAAGCTTTTATTTTCACTCTCATCTTTTGTCTCCCTTA 360

QY 1931 GCACAAATGTAAAAAGAAATAGTAAATACAGAACGAGGAGGATGCTTGTCTGGGAG 1990
Db 361 GCACAAATGTAAAAAGAAATAGTAAATACAGAACGAGGAGGATGCTTGTCTGGGAG 420

QY 1991 CCATCCAGGACACTGGGAGCACAATAGATTCACCCATGTTTGTGAATCTAGATCAT 2050
Db 421 CCATCCAGGACACTGGGAGCACAATAGATTCACCCATGTTTGTGAATCTAGATCAT 480

QY 2051 TCTCATGCTTTCTTTATATTCACACATATGATAGTAAAGTCTTCTAGTAATCTCTAGTAATGT 2110
Db 481 TCTCATGCTTTCTTTATATTCACACATATGATAGTAAAGTCTTCTAGTAATGT 540

QY 2111 TGATACACATAGCCCAATATAGTAAAGTCTTCTAGTAATCTCTAGTAATCTCTAGTAATGT 2170
Db 541 TGATACACATAGCCCAATATAGTAAAGTCTTCTAGTAATCTCTAGTAATCTCTAGTAATGT 600

QY 2171 TAGAGATGCTATTGTATACAACTGTGCCATGACTCAGGAAGGAGCTCAGCCACAGAGA 2230
Db 601 TAGAGATGCTATTGTATACAACTGTGCCATGACTCAGGAAGGAGCTCAGCCACAGAGA 660

QY 2231 CTGGGCTGCTCTCCGAGGCCAAACCCAAAGAGTCTGGCAAGTCTAGGCTCAGGAGGA 2290
Db 661 CTGGGCTGCTCTCCGAGGCCAAACCCAAAGAGTCTGGCAAGTCTAGGCTCAGGAGGA 720

QY 2291 CTCTGCCCTGCTGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTCCTTGAACA 2350
 Db 721 CTCTGCCCTGCTGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTCCTTGAACA 780
 QY 2351 GAGGGGTCTCAAGACATCTCTCCCTACCTATTAGCTTTTCTTTATTTTAACTTTTGG 2410
 Db 781 GAGGGGTCTCAAGACATCTCTCCCTACCTATTAGCTTTTCTTTATTTTAACTTTTGG 840
 QY 2411 GGGGAAAGTATTTTGGAGATTTTGTCTGCAATGATTTTAAATAGTAATAAGTT 2470
 Db 841 GGGGAAAGTATTTTGGAGATTTTGTCTGCAATGATTTTAAATAGTAATAAGTT 900
 QY 2471 TTTACCATTAATAAAA 2486
 Db 901 TTTACCATTAATAAAA 916
 RESULT 7
 US-09-671-325-73
 ; Sequence 73, Application US/09671325
 ; Patent No. 6667154
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedwick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C12
 ; CURRENT APPLICATION NUMBER: US/09/671,325
 ; CURRENT FILING DATE: 2000-09-26
 ; NUMBER OF SEQ ID NOS: 1825
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 73
 ; LENGTH: 916
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-671-325-73
 Query Match 36.7%; Score 914.4; DB 4; Length 916;
 Best Local Similarity 99.9%; Pred. No. 6.2e-209;
 Matches 915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1571 GGAGAAAATAAGGTGGAGTCTCTACTTGTGTTTAAATAATATGTAAGATTTCTAGGG 1630
 Db 1 GGAGAAAATAAGGTGGAGTCTCTACTTGTGTTTAAATAATATGTAAGATTTCTAGGG 60
 QY 1631 CACTCTGGAACTTAAAGGAGGATTTTCGGGCCCTCTCTCAGGAATCTCTCTGAA 1690
 Db 61 CACTCTGGAACTTAAAGGAGGATTTTCGGGCCCTCTCTCAGGAATCTCTCTGAA 120
 QY 1691 GACATGGCCAGTCAAGGCCAGGATGCTTTGCTGCGGCCCTCGTGGGTAGAGGGA 1750
 Db 121 GACATGGCCAGTCAAGGCCAGGATGCTTTGCTGCGGCCCTCGTGGGTAGAGGGA 180
 QY 1751 CAGAGAGCAGGAGAGTCAAGTCCATTCAGAGGATCACAAGTAATGGCAATTC 1810
 Db 181 CAGAGAGCAGGAGAGTCAAGTCCATTCAGAGGATCACAAGTAATGGCAATTC 240
 QY 1811 TTCGATGATGACAGAAAATAGTGTGTTGATGATCAACATCAAGACGAGCTTTATTC 1870
 Db 241 TTCGATGATGACAGAAAATAGTGTGTTGATGATCAACATCAAGACGAGCTTTATTC 300
 QY 1871 TGAGGATAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCTATCTTTTCTCTCTTA 1930
 Db 301 TGAGGATAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCTATCTTTTCTCTCTTA 360
 QY 1931 GCACAATGTAAAAAGAAATAGTAATATCAGAACAGGAGGAGGATGCTTGTCTGGGAG 1990

Db 361 GACATGTAAAAAGAAATAGTAATATCAGAACAGGAGGAGGATGCTTGTCTGGGAG 420
 QY 1991 CCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCA 2050
 Db 421 CCATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAACTTAGAGTCA 480
 QY 2051 TCTCATGCTTTTCTTTATAATTACACATATATGAGAGAAAGATGTTTCTTTGTTAAAT 2110
 Db 481 TCTCATGCTTTTCTTTATAATTACACATATATGAGAGAAAGATGTTTCTTTGTTAAAT 540
 QY 2111 TGTATACACATAGCCCCAAATATATAGTAAGATCTATATAGATATCTAGATGAAATGT 2170
 Db 541 TGTATACACATAGCCCCAAATATATAGTAAGATCTATATAGATATCTAGATGAAATGT 600
 QY 2171 TAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCAGGCCCAGAGA 2230
 Db 601 TAGAGATGCTATATGATACAACTGTGGCCATGACTGAGGAAAGGAGCTCAGGCCCAGAGA 660
 QY 2231 CTGGGCTGCTCTCCGAGAGGCCAAACCCAAAGAGGTCTGGCAAAGTCAAGCTCAGGAGA 2290
 Db 661 CTGGGCTGCTCTCCGAGAGGCCAAACCCAAAGAGGTCTGGCAAAGTCAAGCTCAGGAGA 720
 QY 2291 CTCTGCCCTGTGACAGACTCGGTGTGGACACACGCTCATAGAGCTCTCTTGAACA 2350
 Db 721 CTCTGCCCTGTGACAGACTCGGTGTGGACACACGCTCATAGAGCTCTCTTGAACA 780
 QY 2351 GAGGGTCTCAAGACATTTCTGCTACCTATTAGCTTTTCTTTATTTTAACTTTTGG 2410
 Db 781 GAGGGTCTCAAGACATTTCTGCTACCTATTAGCTTTTCTTTATTTTAACTTTTGG 840
 QY 2411 GGGGAAAAGTATTTTGGAGATTTTGTCTGCAATGATTTTAAATAGTAATAAGTT 2470
 Db 841 GGGGAAAAGTATTTTGGAGATTTTGTCTGCAATGATTTTAAATAGTAATAAGTT 900
 QY 2471 TTTACCATTAATAAAA 2486
 Db 901 TTTACCATTAATAAAA 916
 RESULT 8
 US-09-589-184-73
 ; Sequence 73, Application US/09589184
 ; Patent No. 6686447
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedwick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C8
 ; CURRENT APPLICATION NUMBER: US/09/589,184
 ; CURRENT FILING DATE: 2000-06-05
 ; NUMBER OF SEQ ID NOS: 827
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 73
 ; LENGTH: 916
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-589-184-73
 Query Match 36.7%; Score 914.4; DB 4; Length 916;
 Best Local Similarity 99.9%; Pred. No. 6.2e-209;
 Matches 915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1571 GGAGAAAATAAGGTGGAGTCTCTACTTGTGTTTAAATAATATGTAAGATTTCTAGGG 1630
 Db 1 GGAGAAAATAAGGTGGAGTCTCTACTTGTGTTTAAATAATATGTAAGATTTCTAGGG 60

SEQUENCE CHARACTERISTICS:
LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-482-271-5

Query Match 26.0%; Score 648.4; DB 1; Length 798;
Best Local Similarity 88.4%; Pred. No. 2e-145;
Matches 703; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 193 GCGCGAGCTCGGGGGCTTGGTCCGCTGCGCTGCGAGCGTGGAGCGCGTGCA 252
Db 4 GTGCACTCTTCGAGTTTAGTTCAGTTGTCNTTGTGAACCATGTGATCTCGTCT 63

QY 253 CTGGCCAGTCGCGCGCTCCGCGCGCTGTCGCGAGCTGTGTCGCGAGCCGGCTGC 312
Db 64 CTGTCTCAATGTCTCCACCACAGCTGTTGTGCTGAACCTGTGTCGAACCGGGTGT 123

QY 313 GCGTGTGCTGACGTGGCCTGAGCGAGGCGCCAGCGTGGGATCTACACCGAGCGC 372
Db 124 GGTGTGTGCTGACCTGTGCTCTTCTGAAGTCAACCATGTGTTATTACTGAAGT 183

QY 373 TGTGCTCGCGCTTGTGTCGAGCGCTGCGCGAGCGTGGCGAGCGCGCTGACGCGT 432
Db 184 TGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243

QY 433 CTGGAGCGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
Db 244 CTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303

QY 493 CTGCCAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
Db 304 CTGCCAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363

QY 553 AGTGTGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
Db 364 AGTGTGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423

QY 613 CTCCATTCAAGATATCATCATCAAGAAAGGCGATGCTAAAGACAGCGCGCTACAAA 672
Db 424 CTCCATTCAAGATATCATCATCAAGAAAGGCGATGCTAAAGACAGCGCGCTACAAA 483

QY 673 GTTGACTAGCTCTCAGAGCAGATACCCAGAACTTCTCTCGAGTCCAGCGGAG 732
Db 484 GTTGACTAGCTCTCAGAGCAGATACCCAGAACTTCTCTCGAGTCCAGCGGAG 543

QY 733 ACAGATATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
Db 544 ACAGATATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603

QY 793 AATGTCTGAGTCCAGGGGTGTACATTCCTCACTGTGACAGAGGATTTTATAG 852
Db 604 AATGTCTGAGTCCAGGGGTGTACATTCCTCACTGTGACAGAGGATTTTATAG 663

QY 853 AAAAGCAGTGTGCGCTTCCAAAGCAGAGAGCGGGCTTCTGCTGTGTGTGATAG 912
Db 664 AAAAGCAGTGTGCGCTTCCAAAGCAGAGAGCGGGCTTCTGCTGTGTGTGATAG 723

QY 913 TATGGCAGCTCTTCCAGGCTACACCAAGAGGAGAGGAGCTGCTGCTGCTGCTGCT 972
Db 724 TATGGCAGCTCTTCCAGGCTACACCAAGAGGAGAGGAGCTGCTGCTGCTGCTGCT 783

QY 973 ATGCAGCAAGTAG 987
Db 784 ATGCAGCAAGTAG 798

RESULT 13
US-09-080-120A-3
Sequence 3, Application US/09080120A
Patent No. 6017885
GENERAL INFORMATION:

APPLICANT: BAGI, CEDO M.
APPLICANT: BROMWAGE, ROBERT
APPLICANT: ROSEN, DAVID M.
APPLICANT: ADAMS, STEVEN W.
TITLE OF INVENTION: IGF/IGFBP COMPLEX FOR PROMOTING BONE
TITLE OF INVENTION: FORMATION AND FOR REGULATING BONE REMODELING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,120A
FILING DATE: 14-MAY-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/806,918
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/450,258
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,456
FILING DATE: 20-JUL-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Buffinger, Nicholas
REGISTRATION/DOCKET NUMBER: 39,124
REFERENCE/DOCKET NUMBER: 220955027203
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..792
US-09-080-120A-3

Query Match 25.7%; Score 639.8; DB 3; Length 795;
Best Local Similarity 88.7%; Pred. No. 2.3e-143;
Matches 705; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

QY 193 GCGCGAGCTCGGGGGCTTGGTCCGCTGCGCTGCGAGCGTGGAGCGCGTGCA 252
Db 4 GTGCACTCTTCGAGTTTAGTTCAGTTGTCNTTGTGAACCATGTGATCTCGTCT 63

QY 253 CTGGCCAGTGTGCGCGCTCCGCGCGCTGTCGCGAGCTGTGTCGCGAGCGCGCTGC 312
Db 64 CTGTCTCAATGTG---CTCCACCAGCTGTTTGTGCTGAACCTGTTCTGTAACCGGGTGT 120

QY 313 GCGTGTGCTGCGCTGCGCATGACGAGGCGCCAGCGTGGGATCTACACCGAGCGC 372
Db 121 GGTGTGTGCTGACTTGGCGCACTTCTGAAGGTCAACCATGTGTTATTACTGAAGT 180

QY 373 TGTGCTTCCGCGCTTCTGCTGCGAGCGCTGCGCGAGCGCGAGCGCGCTGCGAGCGCTG 432
Db 181 TGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

RESULT 15
US-09-976-594-877
; Sequence 877, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ. ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 877
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 5673549 253550.20
US-09-976-594-877

Query Match 19.0%; Score 472.8; DB 4; Length 1141;
Best Local Similarity 99.4%; Pred. No. 2.1e-103;
Matches 485; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY	740	ATGTTCCCTGCGGTAGAGAAATGAAGACACACTGAATCACCTGAAGTTCTCAATGTC	799
DB	655	AGGGTCCCTGCGGTAGAGAAATGAAGACACACTGAATCACCTGAAGTTCTCAATGTC	714
QY	800	TGAGTCCCGAGGGGTGTACACATTCCTCAACTGTGACAGAGGGATTTTATAAGAAAAAGC	859
DB	715	TGAGTCCCGAGGGGTGTACACATTCCTCAACTGTGACAGAGGGATTTTATAAGAAAAAGC	774
QY	860	AGTGTGCGCCCTTCCAAAGCAGGAGCGGGCTTCTGCTGTGTGTGATAGTATCGGC	919
DB	775	AGTGTGCGCCCTTCCAAAGCAGGAGCGGGCTTCTGCTGTGTGTGATAGTATCGGC	834
QY	920	AGCCTCTCCAGGCTACACACCACAGGGGAGGAGGAGTGCCTGCTACAGCATGCAGA	979
DB	835	AGCCTCTCCAGGCTACACACCACAGGGGAGGAGGAGTGCCTGCTACAGCATGCAGA	894
QY	980	GCAAGTAGACGCTCCCGCAAGTTAATGTGGAGCTCAATATGCTTATTTTCCACAAA	1039
DB	895	GCAAGTAGACGCTCCCGCAAGTTAATGTGGAGCTCAATATGCTTATTTTCCACAAA	954
QY	1040	AGACTGCCAAGACATGACCCAGCTGCTACAGCTCGATTTATATTTCTGTTGTGG	1099
DB	955	AGACTGCCAAGACATGACCCAGCTGCTACAGCTCGATTTATATTTCTGTTGTGG	1014
QY	1100	TGAAGTGAATTTTTTTTAAACCAAGTTTAGAAGAGTTTTTGAATGCTATGTTTC	1159
DB	1015	TGAAGTGA-TTTTTTTAAACCAAGTTTAGAAGAGTTTTTGAATGCTATGTTTC	1073
QY	1160	TTTGAATGTTAACTGACATCTTTTCCAGTTCAGTAGTCAGCAAGAGCAGTTTGA	1219
DB	1074	TTTGAATGTTAACTGACATCTTTTCCAGTTCAGTAGTCAGCAAGAGCAGTTTGA	1133
QY	1220	TTTTCTTG 1227	
DB	1134	TTTTCTTG 1141	

Search completed: March 11, 2004, 14:41:29
Job time : 117.891 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

M nucleic - nucleic search, using sw model

un on: March 11, 2004, 03:37:21 ; Search time 581.15 Seconds
(without alignments)
15799.545 Million cell updates/sec

title: US-10-084-817-18
erfect score: 2494
equence: 1 ggcgtgagatcagccgctt.....ccattataaaaaaa 2494

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/FCR_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/us06_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/us06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/us07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/FCR05_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/us08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/us09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/us09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/us09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/us09D_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/us10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/us10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/us10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/us10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/us60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/us60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match %	Length	DB ID	Description
1	2494	100.0	2494	14	US-10-084-817-18
2	2478.4	99.4	2617	14	US-10-106-698-1304
3	2472	99.1	2472	14	US-10-247-671-42
4	2461.8	98.7	2617	13	US-10-044-090-775
5	2456	98.5	2496	14	US-10-240-965-195
6	2452.4	98.3	2485	14	US-10-210-120-9
7	2446.2	98.1	2499	14	US-10-171-311-90
8	2446.2	98.1	2499	14	US-10-102-524-1694
9	2446.2	98.1	2499	14	US-10-096-534-32
10	2430.4	97.4	2474	10	US-09-791-196-2
11	2415.8	96.9	3642	15	US-10-063-674-2164
12	2361.8	94.7	2448	15	US-10-094-749-493
13	2162.6	86.7	2355	15	US-10-108-260A-960
14	2099.8	84.2	2327	15	US-10-104-047-1076
15	1977.6	79.3	2192	15	US-10-108-260A-1000

16	1943.8	77.9	2173	15	US-10-108-260A-944
17	1738.4	69.7	1833	9	US-09-925-301-314
18	1459.8	58.5	10884	12	US-09-880-107-2346
19	1459.8	58.5	10884	12	US-10-240-425-1318
20	1459.8	58.5	10884	12	US-10-377-142-2
21	1244.2	49.9	1759	14	US-10-198-846-9856
22	985.4	39.5	985	9	US-09-865-578-12
23	948	38.0	994	12	US-10-210-172-13
24	914.4	36.7	916	9	US-09-736-457-73
25	914.4	36.7	916	9	US-09-902-941-73
26	914.4	36.7	916	9	US-09-849-626-73
27	914.4	36.7	916	10	US-09-476-300-73
28	914.4	36.7	916	14	US-10-017-754-73
29	914.4	36.7	916	14	US-10-113-872-73
30	854.2	34.3	2352	9	US-09-917-800A-1548
31	854.2	34.3	2352	15	US-10-388-934-243
32	854.2	34.3	2352	15	US-10-191-803-22
33	846.8	34.0	3642	15	US-10-062-674-2164
34	593	23.8	603	14	US-10-102-524-1627
35	593.8	23.4	587	14	US-10-103-524-1585
36	593.4	23.4	722	15	US-10-264-049-2138
37	500.4	20.1	502	14	US-10-102-524-486
38	446.2	18.6	798	15	US-10-264-049-2075
39	446.4	17.9	462	9	US-09-738-973-519
40	446.4	17.9	462	9	US-09-854-133-519
41	446.4	17.9	462	14	US-10-144-649A-519
42	441.6	17.7	654	9	US-09-777-564-1399
43	441.6	17.7	654	14	US-10-015-219-1399
44	417.4	16.7	432	12	US-10-085-783A-6713
45	417.4	16.7	432	15	US-10-242-535A-6713

ALIGNMENTS

RESULT 1
US-10-084-817-18
; Sequence 18, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 2494
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 3072333CB1
US-10-084-817-18

Query Match	100.0%;	Score 2494;	DB 14;	Length 2494;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2494;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CGCGTGGATCAGCCGCTTCCTGCTGGATTCCACAGCTTCGCGCGTGTACTGTGCGC	60	
Db	1	CGCGTGGATCAGCCGCTTCCTGCTGGATTCCACAGCTTCGCGCGTGTACTGTGCGC	60	
Qy	61	CCATCCCTGGCGGCCAGCCTGCGAGCGTGCAGCGTCCCGGTTGACGCGTGCACGCG	120	
Db	61	CCATCCCTGGCGGCCAGCCTGCGAGCGTGCAGCGTCCCGGTTGACGCGTGCACGCG	120	


```

2b 2281 CTCAGGAGACTCTGCCCTGCTGCAGACCTCGGTGGGACACACAGCTGCATAGACTCTC 2340
2y 2341 CTTGAAAAAGAGGGGTCTCAAGACATTCGCTCTACCTATCTCTTTCTTTATTTTTT 2400
2b 2341 CTTGAAAAAGAGGGGTCTCAAGACATTCGCTCTACCTATCTCTTTCTTTATTTTTT 2400
2y 2401 AACTTTTGGGGGAAAAAGTATTTTGGAGAGTTTCTCTTGCAATGATTTATTAATAAGT 2460
2b 2401 AACTTTTGGGGGAAAAAGTATTTTGGAGAGTTTCTCTTGCAATGATTTATTAATAAGT 2460
2y 2461 AATAAAGTTTTTACCATTAATAAAAAA 2494
2b 2461 AATAAAGTTTTTACCATTAATAAAAAA 2494

RESULT 2
US-10-106-698-1904
: Sequence 1904, Application US/10108698
: Publication No. US20030109690A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
: FILE REFERENCE: PA005P1
: CURRENT APPLICATION NUMBER: US/10/106,698
: CURRENT FILING DATE: 2002-03-27
: PRIOR APPLICATION NUMBER: PCT/US00/26524
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US 60/157,137
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: US 60/163,280
: PRIOR FILING DATE: 1999-11-03
: NUMBER OF SEQ ID NOS: 8564
: SOFTWARE: PatentIn Ver. 3.0
: SEQ ID NO 1904
: LENGTH: 2617
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-106-698-1904

Query Match 99.4%; Score 2478.4; DB 14; Length 2617;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2490; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

2y 1 GCGCTGAGGATCAGCGCTTCTGCTGCTGATTCACAGCTTCGCGCGGTACTGTCGCC 60
2b 98 GCGCTGAGGATCAGCGCTTCTGCTGCTGATTCACAGCTTCGCGCGGTACTGTCGCC 157
2y 61 CCAATCCCTGCGCGCCAGCTGCAAGACAGCGTGCCTCCCGGTTCGAGCGCTCATGCAAGCG 120
2b 158 CCAATCCCTGCGCGCCAGCTGCAAGACAGCGTGCCTCCCGGTTCGAGCGCTCATGCAAGCG 217
2y 121 GCGCGCCAGCTGCTGGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
2b 218 GCGCGCCAGCTGCTGGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
2y 181 GTGCGCGGGGTGCGCGAGCTCGGGGGGTCTGGGTCCCGGTTCGAGCGCTCGAGCGCGTGC 240
2b 278 GTGCGCGGGGTGCGCGAGCTCGGGGGGTCTGGGTCCCGGTTCGAGCGCTCGAGCGCGTGC 337
2y 241 GACCGCGTGCAGTGGCCAGTGGCGGCTCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
2b 338 GACCGCGTGCAGTGGCCAGTGGCGGCTCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 397
2y 301 GACCGCGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
2b 398 GACCGCGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 457
2y 361 TACACGAGCGCTGTGCTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGG 420
2b 458 TACACGAGCGCTGTGCTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGG 517
2y 421 CTGACGCGGTGTGAGCGCGCGCGGCTCTGCTGCTCAAGCTAGTGCCTGCTGCTGCTGCTGCT 480

```

```

518 CTGAGGCGCTGCTGGAGCGCGCGGCTCTGGTCAAACGCTAGTCCGCTCAGCGCGCTG 577
481 CGCGCTACTGCTGCGCAGCGCGCGCGCTCCAGGAAATGCTAGTGTGAGTGGAGGAAGAC 540
578 CGCGCTACTGCTGCGCAGCGCGCGCGCTCCAGGAAATGCTAGTGTGAGTGGAGGAAGAC 637
541 CGCAGCGCGCGCTGCTGGAGAGCGCGTCCGCTCCTCAGCAGCGACCGGGTGTCTGATCCC 600
638 CGCAGCGCGCGCTGCTGGAGAGCGCGTCCGCTCCTCAGCAGCGACCGGGTGTCTGATCCC 697
601 AAGTCCACCCCTCCATTTCAAAGATATCATCATCAAGAAAGGCGCATGTCTAAAGACAGC 660
698 AAGTTCACCCCTCCATTTCAAAGATATCATCATCAAGAAAGGCGCATGTCTAAAGACAGC 757
661 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCAGATACCCAGAACTTCTCTCCGAG 720
758 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCAGATACCCAGAACTTCTCTCCGAG 817
721 TCCAAGCGGAGACAGAAATGCTCCCTGCGGTAGAGAAATGGAAGACACACTGAATCAC 780
818 TCCAAGCGGAGACAGAAATGCTCCCTGCGGTAGAGAAATGGAAGACACACTGAATCAC 877
781 CTGAAGTTCCTCAATGCTGAGTCCAGGGGTGACACATTCCTCAACTGTGACAGAG 840
878 CTGAAGTTCCTCAATGCTGAGTCCAGGGGTGACACATTCCTCAACTGTGACAGAG 937
841 GGATTTTATAGAAAAAGCAGTGTGCGCTTCCAAGGCGAGGAGCGGGCTTCTGCTGG 900
938 GGATTTTATAGAAAAAGCAGTGTGCGCTTCCAAGGCGAGGAGCGGGCTTCTGCTGG 997
901 TGTGTGATAGTATGGCAGCTCTCCAGGCTACACACCCAGGGGAGGAGGAGCTG 960
998 TGTGTGATAGTATGGCAGCTCTCCAGGCTACACACCCAGGGGAGGAGGAGCTG 1057
961 CACTGCTACAGCATGCAGAGCAAGTAGACGCTCCCGCAAGGTTAATGTGAGGCTCAAT 1020
1058 CACTGCTACAGCATGCAGAGCAAGTAGACGCTCCCGCAAGGTTAATGTGAGGCTCAAT 1117
1021 ATGCTTATTTTGCACAAAGACTGCCAGGACATGACAGCAGCTGCTACAGCTCGA 1080
1118 ATGCTTATTTTGCACAAAGACTGCCAGGACATGACAGCAGCTGCTACAGCTCGA 1177
1081 TTTATATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1140
1178 TTTATATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1236
1141 TTTAAATGCTTATGTTTCTTTGAAATGTTAACTTTGAGCATCTTTTCACTTCCAGTAGT 1200
1237 TTTAAATGCTTATGTTTCTTTGAAATGTTAACTTTGAGCATCTTTTCACTTCCAGTAGT 1296
1201 CAGCAAGAGCAGTTTGAATTTTCTGCTGCTTCTTCAAAATATTCAGAGACTCCGAGC 1260
1297 CAGCAAGAGCAGTTTGAATTTTCTGCTGCTTCTTCAAAATATTCAGAGACTCCGAGC 1356
1261 ACAGCACCAGCTTCAATGCGCGCTGAAATGCTTCAACATGTTGTTGTTGTTGTTGTTGTTG 1320
1357 ACAGCACCAGCTTCAATGCGCGCTGAAATGCTTCAACATGTTGTTGTTGTTGTTGTTGTTG 1416
1321 CCACTGACTTTGCTGCTGAGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1417 CCACTGACTTTGCTGCTGAGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1476
1381 CTCCCGCTACAGTGCAGCGCTTTATCGAGAAATAGGAAACCTTTAAACCCCGGTCT 1440
1477 CTCCCGCTACAGTGCAGCGCTTTATCGAGAAATAGGAAACCTTTAAACCCCGGTCT 1536
1441 CGGACATCCCAAGCATGCTCTGAGCTCAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1537 CGGACATCCCAAGCATGCTCTGAGCTCAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1596
1501 AAGGCGTGGATCCCTCAACCAAGAAATGTTTATGCTTCAAGTCACTGTACTGCTT 1560
1597 AAGGCGTGGATCCCTCAACCAAGAAATGTTTATGCTTCAAGTCACTGTACTGCTT 1656

```

```

QY 1561 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1620
Db 1562 |||||
Db 1563 |||||
QY 1564 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1716
Db 1565 |||||
Db 1566 |||||
QY 1567 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1680
Db 1568 |||||
Db 1569 |||||
QY 1570 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1776
Db 1571 |||||
Db 1572 |||||
QY 1573 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1740
Db 1574 |||||
Db 1575 |||||
QY 1576 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1836
Db 1577 |||||
Db 1578 |||||
QY 1579 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1800
Db 1580 |||||
Db 1581 |||||
QY 1582 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1996
Db 1583 |||||
Db 1584 |||||
QY 1585 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1860
Db 1586 |||||
Db 1587 |||||
QY 1588 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1956
Db 1589 |||||
Db 1590 |||||
QY 1591 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1920
Db 1592 |||||
Db 1593 |||||
QY 1594 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2016
Db 1595 |||||
Db 1596 |||||
QY 1597 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 1980
Db 1598 |||||
Db 1599 |||||
QY 1600 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2076
Db 1601 |||||
Db 1602 |||||
QY 1603 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2040
Db 1604 |||||
Db 1605 |||||
QY 1606 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2136
Db 1607 |||||
Db 1608 |||||
QY 1609 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2100
Db 1610 |||||
Db 1611 |||||
QY 1612 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2196
Db 1613 |||||
Db 1614 |||||
QY 1615 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2160
Db 1616 |||||
Db 1617 |||||
QY 1618 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2256
Db 1619 |||||
Db 1620 |||||
QY 1621 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2220
Db 1622 |||||
Db 1623 |||||
QY 1624 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2316
Db 1625 |||||
Db 1626 |||||
QY 1627 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2280
Db 1628 |||||
Db 1629 |||||
QY 1630 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2376
Db 1631 |||||
Db 1632 |||||
QY 1633 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2340
Db 1634 |||||
Db 1635 |||||
QY 1636 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2436
Db 1637 |||||
Db 1638 |||||
QY 1639 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2400
Db 1640 |||||
Db 1641 |||||
QY 1642 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2496
Db 1643 |||||
Db 1644 |||||
QY 1645 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2460
Db 1646 |||||
Db 1647 |||||
QY 1648 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2556
Db 1649 |||||
Db 1650 |||||
QY 1651 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2494
Db 1652 |||||
Db 1653 |||||
QY 1654 GGGGACTATTGGAGAAATAGGTGGAGTCTACTTGTTHAAAAAATATGTATCTAAGAA 2590
Db 1655 |||||
Db 1656 |||||

```

RESULT 3

US-10-247-671-42
; Sequence 42, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov

APPLICANT: Porter, Gordon, J.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL Program
SEQ ID NO 42
LENGTH: 2472
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030194721A1 3072333CB1
US-10-247-671-42

Query Match 99.1%; Score 2472; DB 14; Length 2472;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGGCTGAGGATCAGCGGCTTCCGCTGGATTCACACAGCTTCGCGCCGCTACTCTCGCC 60
Db 1 GGGCTGAGGATCAGCGGCTTCCGCTGGATTCACACAGCTTCGCGCCGCTACTCTCGCC 60
QY 61 CCATCCCTCGCGCCAGCCTGCCAAGCAGCGTGCCTGGTTCAGAGGCTCATGACGG 120
Db 61 CCATCCCTCGCGCCAGCCTGCCAAGCAGCGTGCCTGGTTCAGAGGCTCATGACGG 120
QY 121 GCGGACCCACGCTCTGGGCGGCTGCGCTGACTCTGCTGGTCTGCTCGGGGGCGCG 180
Db 121 GCGGACCCACGCTCTGGGCGGCTGCGCTGACTCTGCTGGTCTGCTCGGGGGCGCG 180
QY 181 GTGGGCGGCGCTGGGCGGCTGCGGCTGGTTCGCTGGTTCGCTGGAGCCGCTGC 240
Db 181 GTGGGCGGCGCTGGGCGGCTGCGGCTGGTTCGCTGGTTCGCTGGAGCCGCTGC 240
QY 241 GAGCGGCTGACTGGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 300
Db 241 GAGCGGCTGACTGGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 300
QY 301 GAGCGGCTGCGGCTGCTGCTGACGTGCGCACTGAGCGAGGCGCAGCGTGGCGCATC 360
Db 301 GAGCGGCTGCGGCTGCTGCTGACGTGCGCACTGAGCGAGGCGCAGCGTGGCGCATC 360
QY 361 TACCGAGCGCTGTGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 420
Db 361 TACCGAGCGCTGTGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 420
QY 421 CTGCGAGGCTGCTGCGAGCGGCGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCG 480
Db 421 CTGCGAGGCTGCTGCGAGCGGCGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCG 480
QY 481 CGCGCTACTCTGCTGCGAGCGGCGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCG 540
Db 481 CGCGCTACTCTGCTGCGAGCGGCGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCG 540
QY 541 GCGAGCGGCGGCTGCGAGAGCGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 600
Db 541 GCGAGCGGCGGCTGCGAGAGCGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 600
QY 601 AAGTTCCACCCCTCCATTCAGAGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 660
Db 601 AAGTTCCACCCCTCCATTCAGAGGCTTCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 660
QY 661 GAGCGCTACAAAGTTGACTTACGAGTCTCAGAGGCTTCCGCTGCGCTGCGCTGCGCTG 720
Db 661 GAGCGCTACAAAGTTGACTTACGAGTCTCAGAGGCTTCCGCTGCGCTGCGCTGCGCTG 720
QY 721 TCCAGCGGCGAGACAGATATGCTCCCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 780

```

Db 721 TCCAGCGGAGACAGAAATATGGTCCCTGCGGTAGAGAAATGGAGACACACTGAATCAC 780
Qy 781 CTGAAGTTCCTCAATGTCTGAGTCCAGGGGTGTACACATCCCACTGTGACAGAAG 840
Db 781 CTGAAGTTCCTCAATGTCTGAGTCCAGGGGTGTACACATCCCACTGTGACAGAAG 840
Qy 841 GGAATTTATAGAAAAGACAGTGTGCGCCCTTCCAAAGCGCAGGAGCGGGGCTTCTGCTGG 900
Db 841 GGAATTTATAGAAAAGACAGTGTGCGCCCTTCCAAAGCGCAGGAGCGGGGCTTCTGCTGG 900
Qy 901 TGTGTGATAGATAGGCGACCTCTCCAGGCTPACACCAAGGGGAAAGAGGAGCGTG 960
Db 901 TGTGTGATAGATAGGCGACCTCTCCAGGCTPACACCAAGGGGAAAGAGGAGCGTG 960
Qy 961 CACTGTCTACGACATGACAGCAAGTACAGCCCTGCGCAGAGGTTATGTGGAGCTCAAT 1020
Db 961 CACTGTCTACGACATGACAGCAAGTACAGCCCTGCGCAGAGGTTATGTGGAGCTCAAT 1020
Qy 1021 ATGCTTTATTTGCAAAAAGACTGCCAAGGACATGACAGAGCTGGCTPACAGCCTCGA 1080
Db 1021 ATGCTTTATTTGCAAAAAGACTGCCAAGGACATGACAGAGCTGGCTPACAGCCTCGA 1080
Qy 1081 TTTATATTTCTGTTTGGTGAACCTGATTTTTTTTTTAAACCAAAGTTTAAAGAGGTTT 1140
Db 1081 TTTATATTTCTGTTTGGTGAACCTGATTTTTTTTTTAAACCAAAGTTTAAAGAGGTTT 1140
Qy 1141 TTGAAATGCTATGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTCCAGTAGT 1200
Db 1141 TTGAAATGCTATGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTCCAGTAGT 1200
Qy 1201 CAGCAAGAGGAGTTTGAATTTCTTGTGCTGCTTCCCTATCAAAATATTCAGAGCTGAGC 1260
Db 1201 CAGCAAGAGGAGTTTGAATTTCTTGTGCTGCTTCCCTATCAAAATATTCAGAGCTGAGC 1260
Qy 1261 ACAGCAACCCAGACTTCATGCGCCGCTGGAATGCTCACCACATGTTGTCGAAGCGGCCGA 1320
Db 1261 ACAGCAACCCAGACTTCATGCGCCGCTGGAATGCTCACCACATGTTGTCGAAGCGGCCGA 1320
Qy 1321 CCAGTACTTTGTGACTTAGCGGCTGTGTTGCTATGTAGAGAACACGCTTCAACCCCA 1380
Db 1321 CCAGTACTTTGTGACTTAGCGGCTGTGTTGCTATGTAGAGAACACGCTTCAACCCCA 1380
Qy 1381 CTCCTCCGTACAGTCGACAGGCTTTATCAGAAATAGGAAACCTTTAAACCCCGTCAAT 1440
Db 1381 CTCCTCCGTACAGTCGACAGGCTTTATCAGAAATAGGAAACCTTTAAACCCCGTCAAT 1440
Qy 1441 CCGGACATCCCAACGATGCTCCTGAGCTCAGAGCTTCTGCTGCTCATTTCTGAAC 1500
Db 1441 CCGGACATCCCAACGATGCTCCTGAGCTCAGAGCTTCTGCTGCTCATTTCTGAAC 1500
Qy 1501 AAGGCGTGGATCCCTCAACCAAGAGAAATGTTATGTCTTCAAGTGACCTGACTGCTT 1560
Db 1501 AAGGCGTGGATCCCTCAACCAAGAGAAATGTTATGTCTTCAAGTGACCTGACTGCTT 1560
Qy 1561 GGGGACTATTGGGAAATAGGTGGAGTCTCTACTTTTAAATAATATGTATCTAAGAA 1620
Db 1561 GGGGACTATTGGGAAATAGGTGGAGTCTCTACTTTTAAATAATATGTATCTAAGAA 1620
Qy 1621 TGTCTAGGCACTCTGGAACTTAAAGCGAGGTATTTCCGGCCCTCTCTCAGGAA 1680
Db 1621 TGTCTAGGCACTCTGGAACTTAAAGCGAGGTATTTCCGGCCCTCTCTCAGGAA 1680
Qy 1681 TCCTTCTGAAGACATGCGCCAGTCCGAAGGCCAGGATGGCTTTTGTGGCGCCCGCTGGG 1740
Db 1681 TCCTTCTGAAGACATGCGCCAGTCCGAAGGCCAGGATGGCTTTTGTGGCGCCCGCTGGG 1740
Qy 1741 GTAGGAGGACAGAGACAGAGGAGTACGCTCCACATTCAGAGCATCAAGTAAT 1800
Db 1741 GTAGGAGGACAGAGACAGAGGAGTACGCTCCACATTCAGAGCATCAAGTAAT 1800
Qy 1801 GGCACAATTTCTCGATGACTGACAGAAAATAGTGTGTTTGTAGTTCAACACTCAAGACGA 1860
Db 1801 GGCACAATTTCTCGATGACTGACAGAAAATAGTGTGTTTGTAGTTCAACACTCAAGACGA 1860

Qy 1861 AGCTTATTTCTGAGGATAAGCTCTTTTAAAGGCAAGCTTTTATTTTCACTCTCATCTTTT 1920
Db 1861 AGCTTATTTCTGAGGATAAGCTCTTTTAAAGGCAAGCTTTTATTTTCACTCTCATCTTTT 1920
Qy 1921 GTCTCTCTTTAGCACAAATGTAAAAAGAAATAGTAAATATCAGAACAGGAGGAAATGGCT 1980
Db 1921 GTCTCTCTTTAGCACAAATGTAAAAAGAAATAGTAAATATCAGAACAGGAGGAAATGGCT 1980
Qy 1981 TGCTGGGAGGCCATCCAGGACATCTGGGAGCACATAGAGATTCAACCATGTTTGTGAAC 2040
Db 1981 TGCTGGGAGGCCATCCAGGACATCTGGGAGCACATAGAGATTCAACCATGTTTGTGAAC 2040
Qy 2041 TTAGAGTCAATTTCTCATGCTTTTCTTTTAAATTCACACATATATCAGAGAAAGATATGTC 2100
Db 2041 TTAGAGTCAATTTCTCATGCTTTTCTTTTAAATTCACACATATATCAGAGAAAGATATGTC 2100
Qy 2101 TTGTTAAACATTTGTATPACAAATAGCCCCCAATATAGTAAGATCTATCTAGATAATCCTA 2160
Db 2101 TTGTTAAACATTTGTATPACAAATAGCCCCCAATATAGTAAGATCTATCTAGATAATCCTA 2160
Qy 2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCCATGACTGAGGAAAGAGCTCA 2220
Db 2161 GATGAAATGTTAGAGATGCTATTTGATACAACTGTGCCCATGACTGAGGAAAGAGCTCA 2220
Qy 2221 CGCCAGAGACTGTGGCTGCTCTCCCGGAGGCCAAACCCCAAGGCTCTGGCAAGTCAAG 2280
Db 2221 CGCCAGAGACTGTGGCTGCTCTCCCGGAGGCCAAACCCCAAGGCTCTGGCAAGTCAAG 2280
Qy 2281 CTCAGGAGACTGTGCCCTGCTGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2340
Db 2281 CTCAGGAGACTGTGCCCTGCTGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2340
Qy 2341 CTTGAAAAACAGAGGGGTCTCAAGACATTTCTGCCCTACCTATTAGTCTTTTCTTTTATTTT 2400
Db 2341 CTTGAAAAACAGAGGGGTCTCAAGACATTTCTGCCCTACCTATTAGTCTTTTCTTTTATTTT 2400
Qy 2401 AACTTTTTGGGGGAAAGTATTTTTCAGAAAGTTTGTCTTCAATGTATTTATTAATAGT 2460
Db 2401 AACTTTTTGGGGGAAAGTATTTTTCAGAAAGTTTGTCTTCAATGTATTTATTAATAGT 2460
Qy 2461 AAATAAAGTTTTT 2472
Db 2461 AAATAAAGTTTTT 2472

RESULT 4

US-10-044-090-775
; Sequence 775, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 775
; LENGTH: 2617
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 253550.17
US-10-044-090-775

Query Match 98.7%; Score 2461.8; DB 13; Length 2617;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2485; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Qy 1 GCGCTGAGGATCAGCGCTTCCCTCGCTGGATTCCACAGCTTCGCGCGTGTACTGTGCGCC 60

QY	1380	ACTCCCGTACAGTGGCGCACAGGCTTTATCGAGAAATAGGAAAAACCTTTAAACCCCGGTCA	1439
DB	1397	ACTCCCGTACAGTGGCGCACAGGCTTTATCGAGAAATAGGAAAAACCTTTAAACCCCGGTCA	1456
QY	1440	TCCGGACATCCCAACGCATGCTCTCGAGGCTCACAGGCTTCTGTGGTGTCAATTTCTGAAA	1499
DB	1457	TCCGGACATCCCAACGCATGCTCTCGAGGCTCACAGGCTTCTGTGGTGTCAATTTCTGAAA	1516
QY	1500	CAAGGGGTGGATCCCTCAACCAAGAAAGATGTTTATGTCTTCAAGTGAAGCTGATCTGCT	1559
DB	1517	CAAGGGGTGGATCCCTCAACCAAGAAAGATGTTTATGTCTTCAAGTGAAGCTGATCTGCT	1576
QY	1560	TGSGGACTATTGAGAAAAATAAGGTGAGTCCTACTTGTTTAAAAAATATGTATCTAAAGA	1619
DB	1577	TGSGGACTATTGAGAAAAATAAGGTGAGTCCTACTTGTTTAAAAAATATGTATCTAAAGA	1636
QY	1620	ATGTTCTAGGGCATCTGTGGAAACCTATAAAGGCAAGTATTTTCGGGCGCTCTCTTCAGGA	1679
DB	1637	ATGTTCTAGGGCATCTGTGGAAACCTATAAAGGCAAGTATTTTCGGGCGCTCTCTTCAGGA	1696
QY	1680	ATCTTCTGAAGACATGGCCCACTCGAAGGCCCAAGATGCGCTTTTGTCTGGGCCCCGTGG	1739
DB	1697	ATCTTCTGAAGACATGGCCCACTCGAAGGCCCAAGATGCGCTTTTGTCTGGGCCCCGTGG	1756
QY	1740	GGTAGGAGGACAGAGAGACAGGAGAGTCAGGCTCCACATTCAGAGGCATCAAAAGTAA	1799
DB	1757	GGTAGGAGGACAGAGAGACAGGAGAGTCAGGCTCCACATTCAGAGGCATCAAAAGTAA	1816
QY	1800	TGSCACAAATCTTTCGGATGACTCGAGAAATAGTGTTTGTAGTTCACAACTCAAGACG	1859
DB	1817	TGSCACAAATCTTTCGGATGACTCGAGAAATAGTGTTTGTAGTTCACAACTCAAGACG	1876
QY	1860	AAGCTTATTCTCAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCATCTTTT	1919
DB	1877	AAGCTTATTCTCAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCATCTTTT	1936
QY	1920	TGTCCTCCTTAGCACAAATGTAAAAAGAAATAGTAATATCAGACACAGGAGGAATGGC	1979
DB	1937	TGTCCTCCTTAGCACAAATGTAAAAAGAAATAGTAATATCAGACACAGGAGGAATGGC	1996
QY	1980	TTGCTGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACGCCATGTTGTGAA	2039
DB	1997	TTGCTGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCACGCCATGTTGTGAA	2056
QY	2040	CTTAGAGTCAATCTCATGCTTTTCTTTAATTCACATATATGACAGAAAGATGTT	2099
DB	2057	CTTAGAGTCAATCTCATGCTTTTCTTTAATTCACATATATGACAGAAAGATGTT	2116
QY	2100	CTTGTTAAACATTTGTATACACATAGCCCCAAATATAGTAAGACTATCTAGATAATCCT	2159
DB	2117	CTTGTTAAACATTTGTATACACATAGCCCCAAATATAGTAAGACTATCTAGATAATCCT	2176
QY	2160	AGATGAAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTAGAGAAAGAGCTC	2219
DB	2177	AGATGAAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTAGAGAAAGAGCTC	2236
QY	2220	ACGCCAGAGACTGGGTGCTCTCCGGAGGCCAAACCCAAAGAGGTCTCGGCAAGTCTAG	2279
DB	2237	ACGCCAGAGACTGGGTGCTCTCCGGAGGCCAAACCCAAAGAGGTCTCGGCAAGTCTAG	2296
QY	2280	GCTCAGGGAGACTCTGCGCTGTCTGAGACCTCGGTGTGGACACACGCTGATAGAGCTCT	2339
DB	2297	GCTCAGGGAGACTCTGCGCTGTCTGAGACCTCGGTGTGGACACACGCTGATAGAGCTCT	2356
QY	2340	CCTTGAAGAACAGAGGGGTCTCAAGACATTCGCTACCTATTAGCTTTTCTTTATTTTTT	2399
DB	2357	CCTTGAAGAACAGAGGGGTCTCAAGACATTCGCTACCTATTAGCTTTTCTTTATTTTTT	2416
QY	2400	TAACTTTTTGGGGGAAAAAGTATTTTTGAGAGAGTTTGTCTGCAATGTATTTATAAATAG	2459
DB	2417	TAACTTTTTGGGGGAAAAAGTATTTTTGAGAGAGTTTGTCTGCAATGTATTTATAAATAG	2476

QY	2460	TAAATAAAGTTTTTACCATT	2479
Db	2477	TAAATAAAGTTTTTACCATT	2496
RESULT 6			
US-10-210-120-9			
; Sequence 9, Application US/10210120			
; Publication No. US20030175736A1			
; GENERAL INFORMATION:			
; APPLICANT: Chinnaiyan, Arul M.			
; APPLICANT: Rubini, Mark A.			
; APPLICANT: Steekumar, Arun			
; TITLE OF INVENTION: Expression Profile of Prostate Cancer			
; FILE REFERENCE: UM-07221			
; CURRENT APPLICATION NUMBER: US/10/210,120			
; CURRENT FILING DATE: 2002-08-01			
; PRIOR APPLICATION NUMBER: US 60/309,581			
; PRIOR FILING DATE: 2001-08-02			
; PRIOR APPLICATION NUMBER: US 60/334,468			
; PRIOR FILING DATE: 2001-11-15			
; NUMBER OF SEQ ID NOS: 123			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 9			
; LENGTH: 2465			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-210-120-9			
Query Match 98.3%; Score 2452.4; DB 14; Length 2465;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 2484; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
QY	14	GGCGTTCTCGCTGGATTCCACAGCTTCCGCGCGTGTA	CTGTGCGCCCATCCCTGCGCG 73
Db	1	GGCGTTCTCGCTGGATTCCACAGCTTCCGCGCGTGTA	CTGTGCGCCCATCCCTGCGCG 60
QY	74	CCACAGCTCCCAAGCAGCTGCCCGGTTGCAGGCGCTCAT	GCAGCGCGGCGCACCCACGC 133
Db	61	CCACAGCTCCCAAGCAGCTGCCCGGTTGCAGGCGCTCAT	GCAGCGCGGCGCACCCACGC 120
QY	134	TCGTGGCCCGCTGCGCTGACTCTGCTGGTGCTGTCTCG	CGCGCCGCGCGCTGCGCGGCGCTG 193
Db	121	TCGTGGCCCGCTGCGCTGACTCTGCTGGTGCTGTCTCG	CGCGCCGCGCGCTGCGCGGCGCTG 180
QY	194	GGCGAGCTTCGGGGGCTTGGGTCCCGTGGTGGCGCTTC	CGAGCCGTGCAGCGCGCGCTGCAC 253
Db	181	GGCGAGCTTCGGGGGCTTGGGTCCCGTGGTGGCGCTTC	CGAGCCGTGCAGCGCGCGCTGCAC 240
QY	254	TGSCCCAGTGCGCCTCCGCGCCCGCTTGGCGCGAGTGT	GTGTCGCGAGACGCCCGGCTGCG 313
Db	241	TGSCCCAGTGCGCCTCCGCGCCCGCTTGGCGCGAGTGT	GTGTCGCGAGACGCCCGGCTGCG 300
QY	314	GCTGTCTCTGACGTGCGCACTGAGCGAGGCGCAGCCGT	TCGGGCATCTACACGAGGCT 373
Db	301	GCTGTCTCTGACGTGCGCACTGAGCGAGGCGCAGCCGT	TCGGGCATCTACACGAGGCT 360
QY	374	GTGGCTCCGGCCCTTCGCTGCGCAGCCGTCCGCCGCA	CGAGCGCTGCAGCGCGCTGC 433
Db	361	GTGGCTCCGGCCCTTCGCTGCGCAGCCGTCCGCCGCA	CGAGCGCGCTGCAGCGCGCTGC 420
QY	434	TGAGCGGCGCGGCTCTCGGCTCAACGCTAGTGCCTGAC	CGCCCTGCGGCGCTACCTGC 493
Db	421	TGAGCGGCGCGGCTCTCGGCTCAACGCTAGTGCCTGAC	CGCCCTGCGGCGCTACCTGC 480
QY	494	TGCGACGCGCGCAGCTCCAGGAAATGCTAGTTCGAGGAA	AGACCGCAGCGCGCGCA 553
Db	481	TGCGACGCGCGCAGCTCCAGGAAATGCTAGTTCGAGGAA	AGACCGCAGCGCGCGCA 540
QY	554	GTGTGAGAGCGCGTCCGTCTCCAGCACGACCGGGTGCT	TGATCCCAAGTTCCACCCC 613
Db	541	GTGTGAGAGCGCGTCCGTCTCCAGCACGACCGGGTGCT	TGATCCCAAGTTCCACCCC 600

iy	614	TCCATTCAAGATAAATCATCATCAAGAAAGGGCATGCTAAAGACAGCAGCGCTTACAAG	673
ib	601	TCCATTCAAGATAAATCATCATCAAGAAAGGGCATGCTAAAGACAGCAGCGCTTACAAG	660
iy	674	TTGACTACGAGTCTCAGAGCACAGATACCGACAATTCTCCTCCGAGTCCAAAGCGGAGA	733
ib	661	TTGACTACGAGTCTCAGAGCACAGATACCGACAATTCTCCTCCGAGTCCAAAGCGGAGA	720
iy	734	CAGAATAATGTCTCGCTGGCGTAGAGAAATGGAAAGACACACTGAAATCACTGAAAGTTCCTCA	793
ib	721	CAGAATAATGTCTCGCTGGCGTAGAGAAATGGAAAGACACACTGAAATCACTGAAAGTTCCTCA	780
iy	794	ATGTGCTGAGTCCCGAGGGGTACATATCCCAACTGTGACAAAGAGGGAATTTTATAGA	853
ib	781	ATGTGCTGAGTCCCGAGGGGTACATATCCCAACTGTGACAAAGAGGGAATTTTATAGA	840
iy	854	AAAAGCAGTGTGCGCCTTCCAAAGGCAGGAAGCGGGCTTCTGCTGCTGATTAAGT	913
ib	841	AAAAGCAGTGTGCGCCTTCCAAAGGCAGGAAGCGGGCTTCTGCTGCTGATTAAGT	900
iy	914	ATGGGCAGCTCTCCAGGCTACACACCAAGGGGAGGAGACGTGCACCTGCTACAGCA	973
ib	901	ATGGGCAGCTCTCCAGGCTACACACCAAGGGGAGGAGACGTGCACCTGCTACAGCA	960
iy	974	TGCAGAGCAAGTAGACGCCCTGCCGCAAGGTTAATGTGAGAGCTCAAAATATGCCCTTATTTTG	1033
ib	961	TGCAGAGCAAGTAGACGCCCTGCCGCAAGGTTAATGTGAGAGCTCAAAATATGCCCTTATTTTG	1020
iy	1034	CACAAAAGACTGCCAAGGACATGACACAGCAGCTGGCTACAGCCTCGATATATTTCTGT	1093
ib	1021	CACAAAAGACTGCCAAGGACATGACACAGCAGCTGGCTACAGCCTCGATATATTTCTGT	1080
iy	1094	TTGTGGTGAACGTGATTTTTTTTTTAAACCAGAAAGTTTAGAAAGAGGTTTTGAAATGCCTAT	1153
ib	1081	TTGTGGTGAACGTG- TTTTTTTTAAACCAAGTTTAGAAAGAGGTTTTGAAATGCCTAT	1139
iy	1154	GGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAGAGCAG	1213
ib	1140	GGTTTCTTTGAATGGTAAACTTGAGCATCTTTTCACTTTCCAGTAGTCAGCAAGAGCAG	1199
iy	1214	TTTGAAATTTTCTGTGCTTCTCATCAAAATATTCAGAGACTCGAGCAGCACGCCAGAC	1273
ib	1200	TTTGAAATTTTCTGTGCTTCTCATCAAAATATTCAGAGACTCGAGCAGCACGCCAGAC	1259
iy	1274	TTCATGCGCCCGTGGAAATGCTCACCACATGTTGGTGAAGCGCGCAGCACCTGACTTTGT	1333
ib	1260	TTCATGCGCCCGTGGAAATGCTCACCACATGTTGGTGAAGCGCGCAGCACCTGACTTTGT	1319
iy	1334	GACTTAGCGGCTGTGTTGCTATGTAGAGAACACGCTTCACCCCACTCCCGCTACAGT	1393
ib	1320	GACTTAGCGGCTGTGTTGCTATGTAGAGAACACGCTTCACCCCACTCCCGCTACAGT	1379
iy	1394	CGGCACAGGCTTTATCGAGAAATAGGAAAAACCTTTAAACCCCGGTCACTCGGACATCCCAA	1453
ib	1380	CGGCACAGGCTTTATCGAGAAATAGGAAAAACCTTTAAACCCCGGTCACTCGGACATCCCAA	1439
iy	1454	CGCATGCTCTCGAGCTCACAGCCTTCTGTGTTGTCATTTCTGAAACCAAGGGCTGGATC	1513
ib	1440	CGCATGCTCTCGAGCTCACAGCCTTCTGTGTTGTCATTTCTGAAACCAAGGGCTGGATC	1499
iy	1514	CCTCAACCAAGAGAAATGTTTATGCTTCAAGTGACCTGACTGCTCGGGACACTATTGGA	1573
ib	1500	CCTCAACCAAGAGAAATGTTTATGCTTCAAGTGACCTGACTGCTCGGGACACTATTGGA	1559
iy	1574	GAAATAAGGTGGAGTCCCTACTTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGGCAC	1633
ib	1560	GAAATAAGGTGGAGTCCCTACTTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGGCAC	1619
iy	1634	TCTGGGAACCTATAAGGACAGTATTTGGGCCCTCCTCTTCAGAAATCTCTCGAGAC	1693
ib	1620	TCTGGGAACCTATAAGGACAGTATTTGGGCCCTCCTCTTCAGAAATCTCTCGAGAC	1679
iy	1694	ATGGCCCAAGTCGAAGGCCCAAGATGCGCTTTTGCTGGCGCCCGTGGGTAGGAGGACAG	1753

1680	ATGCGCCAGTCGAAAGCCCGAGGATGCTTTGCTGGGCCCGGTGGGTAGGAGGACAG	1739
1754	AGAGACAGGAGAGTCCAGCTCCACATTCAGAGGCATCAACGTAATGGCACAAATCTTTC	1813
1740	AGAGACAGGAGAGTCCAGCTCCACATTCAGAGGCATCAACGTAATGGCACAAATCTTTC	1799
1814	GGATGACTGCAGAAAATAGTGTGTTAGTTCACAACTCAACAGCAAGCTTATTTCTGA	1873
1800	GGATGACTGCAGAAAATAGTGTGTTAGTTCACAACTCAACAGCAAGCTTATTTCTGA	1859
1874	GGATAAGCTCTTTAAAGGCAAGCTTATTTTCATCTCTCATCTTTTGTCTCTCTTAGCA	1933
1860	GGATAAGCTCTTTAAAGGCAAGCTTATTTTCATCTCTCATCTTTTGTCTCTCTTAGCA	1919
1934	CAATGTAAAAAAGATAGTAATATCAACAGAGGAGGAATGGCTTGTCTGGGAGCCCC	1993
1920	CAATGTAAAAAAGATAGTAATATCAACAGAGGAGGAATGGCTTGTCTGGGAGCCCC	1979
1994	ATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAATAGAGTCATTCT	2053
1980	ATCCAGGACACTGGGAGCACATAGAGATTCACCCATGTTTGTGAATAGAGTCATTCT	2039
2054	CATGCTTTTCTTTATTAATTCACACATATATGCAGAGGAAGATATGTTCTTGTTAACTTGT	2113
2040	CATGCTTTTCTTTATTAATTCACACATATATGCAGAGGAAGATATGTTCTTGTTAACTTGT	2099
2114	ATACACATAGCCCCAAATATAGTAGAGTCTATCTAGATATCTCTAGATGAATGTTAG	2173
2100	ATACACATAGCCCCAAATATAGTAGAGTCTATCTAGATATCTCTAGATGAATGTTAG	2159
2174	AGATGCTATTGTGATCAAACTGTGCGCATGACTCAGGAAAGGAGCTCACGCCACAGACTG	2233
2160	AGATGCTATTGTGATCAAACTGTGCGCATGACTCAGGAAAGGAGCTCACGCCACAGACTG	2219
2234	GGTGTCTCTCCGGAGGCCAAACCCAAAGAGTCTGGCAAAGTCTCAGGCTCAGGGAGACTC	2293
2220	GGTGTCTCTCCGGAGGCCAAACCCAAAGAGTCTGGCAAAGTCTCAGGCTCAGGGAGACTC	2279
2294	TGCGCTGTCTGACACCTCGGTGTGGACACACGCTGCATAGAGCTCTCTTTGAAAAACAGAG	2353
2280	TGCGCTGTCTGACACCTCGGTGTGGACACACGCTGCATAGAGCTCTCTTTGAAAAACAGAG	2339
2354	GGGTCTCAAGACATCTCGGCTACCTATAGCTTTTCTTTATTTTTTTAACTTTTGGGGG	2413
2340	GGGTCTCAAGACATCTCGGCTACCTATAGCTTTTCTTTATTTTTTTAACTTTTGGGGG	2399
2414	GAAGAATTTTTGAGAAGTTTCTCTTGAACTGATTTATTAATAGTAAATAAGTTTTT	2473
2400	GAAGAATTTTTGAGAAGTTTCTCTTGAACTGATTTATTAATAGTAAATAAGTTTTT	2459
2474	ACCATT	2479
2460	ACCATT	2465

RESULT 7
US-10-171-311-90
; Sequence 90, Application US/10171311
; Publication No. US2003008720A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, fan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035

; CURRENT APPLICATION NUMBER: US/10/171.311
 ; CURRENT FILING DATE: 2002-06-12
 ; PRIOR APPLICATION NUMBER: US 60/298,159
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,155
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/335,936
 ; PRIOR FILING DATE: 2001-11-14
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 90
 ; LENGTH: 2499
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-171-311-90

Query Match 98.1%; Score 2446.2; DB 14; Length 2499;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 2465; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY	1	GGCTGAGGATCAGCCGCTTCTGCTGGATTCCACAGCTTCGCGCGGTACTGTGCGC	60
DB	22	GGCTGAGGATCAGCCGCTTCTGCTGGATTCCACAGCTTCGCGCGGTACTGTGCGC	81
QY	61	CGATCCCTCGCGCCAGCTGCGCAAGCAGGTGCGCGGTGAGCGGTATCAGCGG	120
DB	82	CGATCCCTCGCGCCAGCTGCGCAAGCAGGTGCGCGGTGAGCGGTATCAGCGG	141
QY	121	GGCGACCCAGCTCTGGCGCGCTGCGTGAATTCAGCTTCGCGCGGTGAGCGGT	180
DB	142	GGCGACCCAGCTCTGGCGCGCTGCGTGAATTCAGCTTCGCGCGGTGAGCGGT	201
QY	181	GTGGCGCGGTGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGTGAGCGGT	240
DB	202	GTGGCGCGGTGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGTGAGCGGT	261
QY	241	GACGCGCGTGAATTCAGCTTCGCGCGCTGCGTGAATTCAGCTTCGCGCGGT	300
DB	262	GACGCGCGTGAATTCAGCTTCGCGCGCTGCGTGAATTCAGCTTCGCGCGGT	321
QY	301	GAGCGCGGTGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGTGAGCGGT	360
DB	322	GAGCGCGGTGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGTGAGCGGT	381
QY	361	TACACCGAGCGTGTGGCTTCGCGCGCTGCGTGAATTCAGCTTCGCGCGGT	420
DB	382	TACACCGAGCGTGTGGCTTCGCGCGCTGCGTGAATTCAGCTTCGCGCGGT	441
QY	421	CTGCGAGCGCTGTGGAGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGT	480
DB	442	CTGCGAGCGCTGTGGAGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGT	501
QY	481	CGCGCTTACCTGCTCCAGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGT	540
DB	502	CGCGCTTACCTGCTCCAGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGT	561
QY	541	CGCGCGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGTGAGCGGT	600
DB	562	CGCGCGCGCGCGCTGCGTGAATTCAGCTTCGCGCGGTGAGCGGT	621
QY	601	AAATTTCCACCCCTCCATTCAAAGATATCATCAAGAAAGGCGATGCTAAAGACAGC	660
DB	622	AAATTTCCACCCCTCCATTCAAAGATATCATCAAGAAAGGCGATGCTAAAGACAGC	681
QY	661	CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCAGATACCGAGAACTTCTCTCCGAG	720
DB	682	CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCAGATACCGAGAACTTCTCTCCGAG	741
QY	721	TCCAGCGGAGACAGATATGCTCCCTGAGAAATGGAGACACACTGAATCAC	780
DB	742	TCCAGCGGAGACAGATATGCTCCCTGAGAAATGGAGACACACTGAATCAC	801
QY	781	CTGAAGTTCTCTCAATGTGTGAGTCCCGGGGTGTACACATTCCTCCAACTGTGACAGAAG	840

DB	802	CTGAAGTTCTCTCAATGTGTGAGTCCAGGGGTGTACACATTCCTCCAACTGTGACAGAAG	861
QY	841	GGATTTTATAAGAAAAGCAGTGTGCGCTTCCAAAGCAGGAAGCGGGCTTCTGCTGG	900
DB	862	GGATTTTATAAGAAAAGCAGTGTGCGCTTCCAAAGCAGGAAGCGGGCTTCTGCTGG	921
QY	901	TGTGTGATAAGTATGCGGCGAGCTCTCCAGGCTACACACCAGGGAAGGAGGACGTG	960
DB	922	TGTGTGATAAGTATGCGGCGAGCTCTCCAGGCTACACACCAGGGAAGGAGGACGTG	981
QY	961	CATGCTACAGCATGAGAGCAAGTAGAGCTGCGCAAGGTAAATGTGAGAGCTCAAT	1020
DB	982	CATGCTACAGCATGAGAGCAAGTAGAGCTGCGCAAGGTAAATGTGAGAGCTCAAT	1041
QY	1021	ATGCGCTTATTTTGCACAAAAGACTGCGCAAGGATGACAGCAGCTGGTACAGCTCGA	1080
DB	1042	ATGCGCTTATTTTGCACAAAAGACTGCGCAAGGATGACAGCAGCTGGTACAGCTCGA	1101
QY	1081	TTTATATTTCTGTTTGTGTGAATTTTCTTTTAACTTAACTTAACTTAACTTAACTT	1140
DB	1102	TTTATATTTCTGTTTGTGTGAATTTTCTTTTAACTTAACTTAACTTAACTTAACTT	1160
QY	1141	TTGAAATGCTATGTTTCTTTTGAATTTTCTTTTAACTTAACTTAACTTAACTTAACTT	1200
DB	1161	TTGAAATGCTATGTTTCTTTTGAATTTTCTTTTAACTTAACTTAACTTAACTTAACTT	1220
QY	1201	CAGCAAGAGCAGTGTGAATTTTCTTTTGAATTTTCTTTTAACTTAACTTAACTTAACTT	1260
DB	1221	CAGCAAGAGCAGTGTGAATTTTCTTTTGAATTTTCTTTTAACTTAACTTAACTTAACTT	1280
QY	1261	ACAGCAGCAGCAGCTTATGCGCGCGTGAATTTTCTTTTGAATTTTCTTTTAACTTAACTT	1320
DB	1281	ACAGCAGCAGCAGCTTATGCGCGCGTGAATTTTCTTTTGAATTTTCTTTTAACTTAACTT	1340
QY	1321	CCAATGACTTTGTGACTTAGCGCGTGTTCCTTATGAGAGACAGCTTCAACCCCA	1380
DB	1341	CCAATGACTTTGTGACTTAGCGCGTGTTCCTTATGAGAGACAGCTTCAACCCCA	1400
QY	1381	CTCCCGTACAGTGGCGCAGAGCTTATGAGAGATGAGAAACCTTTAAACCCCGGTAT	1440
DB	1401	CTCCCGTACAGTGGCGCAGAGCTTATGAGAGATGAGAAACCTTTAAACCCCGGTAT	1460
QY	1441	CGGACATCCCAACGATGCTCTGAGAGCTACAGCTTCTGTGTGATCTTCTGAAC	1500
DB	1461	CGGACATCCCAACGATGCTCTGAGAGCTACAGCTTCTGTGTGATCTTCTGAAC	1520
QY	1501	AGGGCGTGGATCCCTCAACGAGAGATGTTTATGCTTCAAGTACCTGCTGCTT	1560
DB	1521	AGGGCGTGGATCCCTCAACGAGAGATGTTTATGCTTCAAGTACCTGCTGCTT	1580
QY	1561	GGGGAATTTGGAGAAAATAAGGTGAGTCTTCTTTTAAATAATGTATCTAAGAA	1620
DB	1581	GGGGAATTTGGAGAAAATAAGGTGAGTCTTCTTTTAAATAATGTATCTAAGAA	1640
QY	1621	TGTTCTAGGCGACTTGGGAACTTAAAGCAGATTTTCGGGCGCTTCTTTCAGGA	1680
DB	1641	TGTTCTAGGCGACTTGGGAACTTAAAGCAGATTTTCGGGCGCTTCTTTCAGGA	1700
QY	1681	TCTTCTGAGACATGCGCCAGTCCGAGGCGCAGGATGCTTTCGGGCGCTTTCGGG	1740
DB	1701	TCTTCTGAGACATGCGCCAGTCCGAGGCGCAGGATGCTTTCGGGCGCTTTCGGG	1760
QY	1741	GTAGGAGGACAGAGAGCAGGAGTCAAGCTTCAATTCAGAGGATCTCAAGATAT	1800
DB	1761	GTAGGAGGACAGAGAGCAGGAGTCAAGCTTCAATTCAGAGGATCTCAAGATAT	1820
QY	1801	GGCACAATTTCTCGGATGACTGAGAAAATAGTGTGTTTGTAGTTCAACAACCTCAAGA	1860
DB	1821	GGCACAATTTCTCGGATGACTGAGAAAATAGTGTGTTTGTAGTTCAACAACCTCAAGA	1880
QY	1861	AGCTTATTTCTGAGGATTAAGCTTTTAAAGGCAAGCTTTATTTTCACTCTCTCTTTT	1920

1141 TTGAATGCTATGTTCTTTTGAATGTAACCTTGAGCATCTTTTCACTTTCCAGTAGT 1200
Db |||
1161 TTGAATGCTATGTTCTTTTGAATGTAACCTTGAGCATCTTTTCACTTTCCAGTAGT 1220
Qy |||
1201 CAGCAAGAGCAGTTTGAATTTTCTTGTGCTTCTATCAAAATATTTCAGAGACTCGAGC 1260
Db |||
1221 CAGCAAGAGCAGTTTGAATTTTCTTGTGCTTCTATCAAAATATTTCAGAGACTCGAGC 1280
Qy |||
1261 ACAGCACCAGACTTCATGCGCGGTGGAATGCTCACACATGTTGCTCGAGCGCGGA 1320
Db |||
1281 ACAGCACCAGACTTCATGCGCGGTGGAATGCTCACACATGTTGCTCGAGCGCGGA 1340
Qy |||
1321 CCAGTACTTTGTGACTTAGCGGCTGTGTTGCCATGTAGAGAACAGCTTTCACCCCA 1380
Db |||
1341 CCAGTACTTTGTGACTTAGCGGCTGTGTTGCCATGTAGAGAACAGCTTTCACCCCA 1400
Qy |||
1381 CTCCTCGTACAGTGGCAGACAGCTTTATCGAGATAGAGAACCTTTARACCCGGTCA 1440
Db |||
1401 CTCCTGTACAGTGGCAGACAGCTTTATCGAGATAGAGAACCTTTARACCCGGTCA 1460
Qy |||
1441 CCGGACATCCCAACGATGCTCTCGAGCTCACAGCCTTCTGTGCTGTCATTTCTGAAC 1500
Db |||
1461 CCGGACATCCCAACGATGCTCTCGAGCTCACAGCCTTCTGTGCTGTCATTTCTGAAC 1520
Qy |||
1501 AAGGCGTGGATCCCTCAACAGAGAGATGTTATGCTTCAAGTACCTGACTGCTT 1560
Db |||
1521 AAGGCGTGGATCCCTCAACAGAGAGATGTTATGCTTCAAGTACCTGACTGCTT 1580
Qy |||
1561 GGGACTATTGAGAAAATAAGTGGAGCTCTACTGTTTAAAAAATATGATCTAAGAA 1620
Db |||
1581 GGGACTATTGAGAAAATAAGTGGAGCTCTACTGTTTAAAAAATATGATCTAAGAA 1640
Qy |||
1621 TGTTCTAGGCACTCTGGAACTTATAAGGAGATATTTCGGGCCCTCTCTTCAGGAA 1680
Db |||
1641 TGTTCTAGGCACTCTGGAACTTATAAGGAGATATTTCGGGCCCTCTCTTCAGGAA 1700
Qy |||
1681 TCTTCTGAAGACATGGCCAGTCAAGGCCAGATGGCTTTTGTGCGGCCCGGTGGG 1740
Db |||
1701 TCTTCTGAAGACATGGCCAGTCAAGGCCAGATGGCTTTTGTGCGGCCCGGTGGG 1760
Qy |||
1741 GTAGAGGAGCAGAGAGACAGGAGAGTCACTCCACATTCAGAGCATCACAGTAAT 1800
Db |||
1761 GTAGAGGAGCAGAGAGACAGGAGAGTCACTCCACATTCAGAGCATCACAGTAAT 1820
Qy |||
1801 GGCACAACTTCTCGGATGACATGCAGAAATAGTGTGTTGTTAGTTCAACAACTCAAGACGA 1860
Db |||
1821 GGCACAACTTCTCGGATGACATGCAGAAATAGTGTGTTGTTAGTTCAACAACTCAAGACGA 1880
Qy |||
1861 AGCTTATTTCTGAGGATAGCTTTTAAAGCAAGCTTTATTTTCACTCTCATCTTTT 1920
Db |||
1881 AGCTTATTTCTGAGGATAGCTTTTAAAGCAAGCTTTATTTTCACTCTCATCTTTT 1940
Qy |||
1921 GTCTCTCTAGCACAATGTAAGAAAGATAGTAATATCAGAACAGGAGGAGGATGGCT 1980
Db |||
1941 GTCTCTCTAGCACAATGTAAGAAAGATAGTAATATCAGAACAGGAGGAGGATGGCT 2000
Qy |||
1981 TGCTGGGAGGCCATCCAGGACACTGGAGCAGACATAGAGATTCACCCATGTTTGTGAAC 2040
Db |||
2001 TGCTGGGAGGCCATCCAGGACACTGGAGCAGACATAGAGATTCACCCATGTTTGTGAAC 2060
Qy |||
2041 TTAGAGTCACTTCTCATGCTTTTCTTATTAATTCACATATATCAGAGAGATATGTC 2100
Db |||
2061 TTAGAGTCACTTCTCATGCTTTTCTTATTAATTCACATATATCAGAGAGATATGTC 2120
Qy |||
2101 TTGTTTAACTTGTATACACATAGCCCCAAATATAGTAAGATCTATAGTAATCTTA 2160
Db |||
2121 TTGTTTAACTTGTATACACATAGCCCCAAATATAGTAAGATCTATAGTAATCTTA 2180
Qy |||
2161 GATGAAATGTTAGAGATGCTATTGATCAACTGTGGCCATGACTGAGGAAGAGCTCA 2220
Db |||
2181 GATGAAATGTTAGAGATGCTATTGATCAACTGTGGCCATGACTGAGGAAGAGCTCA 2240
Qy |||
2221 CGCCAGAGACTGGGCTGCTCTCCCGAGGCGCAACCCAGAGGCTGTGGCAAGTCA 2280

2241 CGCCAGAGACTGGGCTGCTCTCCCGAGGCGCAACCCAGAGGCTGTGGCAAGTCA 2300
Qy |||
2281 CTCAGGAGACTCTGCCCTGTGTCAGAGCTCGGTGTGACACACACCTGCATAGAGCTCTC 2340
Db |||
2301 CTCAGGAGACTCTGCCCTGTGTCAGAGCTCGGTGTGACACACACCTGCATAGAGCTCTC 2360
Qy |||
2341 CTTGAAAACAGAGGGGCTCTCAAGACATTTCTGCTACCTATTAGCTTTCTTTATTTT 2400
Db |||
2361 CTTGAAAACAGAGGGGCTCTCAAGACATTTCTGCTACCTATTAGCTTTCTTTATTTT 2420
Qy |||
2401 AACTTTTTCGGGGGAAAAGTATTTTGAGAACTTTGCTTTGCAATGTTTATAAATAGT 2460
Db |||
2421 AACTTTTTCGGGGGAAAAGTATTTTGAGAACTTTGCTTTGCAATGTTTATAAATAGT 2480
Qy |||
2461 AATAAAGTTTTTACCAAT 2479
Db |||
2481 AATAAAGTTTTTACCAAT 2499

RESULT 9
US-10-096-534-32
; Sequence 32, Application US/10096534
; Publication No. US2003016887A1
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Yates, Karen
; APPLICANT: Mizuno, Shuichi
; APPLICANT: Glowacki, Julie
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
; CURRENT APPLICATION NUMBER: US/10/096,534
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/274,980
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 32
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-096-534-32

Query Match 98.1%; Score 2446.2; DB 14; Length 2499;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2465; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Qy 1 GCGCTGAGGATCAGCGCTTCTGCTGGAATTCACAGCTTCGCGCCCGTGTACTGTCCGC 60
Db 22 GCGCTGAGGATCAGCGCTTCTGCTGGAATTCACAGCTTCGCGCCCGTGTACTGTCCGC 81
Qy 61 CCATCCCTCGCGCCAGCCTGCCAAGCAGCGTGCCTGCTTGCAGGCGTCAATGCAGCGG 120
Db 82 CCATCCCTCGCGCCAGCCTGCCAAGCAGCGTGCCTGCTTGCAGGCGTCAATGCAGCGG 141
Qy 121 GCGGACCCACCGCTCTGGGCGCTCGCTGACTCTGTGCTGCTCCGCGGCGCGCG 180
Db 142 GCGGACCCACCGCTCTGGGCGCTCGCTGACTCTGTGCTGCTCCGCGGCGCGCG 201
Qy 181 GTGGGCGGGCTGGCGCAGCTCGGGGGCTTGGTCCCGTGGTGGTGGTGGTGGTGG 240
Db 202 GTGGGCGGGCTGGCGCAGCTCGGGGGCTTGGTCCCGTGGTGGTGGTGGTGGTGG 261
Qy 241 GACGCGGTGCACTGGCCAGTGCCTCGCGCGCTCGCGCGCTGTGCGCGAGCTGTGGCG 300
Db 262 GACGCGGTGCACTGGCCAGTGCCTCGCGCGCTCGCGCGCTGTGCGCGAGCTGTGGCG 321
Qy 301 GACGCGGTGCGGCTGTGCTGACGTGCGCAGTGCAGGAGGCGCAGCGTGGCGCATC 360
Db 322 GACGCGGTGCGGCTGTGCTGACGTGCGCAGTGCAGGAGGCGCAGCGTGGCGCATC 381
Qy 361 TACACGAGCGTGTGGTTCGGCTTCGCTGCCAGCGCTGCCCGAGCGAGCGGCGGAC 420

1b 382 TACACGAGCGCTGTGGCTCCGGCCCTTCCGTGCCAGCGTCCGCCGACGAGGCGGACCG 441
1b 421 CTGACGCGCTGTGAGCAGCGCCCGGCGTCTCGGTCAACGCTAGTCCCGTCAAGCGCCCTG 480
1b 442 CTGACGCGCTGTGAGCAGCGCCCGGCGTCTCGGTCAACGCTAGTCCCGTCAAGCGCCCTG 501
1b 481 CGCGCTTACCTGTGCTCCAGCGCGCCGAGCTCCAGGAAATGCTAGTGAAGCGAGAGAC 540
1b 502 CGCGCTTACCTGTGCTCCAGCGCGCCGAGCTCCAGGAAATGCTAGTGAAGCGAGAGAC 561
1b 541 CGAGCGCGCGAGTGTGGAGAGCGCGTCCGTCTCCAGCACGACCGCGGTGTCTGATCCC 600
1b 562 CGAGCGCGCGAGTGTGGAGAGCGCGTCCGTCTCCAGCACGACCGCGGTGTCTGATCCC 621
1b 601 AGCTTCCACCCCTCCATTCAAGAGATAATCATCATCAAGAAAGGCGATCTAAAGACAGC 660
1b 622 AGTTCCACCCCTCCATTCAAGAGATAATCATCATCAAGAAAGGCGATCTAAAGACAGC 681
1b 661 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCCTCGAG 720
1b 682 CAGCGCTACAAAGTTGACTACGAGTCTCAGAGCACAGATACCCAGAACTTCTCCCTCGAG 741
1b 721 TCCAAAGCGGAGACAGAAATAGTTCCTGCTGCTAGAGAAATGGAAGACACATCTGAATCAC 780
1b 742 TCCAAAGCGGAGACAGAAATAGTTCCTGCTGCTAGAGAAATGGAAGACACATCTGAATCAC 801
1b 781 CTGAAGTTCTCAATGTGCTGAGTCCAGGGGTGTACACATTCGCCAACTGTGACAAAGAG 840
1b 802 CTGAAGTTCTCAATGTGCTGAGTCCAGGGGTGTACACATTCGCCAACTGTGACAAAGAG 861
1b 841 GGAATTTTAAAGAAAGCAAGTGTGCGCTTCCAAAGGCGAGAGAGCGGGCTTCTGCTGG 900
1b 862 GGAATTTTAAAGAAAGCAAGTGTGCGCTTCCAAAGGCGAGAGAGCGGGCTTCTGCTGG 921
1b 901 TGTGTGTAAGTATGCGGAGCTCTCCAGGCTACACCAAGGGAAGGAGGAGCGTG 960
1b 922 TGTGTGTAAGTATGCGGAGCTCTCCAGGCTACACCAAGGGAAGGAGGAGCGTG 981
1b 961 CATGTCTACAGCATGAGAGCAAGTATAGCGCTGCGCAAGGTTAATGTGGAGCTCAAT 1020
1b 982 CATGTCTACAGCATGAGAGCAAGTATAGCGCTGCGCAAGGTTAATGTGGAGCTCAAT 1041
1b 1021 ATGCTTATTTTCCAAAGAGCTGCCAGGACATGACAGAGCTGGCTACAGCTCGA 1080
1b 1042 ATGCTTATTTTCTCAAAAGACTGCCAAGGACTGCCAAGGACTGCGCTACAGCTCGA 1101
1b 1081 TTTATATTTCTGTTGTGTGTAAGTATGTTTAAACCAAGTTTAAAGAGAGGTTT 1140
1b 1102 TTTATATTTCTGTTGTGTGTAAGTATGTTTAAACCAAGTTTAAAGAGAGGTTT 1160
1b 1141 TTGAATGCTATGTTTCTTTGAATGGTAACTTGAGCATCTTTTCACTTTCCAGTAGT 1200
1b 1161 TTGAATGCTATGTTTCTTTGAATGGTAACTTGAGCATCTTTTCACTTTCCAGTAGT 1220
1b 1201 CAGCAAGAGCAGTTTGAATTTTCTGCTGCTTATCAAAATATTCAGAGACTCGAGC 1260
1b 1221 CAGCAAGAGCAGTTTGAATTTTCTGCTGCTTATCAAAATATTCAGAGACTCGAGC 1280
1b 1261 ACAGCACCAGACTTCATGCGCCCGTGGAAATGCTCCACATGTTGGTGCAGAGCGCGCA 1320
1b 1281 ACAGCACCAGACTTCATGCGCCCGTGGAAATGCTCCACATGTTGGTGCAGAGCGCGCA 1340
1b 1321 CCAGTACTTTGTGACTTAGCGCGCTGTGTGCTATGTAGAGAACACGCTTCACCCCCA 1380
1b 1341 CCAGTACTTTGTGACTTAGCGCGCTGTGTGCTATGTAGAGAACACGCTTCACCCCCA 1400
1b 1381 CTCGCCGTACAGTGGCAGAGCTTTATCAGAGAAATAGGAAACCTTTAAACCCCGGTCA 1440
1b 1401 CTCGCCGTACAGTGGCAGAGCTTTATCAGAGAAATAGGAAACCTTTAAACCCCGGTCA 1460
1b 1441 CCGGACATCCCAAGCATGCTCTCGAGCTTCAGAGCTTCTGTGGTGTCTATTTCTGAAAC 1500
1b 1461 CCGGACATCCCAAGCATGCTCTCGAGCTTCAGAGCTTCTGTGGTGTCTATTTCTGAAAC 1520

RESULT 10

US-09-791-196-2

; Sequence 2, Application US/09791196

1501 AAGCGCTGGATCCCTCAACCAAGAAATGTTTATCTCTTCAAGTCACTGTACTGCTT 1560
1521 AAGCGCTGGATCCCTCAACCAAGAAATGTTTATGTCTTCAAGTCACTGTACTGCTT 1580
1561 GGGGACTATTGGAGAAATTAAGGTGGAGTCTTCTGTTTAAATAATATGTATCTAAGAA 1620
1581 GGGGACTATTGGAGAAATTAAGGTGGAGTCTTCTGTTTCAAAATATGTATCTAAGAA 1640
1621 TGTCTAGGGCACTCTCGGAACTTAAAGGCAAGTATTTGGGGCCCTCTCTTTCAGGAA 1680
1641 TGTCTAGGGCACTCTCGGAACTTAAAGGCAAGTATTTGGGGCCCTCTCTTTCAGGAA 1700
1681 TCTTCCCTGAAGACATGCCAGTCCGAGGCGCCAGATGGCTTTTGTCTGCGGCCCGCTGG 1740
1701 TCTTCCCTGAAGACATGCCAGTCCGAGGCGCCAGATGGCTTTTGTCTGCGGCCCGCTGG 1760
1741 GTAGAGGGGACAGAGACAGGAGGAGTCAAGCTTCCATTCAGAGGACATCAAGTAAT 1800
1761 GTAGAGGGGACAGAGACAGGAGGAGTCAAGCTTCCATTCAGAGGACATCAAGTAAT 1820
1801 GGCAAAATTTCTCGATGACTGCGAGAAATAGTGTGTTTGTAGTTCACAACTCAAGACGA 1860
1821 GGCAAAATTTCTCGATGACTGCGAGAAATAGTGTGTTTGTAGTTCACAACTCAAGACGA 1880
1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCTCATCTTT 1920
1881 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCTCATCTTT 1940
1921 GTCTCTCTTAGCAAAATGTAAGAAATAGTATATATCAGAACAGGAGGAGNATGGCT 1980
1941 GTCTCTCTTAGCAAAATGTAAGAAATAGTATATATCAGAACAGGAGGAGGAGNATGGCT 2000
1981 TGCTGGGAGGCCATCCAGGACACTGGGAGCACATAGAGATTACCCATGTTTGTGAAAC 2040
2001 TGCTGGGAGGCCATCCAGGACACTGGGAGCACATAGAGATTACCCATGTTTGTGAAAC 2060
2041 TTAGAGTCAATCTCATGCTTTTCTTTAATATTCACATATATGACAGAAAGATATGTTTC 2100
2061 TTAGAGTCAATCTCATGCTTTTCTTTAATATTCACATATATGACAGAAAGATATGTTTC 2120
2101 TTGTTAACTTTGTATACAAATAGCCCCCAATATAGTAAGATCTATAGTAATATCTTA 2160
2121 TTGTTAACTTTGTATACAAATAGCCCCCAATATAGTAAGATCTATAGTAATATCTTA 2180
2161 GATGAATGTTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGAGCTCA 2220
2181 GATGAATGTTTAGAGATGCTATGATACAACTGTGGCCATGACTGAGGAAAGAGCTCA 2240
2221 CGCCAGAGACTGGGCTGCTCTCCGAGGCGCAAAACCAAGAGGCTCTGGCAAGTCAAG 2280
2241 CGCCAGAGACTGGGCTGCTCTCCGAGGCGCAAAACCAAGAGGCTCTGGCAAGTCAAG 2300
2281 CTGAGGAGACTCTGCGCTGCTGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2340
2301 CTGAGGAGACTCTGCGCTGCTGAGACCTCGGTGTGGACACACGCTGCATAGAGCTCTC 2360
2341 CTTGAATAACAGAGGGGTCTCAAGACATTTCTGCTACCTATAGCTTTTCTTTATTTTTT 2400
2361 CTTGAATAACAGAGGGGTCTCAAGACATTTCTGCTACCTATAGCTTTTCTTTATTTTTT 2420
2401 AACTTTTTGGGGGAAAGATATTTTTCAGAGGTTTGTCTTGCATATGTAATTAATAATAGT 2460
2421 AACTTTTTGGGGGAAAGATATTTTTCAGAGGTTTGTCTTGCATATGTAATTAATAATAGT 2480
2461 AAATAAAGTTTTTACCATT 2479
2481 AAATAAAGTTTTTACCATT 2499

Publication No. US20030096769A1
GENERAL INFORMATION:
APPLICANT: (countries other than U.S.): Royal Children's Hospital
Research Foundation
(U.S. only): George A. WERTHER and
Christopher J. WRIGHT
TITLE OF INVENTION: A METHOD FOR THE PROPHYLAXIS AND/OR
TREATMENT OF PROLIFERATIVE AND/OR
INFLAMMATORY SKIN DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,196
FILING DATE: 20-AUG-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/666,392
FILING DATE: 20-AUG-1996
APPLICATION NUMBER: PCT/AU95/00410
FILING DATE: 06-JUL-1995
NAME: MacLeod, Janet M.
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A30626-PCT-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
CLONE: Cloning and expression of the growth...
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 110...982
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Wood, W.I., et al.
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-791-196-2
Query Match 97.4%; Score 2430.4; DB 10; Length 2474;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2464; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
QY 12 CAGCCGCTCCCTGCTGATTCACAGCTTCGCGCGTGTACTGTGCGCCCATCCCTGCG 71
DB 10 CAGCCGCTCCCTGCTGATTCACAGCTTCGCGCGTGTACTGTGCGCCCATCCCTGCG 69
QY 72 CGCCGAGCTGCCAAGCAGCGTCCCGGTTGAGCGGTCATGACGCGGCGCGCACCCAC 131
DB 70 CGCCGAGCTGCCAAGCAGCGTCCCGGTTGAGCGGTCATGAGCGGCGCGCACCCAC 129
QY 132 GCTCTGGCGCGTGCCTGACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 191
DB 130 GCTCTGGCGCGTGCCTGACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 189
QY 192 TGGCGCGAGCTCGGGGGGCTTGGTCCCTGCTGCTGCGAGCGCGTGCAGCGCGCTGC 251

DB 190 TGGCGCGAGCTCGGGGGGCTTGGGTCCCGTGTGCTGCGAGCGTGCAGCGCGCTGC 249
QY 252 ACTGGCCCAAGTTCGGCGCTCCCGCCCGCTGTGCGCGAGCTGTGCGCGAGCCCGGCTG 311
DB 250 ACTGGCCCAAGTTCGGCGCTCCCGCCCGCTGTGCGCGAGCTGTGCGCGAGCCCGGCTG 309
QY 312 CGGCTGCTCCTGCTGAGTGTGCGCTGAGCGAGCGCGCGCGCTGCGGCATCTACACGAGG 371
DB 310 CGGCTGCTCCTGCTGAGTGTGCGCTGAGCGAGCGCGCGCGCTGCGGCATCTACACGAGG 369
QY 372 CTGTGCTCCTGCGGCTTTCGCTGCGAGCGCTGCGCGCGAGCGCGCGCTGCGAGCGCT 431
DB 370 CTGTGCTCCTGCGGCTTTCGCTGCGAGCGCTGCGCGCGAGCGCGCGCTGCGAGCGCT 429
QY 432 GCTGAGCGCGCGCGGCTCTGCTGCTCAAGCTAGTGTGCTGCGCGCTGCGCGCGCTGCT 491
DB 430 GCTGAGCGCGCGCGGCTCTGCTGCTCAAGCTAGTGTGCTGCGCGCTGCGCGCGCTGCT 489
QY 492 GCTGCCAGCGCGCGCGCTTCCAGGAAATGCTAGTGTGCTGCGAGGAGAGCGCGAGCGCG 551
DB 490 GCTGCCAGCGCGCGCGCTTCCAGGAAATGCTAGTGTGCGAGGAGAGCGCGAGCGCGCG 549
QY 552 CAGTGTGAGAGCGCGCTGCTGCTCAGCAGCGCGCGGTGTCTGATCCCAAGTTCACCC 611
DB 550 CAGTGTGAGAGCGCGCTGCTGCTCAGCAGCGCGCGGTGTCTGATCCCAAGTTCACCC 609
QY 612 CTCCCATTCAAAGATAATCATCATCAAGAAAGGCGATGCTAAAGAGCAGCGCGCTACAA 671
DB 610 CTCCCATTCAAAGATAATCATCATCAAGAAAGGCGATGCTAAAGAGCAGCGCGCTACAA 669
QY 672 AGTTGACTAGAGTCTCAGAGCAGATACCAGAACTTCTCTCGGAGTCCAAGCGGA 731
DB 670 AGTTGACTAGAGTCTCAGAGCAGATACCAGAACTTCTCTCGGAGTCCAAGCGGA 729
QY 732 GACAGAATATGGTCCCTGCTGCTGAGAGAAATGGAAGACACACTGAATCAGTCAAGTTCT 791
DB 730 GACAGAATATGGTCCCTGCTGCTGAGAGAAATGGAAGACACACTGAATCAGTCAAGTTCT 789
QY 792 CAATGTGCTAGTCCCGAGGGGTGTACATATCCCACTGTGACAAAGAGGATTTATAA 851
DB 790 CAATGTGCTAGTCCCGAGGGGTGTACATATCCCACTGTGACAAAGAGGATTTATAA 849
QY 852 GAAAAGCAGTGTGCGCTTCCAAAGCAGGAGCGGGCTTCTGCTGTGTGTGATAA 911
DB 850 GAAAAGCAGTGTGCGCTTCCAAAGCAGGAGCGGGCTTCTGCTGTGTGTGATAA 909
QY 912 GTATGGCAGCTCTCCCGAGGTACACCAAGGGAAGGAGGAGCGTGCATGCTACAG 971
DB 910 GTATGGCAGCTCTCCCGAGGTACACCAAGGGAAGGAGGAGCGTGCATGCTACAG 969
QY 972 CATGCGAGCAGTGTGAGCGCTGCGCGAGGTTAATGTGAGCTCAATATGCTTATTT 1031
DB 970 CATGCGAGCAGTGTGAGCGCTGCGCGAGGTTAATGTGAGCTCAATATGCTTATTT 1028
QY 1032 TGCACAAAAGACTGCCAAGGACATGACCGAGCTGCGCTACAGCTTCGATTTATTTCT 1091
DB 1029 TGCACAAAAGACTGCCAAGGACATGACCGAGCTGCGCTACAGCTTCGATTTATTTCT 1088
QY 1092 GTTGTGCTGAAGTGTATTTTAAACCAAGTTTAAAGAGGTTTTCGAAATGCT 1151
DB 1089 GTTGTGCTGAAGTGTATTTTAAACCAAGTTTAAAGAGGTTTTCGAAATGCT 1147
QY 1152 ATGCTTCTTTGATGCTAAACTTGAAGCTTTTTCACCTTTCCAGTAGTCAGCAAGAGC 1211
DB 1148 ATGCTTCTTTGATGCTAAACTTGAAGCTTTTTCACCTTTCCAGTAGTCAGCAAGAGC 1207
QY 1212 AGTTGAAATTTCTGCTGCTTCTATCAATATTTTACAGAGCTGCGAGCAGCAGCCAG 1271
DB 1208 AGTTGAAATTTCTGCTGCTTCTATCAAAATATTTTACAGAGCTGCGAGCAGCAGCCAG 1267
QY 1272 ACTTATGCGCGCTGGAATGCTCACACATGTTGTCGAAGCGCGCGAGCTGCTTT 1331

1268 ACTTCATGCCCGCTGGAATGCTCACACATGTTGGTCGAAGCGGCCGACCACTGACTTT 1327
 1332 GTACATTAGCGGCTGTGTCCTATGTAGAGAACAGCTTACCCCACTCCCGGTACA 1391
 1338 GTGACTTAGCGGCTGTGTCCTATGTAGAGAACAGCTTACCCCACTCCCGGTACA 1387
 1392 GTGCGCACAGCTTTATCGAGAAATAGGAAACCTTTAAACCCCGGTATCCCGGACATCC 1451
 1388 GTGCGCACAGCTTTATCGAGAAATAGGAAACCTTTAAACCCCGGTATCCCGGACATCC 1447
 1452 AAGCATGCTCTGGAGCTCACAGCTTCTGGGTGTCATTTCTGAAAACAAGGGGTGA 1511
 1448 AAGCATGCTCTGGAGCTCACAGCTTCTGGGTGTCATTTCTGAAAACAAGGGGTGA 1507
 1512 TCCTCAACCAAGAAATGTTTATGTTCTTCAAGTACCTGACTCTTGGGACTATTG 1571
 1508 TCCTCAACCAAGAAATGTTTATGTTCTTCAAGTACCTGACTCTTGGGACTATTG 1567
 1572 GAGAAATAGGTGGAGTCTACTGTTTAAATAATGTAATTAAGATGTTTAGGGC 1631
 1568 GAGAAATAGGTGGAGTCTACTGTTTAAATAATGTAATTAAGATGTTTAGGGC 1627
 1632 ACTCTGGAACTTATAAGGACAGTATTTGGGCCCTCTCTTCAGGAATCTTCTGAAG 1691
 1628 ACTCTGGAACTTATAAGGACAGTATTTGGGCCCTCTCTTCAGGAATCTTCTGAAG 1687
 1692 ACATGCCAGTCCGAGGCCAGATGGCTTTGCTGGGCCCGCGGGTGGAGGGAC 1751
 1688 ACATGCCAGTCCGAGGCCAGATGGCTTTGCTGGGCCCGCGGGTGGAGGGAC 1747
 1752 AGAGAGACGGGAGAGTACGCTCCCATTCAGAGGCATCAGAGTAATGGACAAATCT 1811
 1748 AGAGAGAC-GGGAGAGTACGCTCCCATTCAGAGGCATCAGAGTAATGGACAAATCT 1806
 1812 TCGGATGACTGCGAGAAATAGTGTGTTGTAGTTTCAACAACTCAAGACGAAGCTATTCT 1871
 1807 TCGGATGACTGCGAGAAATAGTGTGTTGTAGTTTCAACAACTCAAGACGAAGCTATTCT 1866
 1872 GAGGATAAGCTTTTAAAGCAAGCTTTATTTCTCATCTCTCATCTTTGCTCCTTAG 1931
 1867 GAGGATAAGCTTTTAAAGCAAGCTTTATTTCTCATCTCTCATCTTTGCTCCTTAG 1926
 1932 CACAATGTAAAAAGAAATAGTAATATCAGAACAGGAGGAATGGCTTGTGGGAGC 1991
 1927 CACAATGTAAAAAGAAATAGTAATATCAGAACAGGAGGAATGGCTTGTGGGAGC 1986
 1992 CCATCCAGGACACTGGGAGCACATAGAGATTACCCATGTTGTTCAACTTAGAGTCATT 2051
 1987 CCATCCAGGACACTGGGAGCACATAGAGATTACCCATGTTGTTCAACTTAGAGTCATT 2046
 2052 CTCATGCTTTTCTTATAATTCACATATATGAGAGAAATATGTTCTTGTAAACATT 2111
 2047 CTCATGCTTTTCTTATAATTCACATATATGAGAGAAATATGTTCTTGTAAACATT 2106
 2112 GTATACAACTAGCCCCAAATATAGTAAGATCTATATAGTAATCTTAGAGTAATGTT 2171
 2107 GTATACAACTAGCCCCAAATATAGTAAGATCTATATAGTAATCTTAGAGTAATGTT 2166
 2172 AGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAAAGGAGTCAAGCCAGAGAC 2231
 2167 AGAGATGCTATTATGATACAACTGTGGCCATGACTGAGGAAAGGAGTCAAGCCAGAGAC 2226
 2232 TGGGCTGCTCTCCCGAGGCCAAACCCCAAGAGGTCTGGCAAGTCAAGGCTAGGAGAC 2291
 2227 TGGGCTGCTCTCCCGAGGCCAAACCCCAAGAGGTCTGGCAAGTCAAGGCTAGGAGAC 2286
 2292 TCTGCCCTGTGAGACCTCGGTGTGAGACACAGCTGCATAGAGCTCTCTTGAACAG 2351
 2287 TCTGCCCTGTGAGACCTCGGTGTGAGACACAGCTGCATAGAGCTCTCTTGAACAG 2346
 2352 AGGGGTCTCAAGACATCTGCTACCTATTAGCTTTTCTTTATTTTAACTTTTGGG 2411
 2347 AGGGGTCTCAAGACATCTGCTACCTATTAGCTTTTCTTTATTTTAACTTTTGGG 2406

QY 2412 GGGAAAGTATTTTGGAGAGTTTGTCTTCAATGTATTTTATAAATAGTAAATAAGTTTT 2471
 Db 2407 GGGAAAGTATTTTGGAGAGTTTGTCTTCAATGTATTTTATAAATAGTAAATAAGTTTT 2466
 QY 2472 TTACCAIT 2479
 Db 2467 TTACCAIT 2474

RESULT 11
 US-10-062-674-2164
 ; Sequence 2164, Application US/10062674
 ; Publication No. US2004000559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
 ; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
 ; FILE REFERENCE: PA-0026-1 CIP
 ; CURRENT APPLICATION NUMBER: US/10/062,674
 ; PRIOR FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: US 09/625,102
 ; PRIOR FILING DATE: 2000-07-24
 ; NUMBER OF SEQ ID NOS: 2217
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2164
 ; LENGTH: 3642
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US2004000559A1 806690.12
 US-10-062-674-2164

Query Match 96.9%; Score 2415.8; DB 15; Length 3642;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2431; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 50 GTACTGTGCGCCCATCCCTGCGGCCCGCAGCTGCAAGCAGCGTCCCGGTTGCAGGCG 109
 Db 1101 GTGCTCGCATCTCATCCCTGCGGCCCGCAGCTGCAAGCAGCGTCCCGGTTGCAGGCG 1160
 QY 110 TCATGCGAGCGGCGCGACCCACAGCTCTGGGCGGTGCGCTGACTCTGCTGGTGTGCTCC 169
 Db 1161 TCATGCGAGCGGCGCGACCCACAGCTCTGGGCGGTGCGCTGACTCTGCTGGTGTGCTCC 1220
 QY 170 GCGGCGCGCGGTGCGCGGCGCTGCGCGAGCTGCGGGGCTTGGGTCCCGTGGTGGCT 229
 Db 1221 GCGGCGCGCGGTGCGCGGCGCTGCGCGAGCTGCGGGGCGCTTGGGTCCCGTGGTGGCT 1280
 QY 230 GCGAGCGGTGCGAGCGCGCTGCACTGCGCCCGCTGCGCGCTTCCCGCCCGCTGTCGCGG 289
 Db 1281 GCGAGCGGTGCGAGCGCGCTGCACTGCGCCCGCTGCGCGCTTCCCGCCCGCTGTCGCGG 1340
 QY 290 AGCTGTTGCGGAGCGCGGCTGCGGCTGCTGCTGAGCTGCGGCTTCCCGCCCGCTGTCGCGG 349
 Db 1341 AGCTGTTGCGGAGCGCGGCTGCGGCTGCTGCTGAGCTGCGGCTTCCCGCCCGCTGTCGCGG 1400
 QY 350 CGTGGCGCATCTACACGAGCGCTGCTGCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 409
 Db 1401 CGTGGCGCATCTACACGAGCGCTGCTGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 1460
 QY 410 AGGCGGACCCCTGAGCGCTGCTGAGCGCGCGGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 469
 Db 1461 AGGCGGACCCCTGAGCGCTGCTGAGCGCGCGGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 1520
 QY 470 TCAGCGCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 529
 Db 1521 TCAGCGCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 1580
 QY 530 CGGAGGAAGACCGGAGCGCGCTGCTGAGAGCGCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 589
 Db 1581 CGGAGGAAGACCGGAGCGCGCTGCTGAGAGCGCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 1640

QY 590 TGTCTGATCCCAAGTTCCACCCCTCCATTCACAAAGTATCATCATCAAGAAAGGCGATG 649
Db 1641 TGTCTGATCCCAAGTTCCACCCCTCCATTCACAAAGTATCATCATCAAGAAAGGCGATG 1700
QY 650 CTAAGACAGCCAGCGCTACAAAGTTGACTACAGTCTCAGAGCACAGATACCCAGAACT 709
Db 1701 CTAAGACAGCCAGCGCTACAAAGTTGACTACAGTCTCAGAGCACAGATACCCAGAACT 1760
QY 710 TCTCTCCGAGTCCCAAGCGGAGACAGATATGTCCTCCGCTAGAGAAATGGAAGACA 769
Db 1761 TCTCTCCGAGTCCCAAGCGGAGACAGATATGTCCTCCGCTAGAGAAATGGAAGACA 1820
QY 770 CACTGAATCACCTGAAGTTCCCTCAATGTCTCAGTCCCAAGGCGGTACACATCCCAACT 829
Db 1821 CACTGAATCACCTGAAGTTCCCTCAATGTCTCAGTCCCAAGGCGGTACACATCCCAACT 1880
QY 830 GTGACAGAAGGATTTATAGAAAGACAGTGTGCGCTTCCAAAGCGAGGAGCGGG 889
Db 1881 GTGACAGAAGGATTTATAGAAAGACAGTGTGCGCTTCCAAAGCGAGGAGCGGG 1940
QY 890 GCTTCTGCTGGTGTGGGATAAGTATGGCGAGCCTCTCCAGGCTACACCAAGGGGA 949
Db 1941 GCTTCTGCTGGTGTGGATAAGTATGGCGAGCCTCTCCAGGCTACACCAAGGGGA 2000
QY 950 AGGAGACGTGCTGTACAGCATGCGAGCAAGTAGACGCTCCCGCAAGGTTAATGT 1009
Db 2001 AGGAGACGTGCTGTACAGCATGCGAGCAAGTAGACGCTCCCGCAAGGTTAATGT 2060
QY 1010 GGAGCTCAAAATATGCTTATTTTGCACAAAGACATGCCAAGACATGACAGCAGCTGGC 1069
Db 2061 GGAGCTCAAAATATGCTTATTTTGCACAAAGACATGCCAAGACATGACAGCAGCTGGC 2120
QY 1070 TACAGCTCGATTTATATTTCTGTTGGTGAACATGATTTTTTTTAAACCAAGTTTA 1129
Db 2121 TACAGCTCGATTTATATTTCTGTTGGTGAACATG- TTTTTTTTAAACCAAGTTTA 2179
QY 1130 GAAAGAGTTTTTGAATGCTATGTTTCTTGTGAATGCTGAATGCTGATCTTTTCA 1189
Db 2180 GAAAGAGTTTTTGAATGCTATGTTTCTTGTGAATGCTGAATGCTGATCTTTTCA 2239
QY 1190 TTTCCAGTAGTCAGAAAGAGCAGTTGAATTTCTGCTCTCTATCAAAATATTCA 1249
Db 2240 TTTCCAGTAGTCAGAAAGAGCAGTTGAATTTCTGCTCTCTATCAAAATATTCA 2299
QY 1250 GAGACTCGAGCACAGCCAGACTTCATGCGCGGTGGAATGCTCACCACATGTTGGTC 1309
Db 2300 GAGACTCGAGCACAGCCAGACTTCATGCGCGGTGGAATGCTCACCACATGTTGGTC 2359
QY 1310 GAAAGCGCGCACCACTGTTGACTTTAGCGGCTGTGTTGCTATGTAGAGAACAG 1369
Db 2360 GAAAGCGCGCACCACTGTTGACTTTAGCGGCTGTGTTGCTATGTAGAGAACAG 2419
QY 1370 CTTTCAACCCCATCCCGTACAGTCGCGACAGGCTTTATCAGAAATAGGAAACCTTTAA 1429
Db 2420 CTTTCAACCCCATCCCGTACAGTCGCGACAGGCTTTATCAGAAATAGGAAACCTTTAA 2479
QY 1430 ACCCGGCTCATCCGACATCCCAAGCATGCTCTCGAGCTCAGACCTCTGTTGGTGC 1489
Db 2480 ACCCGGCTCATCCGACATCCCAAGCATGCTCTCGAGCTCAGACCTCTGTTGGTGC 2539
QY 1490 ATTCTGAAACAAAGGCGTGGATCCCTCAACCAAGAAATGTTTATGCTTCAAGTGAC 1549
Db 2540 ATTCTGAAACAAAGGCGTGGATCCCTCAACCAAGAAATGTTTATGCTTCAAGTGAC 2599
QY 1550 CTGTACTGCTTGGGACTATTGAGAAAATAAGGTGGAGTCTACTTCTTTTAAAAATAT 1609
Db 2600 CTGTACTGCTTGGGACTATTGAGAAAATAAGGTGGAGTCTACTTCTTTTAAAAATAT 2659
QY 1610 GTATCTAAGATGTTCTAGGGCACTCTGGGAACCTATTAAGGCAAGGTATTTGGGCGCTC 1669
Db 2660 GTATCTAAGATGTTCTAGGGCACTCTGGGAACCTATTAAGGCAAGGTATTTGGGCGCTC 2719
QY 1670 CTCTTCAGGAATCTTCTCTGAAGACATGCCCCAGTCGAAGGCCAGGATGGCTTTTGCTGC 1729

Db 2720 CTCTTCAGGAATCTTCTCTGAAGACATGGCCCGAGTCAAGGCCCGAGATGGCTTTTCTGC 2779
QY 1730 GGCCCGCTGGGTAGGAGGACAGAGAGACAGGAGAGTCAAGCTCCACATTCAGAGGCA 1789
Db 2780 GGCCCGCTGGGTAGGAGGACAGAGAGACAGGAGAGTCAAGCTCCACATTCAGAGGCA 2839
QY 1790 TCACAAGTAAATGSCACAATTTCTCGATGACTGCGAGAAATAGTGTGTTAGTTCACA 1849
Db 2840 TCACAAGTAAATGSCACAATTTCTCGATGACTGCGAGAAATAGTGTGTTAGTTCACA 2899
QY 1850 ACTCAAGACGAAGCTTATTTCTGAGGATAAGTCTTTTAAAGGCAAGCTTTTATTTTATC 1909
Db 2900 ACTCAAGACGAAGCTTATTTCTGAGGATAAGTCTTTTAAAGGCAAGCTTTTATTTTATC 2959
QY 1910 TCTCATCTTTTGTCTTCTTAGCAAAATGTAAAGAAATAGTAAATATCAGAACAGGAAG 1969
Db 2960 TCTCATCTTTTGTCTTCTTAGCAAAATGTAAAGAAATAGTAAATATCAGAACAGGAAG 3019
QY 1970 GAGGAATGGCTTCTCGGAGGCCATCCAGGACATCGGGAGCACATAGAGATTCACCCAT 2029
Db 3020 GAGGAATGGCTTCTCGGAGGCCATCCAGGACATCGGGAGCACATAGAGATTCACCCAT 3079
QY 2030 GTTGTGTAACTTAGAGTCAATTTCTCATGCTTTTCTTTTAAATTCACATATATGCGAG 2089
Db 3080 GTTGTGTAACTTAGAGTCAATTTCTCATGCTTTTCTTTTAAATTCACATATATGCGAG 3139
QY 2090 AAGATATGTTCTTTTAAATTTATACAAATAGCCCCAAATATAGTAAAGTCTATATCT 2149
Db 3140 AAGATATGTTCTTTTAAATTTATACAAATAGCCCCAAATATAGTAAAGTCTATATCT 3199
QY 2150 AGATAATCTTAGATGAATTTTAGAGATCTATTTGATACAACTGTGGCCATGACTGAGG 2209
Db 3200 AGATAATCTTAGATGAATTTTAGAGATCTATTTGATACAACTGTGGCCATGACTGAGG 3259
QY 2210 AAAGGAGCTCAGCCCGAGAGACTGGGCTGCTCTCCCGAGGCGCAACCCCAAGAGTCTG 2269
Db 3260 AAAGGAGCTCAGCCCGAGAGACTGGGCTGCTCTCCCGAGGCGCAACCCCAAGAGTCTG 3319
QY 2270 GCAAGCTAGGCTCAGGAGACTTGCCTCTGTCAGACTCGGTGTGACACACGCTGC 2329
Db 3320 GCAAGCTAGGCTCAGGAGACTTGCCTCTGTCAGACTCGGTGTGACACACGCTGC 3379
QY 2330 ATAGACTCTCTTGAACAGAGGCTCTCAAGCATTTCTGCTTACCTATTAGCTTTTC 2389
Db 3380 ATAGACTCTCTTGAACAGAGGCTCTCAAGCATTTCTGCTTACCTATTAGCTTTTC 3439
QY 2390 TTTATTTTTTAACTTTTGGGGGAAAGTATTTTGAAGAAAGTTTGTCTTCAATGTAT 2449
Db 3440 TTTATTTTTTAACTTTTGGGGGAAAGTATTTTGAAGAAAGTTTGTCTTCAATGTAT 3499
QY 2450 TTATAATAGTAAATAGTATTTTACCATTAAAAAAA 2488
Db 3500 TTATAATAGTAAATAGTATTTTACCATTAAAAAAA 3538

RESULT 12

US-10-094-749-493
; Sequence 493, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO

721	TCC	AAGCGGAGACAGAA	TATGGTCCCTGCCGTAGAGAAATGGAGACACACTCAATCAC	780
690	TCC	AAGCGGAGACAGAA	TATGGTCCCTGCCGTAGAGAAATGGAGACACACTGAATCAC	749
781	CTG	AAGTTCCTCAATGTGCTGAGTCCCAAGGCGTGACAT	TCCCAACTGTGACAAGAAG	840
750	CTG	AAGTTCCTCAATGTGCTGAGTCCCAAGGCGTGACAT	TCCCAACTGTGACAAGAAG	809
841	GGATTTT	TATGAAGAAAGACAGTGTGCCTCCAAAGCGACGAAAGCGGGGCTTCGTCTGG	900	
810	GGATTTT	TATGAAGAAAGACAGTGTGCCTCCAAAGCGACGAAAGCGGGGCTTCGTCTGG	869	
901	TGTGTGAT	TAAGTATGGGACGCTCTCCACAGGCTACACCA	CAAGGGAAGAGACGCTG	960
870	TGTGTGAT	TAAGTATGGGACGCTCTCCACAGGCTACACCA	CAAGGGAAGAGACGCTG	929
961	CAC	TGCTACAGCATGACAGACAGTACGCTCGCGCAAGGTTAATGTGAGCTCAAA	T	1020
930	CAC	TGCTACAGCATGACAGACAGTACGCTCGCGCAAGGTTAATGTGAGCTCAAA	T	989
1021	ATG	CTTTATTTGCACAAAAGACTGCCAAGGACATGAC	CACGACGTGCCTACAGCCTCGA	1080
990	ATG	CTTTATTTGCACAAAAGACTGCCAAGGACATGAC	CACGACGTGCCTACAGCCTCGA	1049
1081	TTT	TATATTTCTGTCTGCTGAGTAACATGATTTTTTTTAAACCAAAAGTTT	TAGAAAGAGGTTT	1140
1050	TTT	TATATTTCTGTCTGCTGAGTAACATGATTTTTTTTAAACCAAAAGTTT	TAGAAAGAGGTTT	1109
1141	TG	AAATGCCTATCGTTTCTTGAAATGGTAAACTT	TGAGCACTTTTTCATCTTTCCAGTAGT	1200
1110	TG	AAATGCCTATCGTTTCTTGAAATGGTAAACTT	TGAGCACTTTTTCATCTTTCCAGTAGT	1169
1201	CAG	CAAAAGACAGTTTGAAATTTTCTTGTGCTTCCCTAT	CAAAATATCAGAGACTCGAGC	1260
1170	CAG	CAAAAGACAGTTTGAAATTTTCTTGTGCTTCCCTA	TCAAATATCAGAGACTCGAGC	1229
1261	AC	ACACCCACAGCTTATCGCCCGCTGGAAATGCT	CACACATGTTGGTTCGAAGCGCGCGGA	1320
1230	AC	ACACCCACAGCTTATCGCCCGCTGGAAATGCT	CACACATGTTGGTTCGAAGCGCGCGGA	1289
1321	CC	ATGACTTTGTGACTTTAGGCGGCTGTGCTGCC	TATGTAGAGAACAGCTTCAACCCCA	1380
1290	CC	ATGACTTTGTGACTTTAGGCGGCTGTGCTGCC	TATGTAGAGAACAGCTTCAACCCCA	1349
1381	CT	CCCGCTACAGTCGCGACAGGCTTTATCGA	AAATAGAGAAACCTTTAAACCCCGCTCAT	1440
1350	CT	CCCGCTACAGTCGCGACAGGCTTTATCGA	AAATAGAGAAACCTTTAAACCCCGCTCAT	1409
1441	CG	GACATCCCAACGATGCTCTCGAGACTCAC	AGCCTTCTGTGGTGTCAATTCGTA	1500
1410	CG	GACATCCCAACGATGCTCTCGAGACTCAC	AGCCTTCTGTGGTGTCAATTCGTA	1469
1501	AAG	GGCGTGAATCCCTCAACCAAGAAAGAAATG	TTATGTCTCAAGTGACCTGTACTGCTT	1560
1470	AAG	GGCGTGAATCCCTCAACCAAGAAAGAAATG	TTATGTCTCAAGTGACCTGTACTGCTT	1529
1561	GG	GACTATTTCGAGAAATTAAGGTGGAGTC	TACTTGTTTAAAAAATATGTATCTA	1620
1530	GG	GACTATTTCGAGAAATTAAGGTGGAGTC	TACTTGTTTAAAAAATATGTATCTA	1589
1621	TG	TCTAGGGCACTCTGGGAAACCTATAA	AGGCAGGTATTTCCGGGCCCTCCTCTTCAG	1680
1590	TG	TCTAGGGCACTCTGGGAAACCTATAA	AGGCAGGTATTTCCGGGCCCTCCTCTTCAG	1649
1681	TC	TTTCTTGAAGACATGCCCCAGTCGAAGGCC	CCAGGATGGCTTTTCTCGCGGCCCGCTGGG	1740
1650	TC	TTTCTTGAAGACATGCCCCAGTCGAAGGCC	CCAGGATGGCTTTTCTCGCGGCCCGCTGGG	1709
1741	GT	AGGAGGGAACAGAGACAGGGAGAGT	CAGCCTCCACATTCAGAGGCATCACAGTAAT	1800
1710	GT	AGGAGGGAACAGAGACAGGGAGAGT	CAGCCTCCACATTCAGAGGCATCACAGTAAT	1769

1801	GGCACAATCTTCGGATGACTGCGAAAAATAGTGTCTTTGTAGTTCAACA	1861	CTCAAGACGA
1770	GGCACAATCTTCGGATGACTGCGAAAAATAGTGTCTTTGTAGTTCAACA	1829	CTCAAGACGA
1861	AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAAGCTTTATTTATCTCTCATCTTTT	1920	
1830	AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAAAGCTTTATTTATCTCTCATCTTTT	1889	
1921	GTCTCTCTTAGCACAATGTAAAAAAGAAATAGTAATATCAGAA	1980	CAGGAAGGAGAAATGGCT
1890	GTCTCTCTTAGCACAATGTAAAAAAGAAATAGTAATATCAGAA	1949	CAGGAAGGAGAAATGGCT
1981	TGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCA	2040	CCCATCTGTTGTTGAAC
1950	TGCTGGGGAGCCCATCCAGGACACTGGGAGCACATAGAGATTCA	2009	CCCATCTGTTGTTGAAC
2041	TTAGAGTCATCTCATGCTTTCTTTTATAAATCACACATATATGC	2100	AGAGATATGTTTC
2010	TTAGAGTCATCTCATGCTTTCTTTTATAAATCACACATATATGC	2069	AGAGATATGTTTC
2101	TTGTTAACATTTGATACAAATAGCCCAATATAGTAAGATCTTACT	2160	AGATAATCTTA
2070	TTGTTAACATTTGATACAAATAGCCCAATATAGTAAGATCTTACT	2129	AGATAATCTTA
2161	GATCAAAATGTTAGAGATGCTATTGTATACAACTGTGGCCATGACT	2220	AGAGAGAGCTCA
2130	GATCAAAATGTTAGAGATGCTATTGTATACAACTGTGGCCATGACT	2189	AGAGAGAGCTCA
2221	CGGCCAGAGACTGGGTGCTCTCCGGAGGCGCAAA	2280	CCCAAGTCAAG
2190	CGGCCAGAGACTGGGTGCTCTCCGGAGGCGCAAA	2249	CCCAAGTCAAG
2281	CTCAGGAGACTCTGGCCCTGCTGCAGACCTCGGTGTGGACACACG	2340	CTGCATAGAGCTCTC
2250	CTCAGGAGACTCTGGCCCTGCTGCAGACCTCGGTGTGGACACACG	2309	CTGCATAGAGCTCTC
2341	CTTGAAAAACAGAGGGGTCTCAAGACATTCCTGCTCACTTAAGCT	2400	CTTTATTTTTTTT
2310	CTTGAAAAACAGAGGGGTCTCAAGACATTCCTGCTCACTTAAGCT	2369	CTTTATTTTTTTT
2401	AACCTTTTGGGGGAAAAAGTATTTTGGAGAAGTTTGTCTTGCAATG	2460	TATTTATAAATAGT
2370	AACCTTTTGGGGGAAAAAGTATTTTGGAGAAGTTTGTCTTGCAATG	2429	TATTTATAAATAGT
2461	AAATAAAGTTTTTACCATT	2479	
2430	AAATAAAGTTTTTACCATT	2448	

```

RESULT 13
US-10-108-260A-960
; Sequence 960, Application US10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 960
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-960

```

```

Query Match      86.7%; Score 2162.6; DB 15; Length 2355;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 2330; Conservative 0; Mismatches 4; Indels 145; Gaps 2;

Qy      1  GCCTGAGGATCAGCCGCTTCCTCCCTGGATTCCACAGTTTCGCGCGGTATCTGTGCGC 60

```

[illegible]

2y 1141 TTGAATGCTATGTTTCTTGAATGTTAACTTGAGCATCTTTTCACTTTCCAGTAGT 1200
 2b 1017 TTGAATGCTATGTTTCTTGAATGTTAACTTGAGCATCTTTTCACTTTCCAGTAGT 1076
 2y 1201 CAGCAAGAGAGAGTTGAAATTTCTTGTGCGTTCCTATCAAAATATTCAGAGACTCGAGC 1260
 2b 1077 CAGCAAGAGAGAGTTGAAATTTCTTGTGCGTTCCTATCAAAATATTCAGAGACTCGAGC 1136
 2y 1261 ACAGCAACCCAGACTTCATGGCGCGTGGAAATGCTCACCATGTTGGTCAAGCGGCCGA 1320
 2b 1137 ACAGCAACCCAGACTTCATGGCGCGTGGAAATGCTCACCATGTTGGTCAAGCGGCCGA 1196
 2y 1321 CCACGTGCTTTGAGACTTAGCGGCTGTGTGCTATGTAGAGAACACGCTTCACCCCCA 1380
 2b 1197 CCACGTGCTTTGAGACTTAGCGGCTGTGTGCTATGTAGAGAACACGCTTCACCCCCA 1256
 2y 1381 CTCGCCGTACAGTCGACAGGCTTTATCAGAAATAGGAAACCTTTAAACCCCGTCAAT 1440
 2b 1257 CTCGCCGTACAGTCGACAGGCTTTATCAGAAATAGGAAACCTTTAAACCCCGTCAAT 1316
 2y 1441 CCGGACATCCAAACGATGCTCTGGAGCTCACAGGCTTCTGTGGTGTCAATTTCTGAAAC 1500
 2b 1317 CCGGACATCCAAACGATGCTCTGGAGCTCACAGGCTTCTGTGGTGTCAATTTCTGAAAC 1376
 2y 1501 AAGGCGTGGATCCCTCAACCAAGAGAAATGTTATGCTCTCAAGTCACTGACTGCTT 1560
 2b 1377 AAGGCGTGGATCCCTCAACCAAGAGAAATGTTATGCTCTCAAGGACCTGACTGCTT 1436
 2y 1561 GGGGACTATTGGAGAAATAGGTGGAGTCTCTACTTGTGTTTAAAAAATATGTATCAAGAA 1620
 2b 1437 GGGGACTATTGGAGAAATAGGTGGAGTCTCTACTTGTGTTTAAAAAATATGTATCAAGAA 1496
 2y 1621 TGTTCTAGGCACTCTGGAACTATTAAGGCAAGTATTTTCGGGCTCTCTCTTCAAGAA 1680
 2b 1497 TGTTCTAGGCACTCTGGAACTATTAAGGCAAGTATTTTCGGGCTCTCTCTTCAAGAA 1556
 2y 1681 TCTTCTTGAAGACATGCGCCAGTCTGAAGGCGCCAGGATGGCTTTTGTGCGGCGCCGTGG 1740
 2b 1557 TCTTCTTGAAGACATGCGCCAGTCTGAAGGCGCCAGGATGGCTTTTGTGCGGCGCCGTGG 1616
 2y 1741 GTAGAGGGGACAGAGACAGGGAGAGTACGCTCCACATTCAGAGCATCAAGATAT 1800
 2b 1617 GTAGAGGGGACAGAGACAGGGAGAGTACGCTCCACATTCAGAGCATCAAGATAT 1676
 2y 1801 GGCACAAATCTTCGGATGACTGCAGAAATAGTGTGTTTGTAGTTCAACAACTCAAGACGA 1860
 2b 1677 GGCACAAATCTTCGGATGACTGCAGAAATAGTGTGTTTGTAGTTCAACAACTCAAGACGA 1736
 2y 1861 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTATCTCTCATCTTTT 1920
 2b 1737 AGCTTATTTCTGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTATCTCTCATCTTTT 1796
 2y 1921 GTCCTCTTAGCACAATGTAAGAAATAGTATATCAAGACAGGAAGAGGATGGCT 1980
 2b 1797 GTCCTCTTAGCACAATGTAAGAAATAGTATATCAAGACAGGAAGAGGATGGCT 1856
 2y 1981 TGCTGGGAGGCCCATCCAGGACACTGGGAGCACATAGAGATTACCCATGTTGTTGAAC 2040
 2b 1857 TGCTGGGAGGCCCATCCAGGACACTGGGAGCACATAGAGATTACCCATGTTGTTGAAC 1916
 2y 2041 TTAGAGTCAATCTCATGCTTTCTTTATATTCACATATATGCAGAGAGATATGTTTC 2100
 2b 1917 TTAGAGTCAATCTCATGCTTTCTTTATATTCACATATATGCAGAGAGATATGTTTC 1976
 2y 2101 TTGTTAACTTGTATACAAATAGCCCAATAGTAAAGATCTTATCTAGATAATCTTA 2160
 2b 1977 TTGTTAACTTGTATACAAATAGCCCAATAGTAAAGATCTTATCTAGATAATCTTA 2036
 2y 2161 GATGAATGTTAGAGAGCTTATTTGATACAACTGTGGCCATGACTGAGGAAGAGCTCA 2220
 2b 2037 GATGAATGTTAGAGAGCTTATTTGATACAACTGTGGCCATGACTGAGGAAGAGCTCA 2096

QY 2221 GCGCCAGAGACTGGGCTCTCTCCGGAGGCGCAACCCAAAGAGTCTGGCAAAAGTCAAG 2280
 Db 2097 GCGCCAGAGACTGGGCTCTCTCCGGAGGCGCAACCCAAAGAGTCTGGCAAAAGTCAAG 2156
 QY 2281 CTCAGGGAGACTTGGCCCTGCTGCAGAGCTCGGTGTGGACACAGCTGCATAGAGCTCTC 2340
 Db 2157 CTCAGGGAGACTTGGCCCTGCTGCAGAGCTCGGTGTGGACACAGCTGCATAGAGCTCTC 2216
 QY 2341 CTTGAAAAACAGAGGGGTCTCAAGACATTTCTGCCCTACCTATTAGCTTTTCTTTATTTT 2400
 Db 2217 CTTGAAAAACAGAGGGGTCTCAAGACATTTCTGCCCTACCTATTAGCTTTTCTTTATTTT 2276
 QY 2401 AACTTTTTGGGGGAAAGTATTTTGGAGAGTTTGTCTTGAATGTATTTTATATAAGT 2460
 Db 2277 AACTTTTTGGGGGAAAGTATTTTGGAGAGTTTGTCTTGAATGTATTTTATATAAGT 2336
 QY 2461 AAATAAAGTTTTTACCATT 2479
 Db 2337 AAATAAAGTTTTTACCATT 2355
 RESULT 14
 US-10-104-047-1076
 ; Sequence 1076, Application US/10104047
 ; Publication No. US20030236392A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 1076
 ; LENGTH: 2327
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-104-047-1076
 Query Match 84.2%; Score 2099.8; DB 15; Length 2327;
 Best Local Similarity 92.9%; Pred. No. 0;
 Matches 2304; Conservative 0; Mismatches 2; Indels 173; Gaps 3;
 QY 1 GGGCTGAGGATCAGCGGCTTCTGCTGGATTCCACAGCTTCGGCGCGGTGACTGTGCGC 60
 Db 22 GCGCTGAGGATCAGCGGCTTCTGCTGGATTCCACAGCTTCGGCGCGGTGACTGTGCGC 81
 QY 61 COATCCCTGCGCGCCAGCTTCGCAAGCAGCGTCCCGCGGTTCAGGCGTTCATGACGCG 120
 Db 82 CCATCCCTGCGCGCCAGCTTCGCAAGCAGCGTCCCGCGGTTCAGGCGTTCATGACGCG 141
 QY 121 GCGGACCCACGCTCTGGCGCGCTGCGTGAATCTGCTGGTGTGCTCCGCGCGCGCGC 180
 Db 142 GCGGACCCACGCTCTGGCGCGCTGCGTGAATCTGCTGGTGTGCTCCGCGCGCGCGC 201
 QY 181 GTGGCGCGGCTGCGGAGCTCGGGGGCTTGGGTCCCGTGGTGGCGAGCGCGTGC 240
 Db 202 GTGGCGCGGCTGCGGAGCTCGGGGGCTTGGGTCCCGTGGTGGCGTACG----- 253
 QY 241 GACGCGCTGCACTGGCCAGTGGCGGCTCCGCGCGCGTGGCGGAGCTGGTGGCG 300
 Db 254 ----- 253
 QY 301 GAGCGGGCTCGGCTGCTGCTGACGTGCGCACTGACGAGGGCCAGCCGTGGCGATC 360
 Db 254 -----AGCCGTGGCGATC 267
 QY 361 TACACCGAGCGCTGTGGCTCCGGCTTCGCTGCCAGCGCGTCCCGCAGCGCGCGACCG 420
 Db 268 TACACCGA----- 275


```

; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560a1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108.260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1000
; LENGTH: 2192
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1000

```

Query Match 79.3%; Score 1977.6; DB 15; Length 2192;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 19; Indels 3; Gaps 3;

Qy	437	ACGCCCGCGGCTCTGCGTCAACGCTAGT-GCGCTCAGCGCGCTTGC	CGCGCTACCTCGT	495
Db	151	ACGCTCTGGGCGGCTGCGCTGACGCTGCTGGACGGCGCGGCTCTGCGCTACCTCGT	210	
Qy	496	CCAGCGCGCGCAGCTCCAGGAAATGCTAGTGAGTCCGAGGAAGACCCAGCGCGGCGAGT	555	
Db	211	CCAGCGCGCGCAGCTCCAGGAAATGCTAGTGAGTCCGAGGAAGACCCAGCGCGGCGAGT	270	
Qy	556	GTGGAGAGCCGCTCCGCTCTCAGACACGACCGGGTGCTGATCCCAAGTTCACACCCCTC	615	
Db	271	GTGGAGAGCCGCTCCGCTCTCAGACACGACCGGGTGCTGATCCCAAGTTCACACCCCTC	330	
Qy	616	CATTCAAAGATAATCATCATCAAGAAAGGGCATGCTATAAGACAGCGGTACAAAGTT	675	
Db	331	CATTCAAAGATAATCATCATCAAGAAAGGGCATGCTATAAGACAGCGGTACAAAGTT	390	
Qy	676	GACTACGAGTCTCAGAGCACAGATACCCAGAACTTCCTCCGAGTCCACAGCGGAGACA	735	
Db	391	GACTACGAGTCTCAGAGCACAGATACCCAGAACTTCCTCCGAGTCCACAGCGGAGACA	450	
Qy	736	GAATATGGTCCCTGCCGTAGAGAAATCGAAGACACACTGAAATCACTGAAAGTTCCTCAAT	795	
Db	451	GAATATGGTCCCTGCCGTAGAGAAATCGAAGACACACTGAAATCACTGAAAGTTCCTCAAT	510	
Qy	796	GTGCTGAGTCCGAGGGGTGTACATTCGCCACTGTGACAAAGAGGATTTTATAAGAAA	855	
Db	511	GTGCTGAGTCCGAGGGGTGTACATTCGCCACTGTGACAAAGAGGATTTTATAAGAAA	570	
Qy	856	AAGCAGTGTGCGCCCTTCCAAAGGCAGGAAGCGGGCTTCGTGGTGTGGATTAAGTAT	915	
Db	571	AAGCAGTGTGCGCCCTTCCAAAGGCAGGAAGCGGGCTTCGTGGTGTGGATTAAGTAT	630	
Qy	916	GGGAGCGCTCTCCAGCGTACACCAAGGGGAAGGAGACGTGCACTGCTACAGCATG	975	
Db	631	GGGAGCGCTCTCCAGCGTACACCAAGGGGAAGGAGACGTGCACTGCTACAGCATG	690	
Qy	976	CAGAGCAAGTAGACGCTGCGCAAGGTTAATGTGGAGCTCAATATGCGCTTATTTTGA	1035	
Db	691	CAGAGCAAGTAGACGCTGCGCAAGGTTAATGTGGAGCTCAATATGCGCTTATTTTGA	750	
Qy	1036	CAAAAGACTGCCAAGGACATGACACAGCAGCTGGCTACAGCGCTCGATTTATTTCTGTTT	1095	
Db	751	CAAAAGACTGCCAAGGACATGACACAGCAGCTGGCTACAGCGCTCGATTTATTTCTGTTT	810	
Qy	1096	GTGGTGAACGTGATTTTTTTTTTAAACCAAAGTTTAGAAAGAGGTTTTTGAATGCTATGG	1155	
Db	811	GTGGTGAACGTGATTTTTTTTTTAAACCAAAGTTTAGAAAGAGGTTTTTGAATGCTATGG	869	
Qy	1156	TTTCTTTGAATGGTAAACTTTGAGCATCTTTTCACTTCCAGTAGTACAGCAAGAGCAGTT	1215	
Db	870	TTTCTTTGAATGGTAAACTTTGAGCATCTTTTCACTTCCAGTAGTACAGCAAGAGCAGTT	929	
Qy	1216	TGAATTTTCTGTGCTTCCCTATCAAAAATATTCAGAGACTCGAGCACAGCAACCCAGACT	1275	
Db	930	TGAATTTTCTGTGCTTCCCTATCAAAAATATTCAGAGACTCGAGCACAGCAACCCAGACT	989	

QY	1276	CATGCGCCCGTGAATGCTCA	CCACATGTTGGTGAAGCGGCGGACCACTGACTTTGTGA	1333
Db	990	CATGCGCCCGTGAATGCTC	CACCACATGTTGGTGAAGCGGCGGACCACTGACTTTGTGA	1049
QY	1336	CTTAGCGCGTGTGTGCTT	CTATGTAGAGAAACGCTTCAACCCCACTCCCGGTACAGTGC	1395
Db	1050	CTTAGCGCGTGTGTGCTT	CTATGTAGAGAAACGCTTCAACCCCACTCCCGGTACAGTGC	1109
QY	1396	GCACAGGCTTTATCGAGAA	TAGGAAAACCTTTAAACCCCGGTCTATCGGACATCCCAAG	1455
Db	1110	GCACAGGCTTTATCGAGAA	TAGGAAAACCTTTAAACCCCGGTCTATCGGACATCCCAAG	1169
QY	1456	CATGCTCTGGAGCTCA	CAGCCTTCTGTGGTGTCTATTTCTGAAAACGAAGGCGTGGATCCC	1515
Db	1170	CATGCTCTGGAGCTCA	CAGCCTTCTGTGGTGTCTATTTCTGAAAACGAAGGCGTGGATCCC	1229
QY	1516	TCNACCAAGAGNATGTT	TATGTCTCAAGTGACCTGTACTGCTGGGACATTTGGAGA	1575
Db	1230	TCNACCAAGAGNATGTT	TATGTCTCAAGTGACCTGTACTGCTGGGACATTTGGAGA	1289
QY	1576	AAATAAGGTGGAGTCT	CTACTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGCGACTC	1635
Db	1290	AAATAAGGTGGAGTCT	CTACTGTTTAAAAAATATGTATCTAAGAAATGTTCTAGGCGACTC	1349
QY	1636	TGGGAACCTTAAAGCG	AGGTATTCGGGCGCTCCTCTTCAGAAATCTTCCTGAAGACAT	1695
Db	1350	TGGGAACCTTAAAGCG	AGGTATTCGGGCGCTCCTCTTCAGAAATCTTCCTGAAGACAT	1409
QY	1696	GGCCCAAGTCEAAGGCC	CAGGATGGCTTTTCTCGCGCCCGCTGGGTAGGAGGACAGAG	1755
Db	1410	GGCCCAAGTCEAAGGCC	CAGGATGGCTTTTCTCGCGCCCGCTGGGTAGGAGGACAGAG	1468
QY	1756	AGACAGGAGAGTCAG	CGCTCCACATTCAGAGGCATCACAAAGTAATGGCAAAATTCCTCGG	1815
Db	1469	AGACAGGAGAGTCAG	CGCTCCACATTCAGAGGCATCACAAAGTAATGGCAAAATTCCTCGG	1528
QY	1816	ATGACTGCAGAAAA	TAGTGTTTGTAGTTTCAACAACTCAAGACGAAGCTTATTTCTGAGG	1875
Db	1529	ATGACTGCAGAAAA	TAGTGTTTGTAGTTTCAACAACTCAAGACGAAGCTTATTTCTGAGG	1588
QY	1876	ATAAGCTCTTTAAG	CGCAAGCTTTATTTTTCATCTCTCATCTTTCTGCTCCTTAGCAC	1935
Db	1589	ATAAGCTCTTTAAG	CGCAAGCTTTATTTTTCATCTCTCATCTTTCTGCTCCTTAGCAC	1648
QY	1936	ATGTAAAAAAGAA	TAGTAATATCAGAACAGGAAGGAATGGCTTGCTGGGAGGCCAT	1995
Db	1649	ATGTAAAAAAGAA	TAGTAATATCAGAACAGGAAGGAATGGCTTGCTGGGAGGCCAT	1708
QY	1996	CACGAGACCTGGG	ACACATAGAGATTCACCCATGTTTGTGAACCTAGAGTCAATTCTCA	2055
Db	1709	CACGAGACCTGGG	ACACATAGAGATTCACCCATGTTTGTGAACCTAGAGTCAATTCTCA	1768
QY	2056	TGCTTTTCTTTA	ATPTCACATATATGCGAGAGAATATGTTCTTGTGTAACTTTGAT	2115
Db	1769	TGCTTTTCTTTA	ATPTCACATATATGCGAGAGAATATGTTCTTGTGTAACTTTGAT	1828
QY	2116	ACAACTAGCCCC	CAATATAGTAAGATCTATCTAGATAATCTCAGATCAAAATGTTAGAG	2175
Db	1829	ACAACTAGCCCC	CAATATAGTAAGATCTATCTAGATAATCTCAGATCAAAATGTTAGAG	1888
QY	2176	ATGCTATTTGAT	ACACTGTGGCCATGACTGAGGAAGAGGCTCAGCCCGACAGACTGGG	2235
Db	1889	ATGCTATTTGAT	ACACTGTGGCCATGACTGAGGAAGAGGCTCAGCCCGACAGACTGGG	1948
QY	2236	CTGCTCTCCCG	GAGGCCAAACCAAGAAGGTCTGGCAAAAGTCAGGCTCAGGGAGACTCTG	2295
Db	1949	CTGCTCTCCCG	GAGGCCAAACCAAGAAGGTCTGGCAAAAGTCAGGCTCAGGGAGACTCTG	2008
QY	2296	CCCTGCTGAG	ACTCTGGTGTGGACACAGCGTGATAGAGCTCTCCTTGAAAACAGAGGG	2355
Db	2009	CCCTGCTGAG	ACTCTGGTGTGGACACAGCGTGATAGAGCTCTCCTTGAAAACAGAGGG	2068
QY	2356	GTCTCAAGA	CATTCTCGCTACCTATTAGCTTTTCTTTATTTTTTTTAACTTTTTTGGGGGA	2415

Db	2069	GTCTCAGACATCTGCCCTACCTATTAGCTTTCTTTATTTTTTTTAACTTTTGGGGGA	2128
Qy	2416	AAAGTATTTTTCGAGAAGTTTGTCTTGCAATGTATTATAAATAGTAAATAAAGTTTTTAC	2475
Db	2129	AAAGTATTTTTCGAGAAGTTTGTCTTGCAATGTATTATAAATAGTAAATAAAGTTTTTAC	2188
Qy	2476	CATT	2479
Db	2189	CATT	2192

Search completed: March 12, 2004, 06:13:23
Job time : 592.261 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2004, 09:18:38 ; Search time 4129.09 seconds

(without alignments)
18036.975 Million cell updates/sec

Title: US-10-084-817-18

Perfect score: 2494
Sequence: 1 ggcgtgagatcagccgctt.....ccatcaaaaaaaaaaaaaa 2494

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: em_eebca:*
2: em_eeahum:*
3: em_eeatin:*
4: em_eeatmu:*
5: em_eeatov:*
6: em_eeatpl:*
7: em_eeatro:*
8: em_eehc:*
9: gb_eeat1:*
10: gb_eeat2:*
11: gb_eeat3:*
12: gb_eeat4:*
13: gb_eeat5:*
14: gb_eeat6:*
15: em_eeatun:*
16: em_eeatun:*
17: em_gss_hum:*
18: em_gss_hum:*
19: em_gss_hum:*
20: em_gss_hum:*
21: em_gss_hum:*
22: em_gss_hum:*
23: em_gss_hum:*
24: em_gss_hum:*
25: em_gss_hum:*
26: em_gss_hum:*
27: em_gss_hum:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
C 1	1115	44.7	1201 9	AL571366 AL571366
C 2	1094.4	43.9	1201 9	AL571366 AL571366
C 3	1075.8	43.1	1201 9	AL545769 AL545769
C 4	1062.6	42.6	1201 9	AL542261 AL542261

C 5	1055.6	42.3	1164 9	AL549091 AL549091
C 6	1038.2	41.6	1201 13	BX366676 BX366676
C 7	1035.6	41.5	1106 9	AL551293 AL551293
C 8	1033.8	41.5	1201 9	AL545693 AL545693
C 9	1027.4	41.2	1045 9	AL574918 AL574918
C 10	1027.4	41.2	1201 9	AL553323 AL553323
C 11	1026.6	41.2	1182 9	AL575300 AL575300
C 12	1014.2	40.7	1201 9	AL553346 AL553346
C 13	1012.2	40.6	1201 13	BX402691 BX402691
C 14	1004.6	40.3	1183 13	BX377586 BX377586
C 15	1001.8	40.2	1201 13	BX364743 BX364743
C 16	999.2	40.1	1201 9	AL577492 AL577492
C 17	995.2	39.9	1201 9	AL545572 AL545572
C 18	993.6	39.8	1201 9	AL542260 AL542260
C 19	991	39.7	1201 9	AL571310 AL571310
C 20	988.8	39.6	1112 9	AL550063 AL550063
C 21	983.6	39.4	1201 9	AL574407 AL574407
C 22	983.2	39.4	1201 13	BX417553 BX417553
C 23	979.4	39.3	1201 9	AL573817 AL573817
C 24	974.2	39.1	1105 9	AL549162 AL549162
C 25	960.6	38.5	1201 9	AL571127 AL571127
C 26	959.2	38.5	1146 9	AL549809 AL549809
C 27	957.2	38.4	1201 9	AL579903 AL579903
C 28	956.8	38.4	1201 9	AL544496 AL544496
C 29	955.2	38.3	1201 13	BX345715 BX345715
C 30	951.6	38.2	1201 9	AL572767 AL572767
C 31	950.8	38.1	1201 9	AL531761 AL531761
C 32	950.8	38.1	1201 13	BX417359 BX417359
C 33	950	38.1	1201 9	AL540851 AL540851
C 34	944.6	37.9	1201 9	AL570558 AL570558
C 35	941	37.7	1087 9	AL574024 AL574024
C 36	939.2	37.7	1201 13	BX417037 BX417037
C 37	932	37.4	1201 9	AL544369 AL544369
C 38	931	37.3	986 9	AL577260 AL577260
C 39	930.2	37.3	1201 9	AL577095 AL577095
C 40	929	37.2	1201 13	BX402692 BX402692
C 41	928.2	37.2	1144 9	AL576242 AL576242
C 42	927.6	37.2	971 9	AL578098 AL578098
C 43	927.2	37.2	1201 9	AL516544 AL516544
C 44	926.6	37.2	1079 9	AL573471 AL573471
C 45	926.2	37.1	1004 13	BX440520 BX440520

ALIGNMENTS

RESULT 1
AL571366/c
LOCUS
DEFINITION
AL571366 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
Accession
AL571366
Version
AL571366.2 GI:31292766
Keywords
EST
Source
Homo sapiens (human)
Organism
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12928590.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4009.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI009CG01NP1c1cluster=4009.r. Contact :
Feng Liang Email : fliang@life.techn.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1015DG03NP1.

FEATURES

source

Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1015YNO1"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 44.7%; Score 1115; DB 9; Length 1201;
 Best Local Similarity 96.7%; Pred. No. 4.7e-192;
 Matches 1150; Conservative 17; Mismatches 17; Indels 5; Gaps 3;

QY 1251 AGACTCGAGCAGCAGCCAGCATTCATGCGCCGCGTGAATGCTCACACATGTTGGTCG 1310
 DB 1198 RRAYCGGCGAGCAGCCAGCATCTAGCG-...CCGGRATGCTCACCATGKTCGG 1142
 QY 1311 AAGCGGCGACCATGACTTTGTGACTTAGCGGGCTGTGCTTATGTAGAGAACGCG 1370
 DB 1141 AAGCGGCGACCAVAGAC-TTKTGACTTAGCGCGCTGTGCTTATGTAGAGAACGCG 1083
 QY 1371 TTCACCCCATCCCGCTACAGTGGCGAGCTTTATCGAGATAGAAACCTTTAAA 1430
 DB 1082 TTCACCCCATCCCGCTACAGTGGCGAGCTTTATCGAGATAGAAACCTTTAAA 1023
 QY 1431 CCCCGTTCATCGGACATCCCAACGATCTCTCGAGCTCACAGCCTTCGTGTGTC 1490
 DB 1022 CCCCGTTCATCGGACATCCCAACGATCTCTCGAGCTCACAGCCTTCGTGTGTC 963
 QY 1491 TTTCTGAACAGGCGCTGGATCCCTCAACAGAGATGTTATGCTTCTCAAGTACC 1550
 DB 962 TTTCTGAACAGGCGCTGGATCCCTCAACAGAGATGTTATGCTTCTCAAGTACC 903
 QY 1551 TGTACTGCTTGGGGACTATTGGAGAAATAAGTGGAGTCTTACTGTTTAAAAAATG 1610
 DB 902 TGTACTGCTTGGGGACTATTGGAGAAATAAGTGGAGTCTTACTGTTTAAAAAATG 843
 QY 1611 TATCTAAGNATGTTCTAGGGACTCTGGACCTTAAGCAGGATTTTCGGGCGCTCC 1670
 DB 842 TATCTAAGNATGTTCTAGGGACTCTGGACCTTAAGCAGGATTTTCGGGCGCTCC 783
 QY 1671 TCTTCAGGAATCTCTGAAGACATGCGCCAGTCAAGGCGCCAGGATGGCTTTTGTGCG 1730
 DB 782 TCTTCAGGAATCTCTGAAGACATGCGCCAGTCAAGGCGCCAGGATGGCTTTTGTGCG 723
 QY 1731 GCCCGTGGGGTAGAGGACACAGAGACAGGAGATCAGGCTCCACATTCAGAGGAT 1790
 DB 722 GCCCGTGGGGTAGAGGACACAGAGACAGGAGATCAGGCTCCACATTCAGAGGAT 663
 QY 1791 CACAAGTATGACCAATCTTCGGATGACTCGAGAAATAGTGTGTTAGTGTCAACAA 1850
 DB 662 CACAAGTATGACCAATCTTCGGATGACTCGAGAAATAGTGTGTTAGTGTCAACAA 603
 QY 1851 CTCAGACGAAAGCTTATTTCTGAGATAGCTCTTTAAAGGCAAGCTTATTTTCATCT 1910
 DB 602 CTCAGACGAAAGCTTATTTCTGAGATAGCTCTTTAAAGGCAAGCTTATTTTCATCT 543
 QY 1911 CTCATCTTTTCTCTCTTAGCACAATGTAAGAAAGATAGTAATATCAGAACGAGG 1970
 DB 542 CTCATCTTTTCTCTCTTAGCACAATGTAAGAAAGATAGTAATATCAGAACGAGG 483
 QY 1971 AGGAATGGCTTGTGGGGAGCCATCCAGACACTGGGAGCATAGAGATTCCACCATG 2030
 DB 482 AGGAATGGCTTGTGGGGAGCCATCCAGACACTGGGAGCATAGAGATTCCACCATG 423
 QY 2031 TTTGTTGAACCTAGATCATCTCTGCTTTCTTTTATATTCACACATATATGACAGAGA 2090

DB 422 TTTGTTGMACTCAGAGTCACTCTCATGTTCTTTTATATTCACATATATGACAGAGA 363
 QY 2091 AGATATGTTCTTTTAAACATTTGTATACAAATAGAGCCCAATATAGTAAATCTACTA 2150
 DB 362 AGATATGTTCTTTTAAACATTTGTATACAAATAGAGCCCAATATAGTAAATCTACTA 303
 QY 2151 GATAATCCTAGATGAATTTAGAGATGCTATTTCATCAACTGTGGCATGACCTGAGA 2210
 DB 302 GATAATCCTAGATGAATTTAGAGATGCTATTTCATCAACTGTGGCATGACCTGAGA 243
 QY 2211 AAGGAGCTCACGCCAGAGACTGGGCTCTCTCCCGAGGCGAAACCCAAAGAGCTCTGG 2270
 DB 242 AAGGAG-TCAAGGCTCACGCCAGAGACTGGGCTCTCTCCCGAGGCGAAACCCAAAGAGCTCTGG 184
 QY 2271 CAAAGTCAGGCTCAGGAGACTCTGCCCTGCTGAGAGCTCGTGTGGACACACGCTGCA 2330
 DB 183 CAAAGTCAGGCTCAGGAGACTCTGCCCTGCTGAGAGCTCGTGTGGACACACGCTGCA 124
 QY 2331 TAGAGCTCTCTTGAAGAACAGAGGGGCTCTCAAGACATTCGCTACCTATTAGCTTTCT 2390
 DB 123 TAGAGCTCTCTTGAAGAACAGAGGGGCTCTCAAGACATTCGCTACCTATTAGCTTTCT 64
 QY 2391 TTATTTTAACTTTTGGGGGAAAGTATTTTGGAGAGTTTGTCT 2439
 DB 63 TTATTTTAACTTTTGGGGGAAAGTATTTTGGAGAGTTTGTCT 15

RESULT 2

AL571232/c

LOCUS

DEFINITION

AL571232 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

ACCESSION

AL571232

VERSION

AL571232.2

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

JOURNAL

COMMENT

On Feb 16, 2001 this sequence version replaced gi:12928322.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 4009.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0D1015DG03NP1&cluster=4009.r. Contact :

Feng Liang Email : fliang@life.techn.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paraday Avenue Genoscope sequence ID : CS0D1015DG03NP1.

Location/Qualifiers

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1015YNO6"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match

Best Local Similarity

43.9%; Score 1094.4; DB 9; Length 1201;

95.9%; Pred. No. 2.6e-188;

	Matches 1130;	Conservative 30;	Mismatches 14;	Indels 4;	Gaps 4;
1295	Y	CACCACATGTTGGTCGAAAGCGGCCGACCACTGACTTTGTGACTTAGCGGCTGTGTTGCC			1354
1177	b	CCCCCCAMWTKTGGYSAVSCGSCMCCAMTAAATTTKTAHTTTAGGCGGCTGTGTTSCC			1118
1355	Y	TATGTAGAGAACCGCTTACACCCCACTCCCC-GTACAGTGGCAGACAGGCTTATC-GAG			1412
1117	b	TAKAAPAPAAACMSYTCGCCCCCACTCCCSGTACAGKGGHACAGGCTTTWCSGAG			1058
1413	Y	AATAGGAAACCTTTAAACCCCGGTGAT-CGGGACATCCCAACGCATGCTCCTGGAGCTC			1471
1057	b	AATAGGAAACCTTTAAACCCCGGTGATCCGGGACATCCCAACGCATGCTCCTGGAGCTM			998
1472	Y	ACAGCCTTCTGTGGTGCATTTCTGAAACAGAGGGGTGGATCCCTCAACCAAGAAGATG			1531
997	b	ACAGCCTTCTGTGGTGCATTTCTGAAACAGAGGGGTGGATCCCTCAACCAAGAAGATG			938
1532	Y	TTTATGCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGAGAAATTAAGTGGAGTCC			1591
937	b	TTTATGCTTCAAGTGACCTGTACTGCTTGGGGACTATTGGAGAAATTAAGTGGAGTCC			878
1592	Y	TACTTGTTTAAAAAATATGTATCTAAGAAATGTTTCTAGGGCACTCTGGGAACTATAAAGG			1651
877	b	TACTTGTTTAAAAAATATGTATCTAAGAAATGTTTCTAGGGCACTCTGGGAACTATAAAGG			818
1652	Y	CAGGTATTTGGGGCCCTCTCTTCAGGAATCTTCTCGAAGACATGGCCCCAGTCCGAAGGCC			1711
817	b	CAGGTATTTGGGGCCCTCTCTTCAGGAATCTTCTCGAAGACATGGCCCCAGTCCGAAGGCC			758
1712	Y	CAGGATGGCTTTTGTCTCGCGCCCGCTGGGGTAGGAGGACAGAGAGACAGGGAGAGTCAG			1771
757	b	CAGGATGGCTTTTGTCTCGCGCCCGCTGGGGTAGGAGGACAGAGAGACAGGGAGAGTCAG			698
1772	Y	CCTCCACATTCAGAGGCATCACAAAGTAATGGACCAATCTTCCGATGACTCGAGAAATA			1831
697	b	CCTCCACATTCAGAGGCATCACAAAGTAATGGACCAATCTTCCGATGACTCGAGAAATA			638
1832	Y	GTGTTTTGTAGTCTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTTAAAGG			1891
637	b	GTGTTTTGTAGTCTCAACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTCTTTAAAGG			578
1892	Y	CAAGCTTTATTTTCATCTCTCATCTTTGTCTCTCTTAGCNCATGTAAAAAGATAG			1951
577	b	CAAGCTTTATTTTCATCTCTCATCTTTGTCTCTCTTAGCNCATGTAAAAAGATAG			518
1952	Y	TAAATCAGAACAGGAAGGAGTAATGGCTTGTGGGGAGCCCATCCAGGACACTGGGAGC			2011
517	b	TAAATCAGAACAGGAAGGAGTAATGGCTTGTGGGGAGCCCATCCAGGACACTGGGAGC			458
2012	Y	ACATAGAGATTCACCCATGTTCTTCAACTTAGAGTCAATCTCATGCTTTCTTTTATAAT			2071
457	b	ACATAGAGATTCACCCATGTTGTGAACTTAGAGTCAATCTCATGCTTTCTTTTATAAT			398
2072	Y	TCACACATATATGAGAGAAAGATATGTTCTGTGTAAATTTGATACAAATAGCCCCAAA			2131
397	b	TCACACATATATGAGAGAAAGATATGTTCTGTGTAAATTTGATACAAATAGCCCCAAA			338
2132	Y	TATAGTAAGATCTATCTAGNTAATCTATAGATGAATGTTAGAGATGCTATTTCATACAA			2191
337	b	TATAGTAAGATCTATCTAGNTAATCTATAGTGAATGTTAGAGATGCTATTTCATACAA			278
2192	Y	CTGTGGCCATCACTGAGGAAAGAGGCTCAAGCCAGAGACTGGGTGCTCTCCCCGGAGGC			2251
277	b	CTGTGGCCATCACTGAGGAAAGGA-SFCAAGCCAGAGACTGGGTGCTCTCCCCGGAGGC			219
2252	Y	CAAAACCAAGAGGCTTGGCAAAGTCAAGGCTCAGGGAGAGCTCTGCCCTGTGTGACAGCTC			2311
218	b	CAAAACCAAGAGGCTTGGCAAAGTCAAGGCTCAGGGAGAGCTCTGCCCTGTGTGACAGCTC			159
2312	Y	GGTGTGGACACACGCTGCATAGAGCTCTCTTGAATAACAGAGGGGTCTCAAGACATTTCTG			2371
158	b	GGTGTGGACACACGCTGCATAGAGCTCTCTTGAATAACAGAGGGGTCTCAAGACATTTCTG			99

Qy 2372 CCGACCTAATAGCTTCTTTATTTTTTAACTTTTGGGGGAAAAAGTATTTTTTGAA 2433

Db 98 CCTACCTAATAGCTTCTTTATTTTTTAACTTTTGGGGGAAAAAGTATTTTTTGAA 39

Qy 2432 GTTTGTCTTCCAATGTATTTATAAATAGTAAATAAAGT 2469

Db 38 GTTTGTCTTCCAATGTATTTATAAATAGTAAATAAAGT 1

RESULT 3

AL545769

LOCUS

DEFINITION

AL545769 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

Clone CS0D1009YN01 5-PRIME, mRNA sequence.

ACCRSSION

AL545769

VERSION

AL545769.2 GI:31267604

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1. (Bases 1 to 1201)

AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

On Feb 19, 2001 this sequence version replaced gi:12878251.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 4009.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0D1009YN01&cluster=4009.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0D1009CG01QF1.

Location/Qualifiers

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1009YN01"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 43.1%; Score 1075.8; DB 9; Length 1201;

Best Local Similarity 98.7%; Pred. No. 6e-185;

Matches 1099; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

Qy 1 GCGCTGAGGATCAGCCGCTTCCCTCGCTCGGATTCACAGCTTCGCGCGGTGACTGTGCC 60

Db 62 GCGCTGAGGATCAGCCGCTTCCCTCGCTCGGATTCACAGCTTCGCGCGGTGACTGTGCC 121

Qy 61 CCATCCTTGCGCGCCAGCTGCGCAAGCAGCGTGCCCGGTTCAGCGCGTCATCAGCGG 120

Db 122 CCATCCTTGCGCGCCAGCTGCGCAAGCAGCGTGCCCGGTTCAGCGCGTCATCAGCGG 181

Qy 121 GCGGACCCACAGCTCTCGGCGCGTGCCTGACTCTGCTGCTGCTGCTCCGCGGCGCCCG 180

Db 182 GCGGACCCACAGCTCTCGGCGCGTGCCTGACTCTGCTGCTGCTGCTCCGCGGCGCCCG 241

Qy 181 GTGCGCGGCGTGCAGCGAGCTCGGGGGCTTGCGTCCCGTGTGCTGCGCTGCGAGCGCTGC 240

Db 242 GTGCGCGGCGTGCAGCGAGCTCGGGGGCTTGCGTCCCGTGTGCTGCTGCGCTGCGAGCGCTGC 301

Oy		241	GACGCGCGGCACTGAGCCCAAGTGCAGCGACTCCGCCGCGATGTGGCGGAAAGTGTTGGC	300
Db		302	CACGCGCTGCACTGACCAGTGCAGCGCTCCGCCGCGATGTGGCGGAAAGTGTTGGC	360
Oy		301	GAGCCGGGCTGCGCTGCTGCTGAAGTCGTGCGCATGAGCGAAGGCGCACCGTGGCATC	360
Db		361	GA- CCGGCGCTGCGCTGCTGCTGATTAGTGGCATGAGCGAAGGCGCACCGTGGCATC	419
Oy		361	TACACCGAGCGGTGAGGCTCCGGGCGTTGGCTGCGCAGCGCTGCGCCGAGAGGCGGACG	420
Db		420	TACACCGAGCGGTGAGGCTCCGGGCGTTGGCTGCGCAGCGCTGCGCCGAGAGGCGGACG	479
Oy		421	CTGCAGCGCTGCTGAGCGGCGCGGCTTGGCTGCAA CGCTAGTGGCGTCAAGCGGCTG	480
Db		480	CTGCAGCGGCTGCTGAGCGGCGCGGCTTGGCTGCAA CGCTAGTGGCGTCAAGCGGCTG	539
Oy		481	CGCGCTTACTGCTGCTGCAAGCGCGCCAGCTCCAAGAATGCTTAGTGAATCGAGGAAGAC	540
Db		540	CGCGCTTACTGCTGCTGCAAGCGCGCCAGCTCCAAGAATGCTTAGTGAATCGAGGAAGAC	599
Oy		541	CGCAGCGCGGAGTGTGGAGAGCCCGTCCGTCCAGACA GCAACCGGATGCTGATCCC	600
Db		600	CGCAGCGCGGAGTGTGGAGAGCCCGTCCGTCCAGACA GCAACCGGATGCTGATCCC	659
Oy		601	AAGTTCACCCCTCCATTCAAGAATATCATCATCAAGAAAGGCGATGCTTAAGACAGC	660
Db		660	AAGTTCACCCCTCCATTCAAGAATATCATCATCAAGAAAGGCGATGCTTAAGACAGC	719
Oy		661	CAGCGCTCAAAA GTTGACTAGAGTCTCAGAGCAGATA TCCCAAACTTCTCCCGCAG	720
Db		720	CAGCGCTCAAAA GTTGACTAGAGTCTCAGAGCAGATA TCCCAAACTTCTCCCGCAG	779
Oy		721	TCCAAGCGGAGACAGAA TATGTCCTCCGCTAGAGAA TGAAGACACACTGATATAC	780
Db		780	TCCAAGCGGAGACAGAA TATGTCCTCCGCTAGAGAA TGAAGACACACTGATATAC	839
Oy		781	CTGAAGTTCCTCAATGTGTGATGCCAGGGGTGAACAT TTCCCACTGTGACAAAGAG	840
Db		840	CTGAAGTTCCTCAATGTGTGATGCCAGGGGTGAACAT TTCCCACTGTGACAAAGAG	899
Oy		841	GGATTTTAAAGAAAAAGCAGTGTGCGCTTCCAAAGCAGAGAACGGGCGTTCTGTGCG	900
Db		900	GGATTTTAAAGAAAAAGCAGTGTGCGCTTCCAAAGCAGAGAACGGGCGTTCTGTGCG	959
Oy		901	TGTGTGATTAAGTATGAGGCAAGCTTCTCCAGGCTACCA CCAAGGGGAAAGAGAGCTG	960
Db		960	TGTGTGATTAAGTATGAGGCAAGCTTCTCCAGGCTACCA CCAAGGGGAAAGAGAGAGCTG	1019
Oy		961	CACCTCTACAGATGACAGAGCAAGTGAAGCGCTGCGGA AGGTTTAATGAGAGCTCAAT	1020
Db		1020	CACCTCTACAGATGACAGAGCAAGTGAAGCGCTGCGGA AGGTTTAATGAGAGCTCAAT	1079
Oy		1021	ATGCTTAATTTTGCACAAAGACTGSCCAAGGACATGAC CAGAGCTGCTACAGCTCGA	1080
Db		1080	ATGCTTAATTTTGCACAAAGACTGSCCAAGGACATGAC CAGAGCTGCTACAGCTCGA	1139
Oy		1081	TTTATATTCTGTTGTGCTGAGACGATTTTTT	1113
Db		1140	TTTATATTCTGTTGTGCTGAGTATTTTTT	1172

RESULT 4
AL542261 1201 bp mRNA linear EST 12-WAY-2003

LOCUS AL542261 Homo sapiens PLACENTA Homo sapiens cDNA clone CSDBE08YI08

DEFINITION 5-PRIME, mRNA Sequence.

ACCESSION AL542261

VERSION AL542261.2 GI:30547237

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
(bases 1 to 1201)	Li, W.-F., Gruber, C., Jessee, J. and Polyzakis, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	
		On Feb 15, 2001 this sequence version replaced gi:12874131.		
	Contact: Genoscope			
	Genoscope - Centre National de Sequencage			
	BP 191 91006 Evry cedex - France			
	Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr			
	Library was constructed by Life Technologies, a division of			
	Invitrogen. This sequence belongs to sequence cluster 4009.r			
	For more information about this cluster, see			
	http://www.genoscope.cns.fr/			
	cgi-bin/cluster.cgi?seq=CS0DE008BE04QP1&cluster=4009.r.			
	Feng Liang Email : fliang@lifeotech.com URL :			
	http://fulllength.invitrogen.com/Invitrogen Corporation 1600			
	Faraday Avenue Genoscope sequence ID : CS0DE008BE04QP1.			
FEATURES	source	Location/Qualifiers		
		1..1201		
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="CS0DE008Y108"			
	/issue_type="PLACENTA"			
	/clone_id="Homo sapiens PLACENTA"			
	/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed			
	with a NotI-oligo(dT) primer. Five prime and enriched,			
	double-strand cDNA was digested with Not I and cloned into			
	the Not I and EcoRV sites of the pCMVSPORT 6 vector.			
	Library was not normalized."			
ORIGIN				
Query Match	42.6%; Score 1062.6; DB 9; Length 1201;			
Best Local Similarity	96.4%; Pred. No. 1.5e-182;			
Matches 1098; Conservative 17; Mismatches 21; Indels 3; Gaps 3;				
4	CTGAGGATCAAGCCCTTCTGCTGCTGATTCACAGCTTCGGCGCTGATCTGTGGCCCCA	63		
Db	65 CTGAGGATCAAGCCCTTCTGCTGCTGATTCACAGCTTCGGCGCTGATCTGTGGCCCCA	124		
QY	64 TCCCTGCGCGCCACAGCTGCCACAGAGCTCCCGGTTGCAGGCGTATGACAGCGGCG	123		
Db	125 TCCCTGCGCGCCACAGCTGCCACAGAGGTCGCCGGTTGCAGGCGTATGACAGGCGG	184		
QY	124 CGACCCAGCTCTTGAGGCGCGCTGCGCTGACTTGTCTGCTGCTCTCCGCGGCGCGGCTG	183		
Db	185 CGACCCAGCTCTTGAGGCGCGCTGCGCTGACTTGTCTGCTGCTCTCCGCGGCGCGGCTG	244		
QY	184 GCGCGGCGTGGCGGAGAGCTCGGCGGCGGAGTCCCGTGGCGCGTGGCGGAGCGGTCAC	243		
Db	245 GCGCGGCGTGGCGGAGAGCTCGGCGGCGGAGTCCCGTGGCGCGTGGCGGAGCGGTCAC	304		
QY	244 GCGCGTGCATGAGCCACAGTGGCGGCTTCGCGCGCGCTGTGCGGAGAGCTGTGCGCGAG	303		
Db	305 GCGCGTGCATGAGCCACAGTGGCGGCTTCGCGCGCGCTGTGCGGAGAGTGTGCGCGAG	362		
QY	304 CCGGCGCTGCGGCTGCTGCTGACGTGGGCACTGAGCGAGGCGGAGCGGTCGGGATCTAC	363		
Db	363 SCGGGCTGCGGCTGCTGCTGACGTGGGCGCTTGAAGCGAGGCGGAGCGGTCGGGATCTAC	422		
QY	364 ACCGAGCGCTGTGCTCGGCGCTTCGCTGCCAGCGCTTCGCCGAGCGGAGCGGTCGCTG	423		
Db	423 ACCGAGCGCTGTGCTCGGCGCTTCGCTGCCAGCGCTTCGCCGAGCGGAGCGGTCGCTG	482		
QY	424 CAGGCGCTGTGACACGCGCGCGGCGCTTGTGCTCAACGCTATGCGCTGACGCGCTGCGC	483		
Db	483 CAGGCGCTGTGACACGCGCGCGGCGCTTGTGCTCAACGCTATGCGCTGACGCGCTGCGC	542		
QY	484 GCTTACCTGTGCGGAGCGCGCGGAGCTTCAGGAATGTAGTGTGCGGAGGAAGACGCG	543		
Db	543 GCTTACCTGTGCGGAGCGCGCGGAGCTTCAGGAATGTAGTGTGCGGAGGAAGACGCG	602		
QY	544 AGCGCGGAGTGTGAGAGCCCGCTCCGTCTCCACACGACCGGAGTGTGATCTCCAG	603		

603	AGCGCGGCGAGT	TTGGAGAGCCGTC	CGTCTCCAGCAGC	ACCGGGTCTCTGAT	CCCCAAG	662	
604	TTCCACGCCCT	TCCATTCAAAGATAAT	CATCATCAAGAAAGG	GCATGCTAAAGACAG	CCAG	663	
663	TTCCACGCCCT	TCCATTCAAAGATAAT	CATCATCAAGAAAGG	GCATGCTAAAGACAG	CCAG	722	
664	CGCTACAAAG	TGTACTACGAGTCT	CAGAGCAGATAC	CCAGAACTTCTCT	CCGAGTCC	723	
723	CGCTACAAAG	TGTACTACGAGTCT	CAGAGCAGATAC	CCAGAACTTCTCT	CCGAGTCC	782	
724	AAGCGGAGAC	GAGAAATATGTCCT	CGCTAGAGAAATG	GAAGACACACTCAAT	CACTG	783	
783	AAGCGGAGAC	GAGAAATATGTCCT	CGCTAGAGAAATG	GAAGACACACTCAAT	CACTG	842	
784	AAGTTCTCAAT	GTGTGAGTCC	AGGGGTGTACAT	TCCAACTGTGAC	AAAGGGA	843	
843	AAGTTCTCAAT	GTGTGAGTCC	AGGGGTGTACAT	TCCAACTGTGAC	AAAGGGA	902	
844	TTTTATAAGAA	AAAGCAGTGTG	CGCCCTTCCAAGGC	AGAGCGGGCTTCTGT	-GGTG	902	
903	TTTTATAAGAA	AAAGCAGTGTG	CGCCCTTCCAAGGC	AGAGCGGGCTTCTGT	GGGTG	962	
903	TGTGGATAAG	TATGGGCAGCGCT	CTCCAGGCTACAC	CAACGAGGGAAGG	AGGACGTGCA	962	
963	TGTGGATAAG	TATGGGCAGCGCT	CTCCAGGCTACAC	CAACGAGGGAAGG	AGGACGTGCA	1022	
963	CTGCTACAGCA	TGAGAGCAAGTAG	ACGCCCTGCGGCAAG	GTTAATGTGGAGCTCA	AAATAT	1022	
1023	CTGCTACAGCA	TGAGAACCAAGTAG	ACGCCCTGCGGCAAG	GTTAATGTGGAGCTCA	AAATAT	1082	
1023	GCGTTATTTTC	CAAAAGACTGCG	CAAGGACATGAC	CAGCAGCTGGCTAC	AGCCTCGATT	1082	
1083	TCCITATTTT	KWC	CAAAAGATGCT	AAGACATGAC	CMAGARCTGGCTAC	ACSCCGGTT	1142
1083	TATATTTCTG	TTTGTGTGACTG	ATTTTTTTTTTAA	CCAAAGTTT	TAGAAAGAGTTTT	1141	
1143	TATATTTT	TKTTTTGTG	KGAGTGTWTTTT	TTTTTAAACAAA	AWRTTTAGAAAGAGTTT	1201	

RESULT 5					
AL549091/c	AL549091	Homo sapiens	linear	EST 31-MAY-2003	
LOCUS			1164 bp		
DEFINITION	AL549091 Homo sapiens PLACENTA COT 25-NORMALIZED Hmo sapiens CDNA clone CS01051Yt13 3-PRIME. mRNA sequence.				

FEATURES source

ORIGIN	Query Match	Score	DB	Length
	Best Local Similarity	97.5%;	Pred. No. 2.8e-181;	
	Matches 1080;	Conservative 11;	Mismatches 15;	Indels 2; Gaps 2;
Qy	1337	TTAGCGCGTGTTCGCTATGTAGAGACACGCTTCA	CCGCCACCTCCCGTCACAGTGGC	1396
Db	1107	TRWYKGGCGGTGTGCTTATGAGACACACGCTTCA	CCGCCACCTCCCGTCACAGTGGC	1049
Qy	1397	CACAGGCTTTATCGAATAAGGAAAAACCTTTAAAC	CCCGGTCATCC- GGACATCCCAACG	1455
Db	1048	CACAGGTTTATCGAATAAGGAAAAACCTTTAAAC	CCCGGTCATCCCGGACATCCCAACG	989
Qy	1456	CATGCTCTGGAGCTCACAGCCTTCTGTGTGTATTT	CTGAAACAAGCGCGTGGATCCC	1515
Db	988	CATGCTCTGGAGCTCACAGCCTTCTGTGTGTATTT	CTGAAACAAGCGCGTGGATCCC	929
Qy	1516	TCACCAAGAAGAAATGTTATGCTTCAAGTAGACCT	GTACTGCTTGGGACTATTGGAGA	1575
Db	928	TCACCAAGAAGAAATGTTATGCTTCAAGTAGACCT	GTACTGCTTGGGACTATTGGAGA	869
Qy	1576	AAATAAGGTGGAGTCCTACTTGTTTAAAAAATAT	TATCTAAGAATGTTCTAGGGCACTC	1635
Db	868	AAATAAGGTGGAGTCCTACTTGTTTAAAAAATAT	TATCTAAGAATGTTCTAGGGCACTC	809
Qy	1536	TGGGAACCTATAAAGGACGATTTTGGGCGCCTT	CTCTTCAGGAATCTTCTCGAAGCAT	1695
Db	808	TGGGAACCTATAAAGGACGATTTTGGGCGCCTT	CTCTTCAGGAATCTTCTCGAAGCAT	749
Qy	1696	GGCCAGTCGAAGGCCACGATGGCTTTTCTCGGG	CCCGCGTGGGTAGAGGGACAGAG	1755
Db	748	GGCCAGTCGAAGGCCACGATGGCTTTTCTCGGG	CCCGCGTGGGTAGAGGGACAGAG	689
Qy	1756	AGACAGGGAGATCAGCCTCCACATTCAGAGGAT	CTCAAGATTAATGGCAATCTTCG	1815
Db	688	AGACAGGGAGATCAGCCTCCACATTCAGAGGAT	CTCAAGATTAATGGCAATCTTCG	629
Qy	1816	ATGACTCGAATAATAGTGTTTGTAGTTCAACAA	CTCAAGAGAACTTATTTCTGAGG	1875
Db	628	ATGACTCGAATAATAGTGTTTGTAGTTCAACAA	CTCAAGAGAACTTATTTCTGAGG	569
Qy	1876	ATAAGCTCTTTAAAGGCAAAAGCTTTATTTTCA	TCTCTCATCTTTTGTCTCTTAGACA	1935
Db	568	ATAAGCTCTTTAAAGGCAAAAGCTTTATTTTCA	TCTCTCATCTTTTGTCTCTTAGACA	509
Qy	1936	ATGTAAAAAAGAAATAGTAATATCAGAACGAA	AGGAGGATGGCTTCTGGGAGGCCAT	1995
Db	508	ATGTAAAAAAGAAATAGTAATATCAGAACGAA	AGGAGGATGGCTTCTGGGAGGCCAT	449
Qy	1996	CCAGGACACTGGGAGCACATAGAGATTCA	CCCCCATGTTTGTGAACCTTAGAGTCA	2055
Db	448	CCAGGACACTGGGAGCACATAGAGATTCA	CCCCCATGTTTGTGAACCTTAGAGTCA	389
Qy	2056	TGCTTTTCTTTAATTACACATATATGACAGAA	GAGATATGTTCTTTGTTAACTTGTAT	2115
Db	388	TGCTTTTCTTTAATTACACATATATGACAGAA	GAGATATGTTCTTTGTTAACTTGTAT	329
Qy	2116	ACAACATAGCCCCAAATATAGTAAGATCTATCT	ATAGATAATCTCTAGATGAATGTTAGAG	2175
Db	328	ACAACATAGCCCCAAATATAGTAAGATCTATCT	ATAGATAATCTCTAGATGAATGTTAGAG	269
Qy	2176	ATGCTATTTGATACAACTGTGGCCATGACTGAG	AAAGAGGCTCAAGCCAGAGACTGGG	2235
Db	268	ATGCTATTTGATACAACTGTGGCCATGACTGAG	AAAGAGGCTCAAGCCAGAGACTGGG	209

QY 2236 CTGCTCTCCCGAGGSCCAACCAAGAGTCTGCAAGTCAAGGAGAGCTGTG 2295
 DB 208 CTGCTCTCCCGAGGSCCAACCAAGAGTCTGCAAGTCAAGGAGAGCTGTG 149
 QY 2296 CCTGTCTGACAGCTTGGTGTGACACAGCTGCTCATAGAGCTCTCTGAAAACAGAGG 2355
 DB 148 CCTGTCTGACAGCTTGGTGTGACACAGCTGCTCATAGAGCTCTCTGAAAACAGAGG 89
 QY 2356 GTCTCAAGACATTTCTCTACTACTATAGCTTTTCTTTATTTTAACTTTTGGGGGGA 2415
 DB 88 GTCTCAAGACATTTCTCTACTACTATAGCTTTTCTTTATTTTAACTTTTGGGGGGA 29
 QY 2416 AAAGTATTTTGAAGAGTTTGTCTTGA 2443
 DB 28 AAAGTATTTTGAAGAGTTTGTCTTGA 1

RESULT 6

BX366676/c 1201 bp mRNA linear EST 08-MAY-2003
 LOCUS BX366676 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
 DEFINITION clone CS0D1025YM22 3-PRIME, mRNA sequence.
 ACCESSION BX366676
 VERSION BX366676.1 GI:30444830
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
 COMMENT Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 4009.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0A1025BGI1NP1&cluster=4009.r. Contact :
 Feng Liang Email : fliang@life.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0A1025BGI1NP1.

FEATURES

Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1025YM22"
 /cruise_type="PLACENTA COT 25-NORMALIZED"
 /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="First strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 41.6%; Score 1038.2; DB 13; Length 1201;
 Best local Similarity 97.4%; Pred. No. 4e-178;
 Matches 1067; Conservative 6; Mismatches 20; Indels 2; Gaps 2;
 QY 1376 CCCCACTCCCGGACAGTGGCGACAGGCTTTATCGAGATAGAAAACCTTTAAACCCCG 1435
 DB 1093 MCCCCACCCCGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1035
 QY 1436 GTATCCGAGACATCCCAAGCATGCTCTGAGAGCTCAAGCCCTTGTGTGATCAATTTCT 1495
 DB 1034 GTATCCGAGACATCCCAAGCATGCTCTGAGAGCTCAAGCCCTTGTGTGATCAATTTCT 975
 QY 1496 GAAACAAAGGGGCTGATCCTCAACCAAGAGATGTTATGCTTCAAGTACCTGTAC 1555

DB 974 GAAACAAAGGGGCTGATCCTCAACCAAGAGATGTTATGCTTCAAGTACCTGTAC 915
 QY 1556 TGCTGGGAGACTATGGAGAAATTAAGTGAAGTCTTACTGTTTAAAAATATATATCT 1615
 DB 914 TGCTT-GGACATTTGGAGAAATTAAGTGAAGTCTTACTGTTTAAAAATATATATCT 856
 QY 1616 AAGATGTTCTAGGGCACTCTGGGAACTATTAAGGAGAGTATTTGGGGCCCTCTCTTC 1675
 DB 855 AAGATGTTCTAGGGCACTCTGGGAACTATTAAGGAGAGTATTTGGGGCCCTCTCTTC 796
 QY 1676 AAGATGTTCTAGGCAATGGCCAGTGGAGGCCAGATGGCTTTTGTGCGGGCCCC 1735
 DB 795 AAGATGTTCTAGGCAATGGCCAGTGGAGGCCAGATGGCTTTTGTGCGGGCCCC 736
 QY 1736 GTGGGATGAGAGGAGACAGAGACAGAGAGAGTCAAGCTTCAAGAGCATACAA 1795
 DB 735 GTGGGATGAGAGGAGACAGAGACAGAGAGAGTCAAGCTTCAAGAGCATACAA 676
 QY 1796 GTAAAGGCAATTTCTGGATGAGTGAAGAAATAGTGTGTTGTAGTTCACACTCA 1855
 DB 675 GTAAAGGCAATTTCTGGATGAGTGAAGAAATAGTGTGTTGTAGTTCACACTCA 616
 QY 1856 GACGAGCTTATTTCTGAGATAGCTTTTAAAGCAAGCTTATTTTATCTCTCAT 1915
 DB 615 GACGAGCTTATTTCTGAGATAGCTTTTAAAGCAAGCTTATTTTATCTCTCAT 556
 QY 1916 CTTTGTCTCTCTTACAGCAATGTAATAAGAAATATATATATAGAAACAGAGAGGAA 1975
 DB 555 CTTTGTCTCTCTTACAGCAATGTAATAAGAAATATATATATAGAAACAGAGAGGAA 496
 QY 1976 TGAGTTGCTGGGAGGCCATTCAGACACTGGGAGACATAGAGATTCACCATGTTGT 2035
 DB 495 TGAGTTGCTGGGAGGCCATTCAGACACTGGGAGACATAGAGATTCACCATGTTGT 436
 QY 2036 TGAATAGTATCTATCTATCTATCTTTTCTTATATATGACATATATAGAGAGAT 2095
 DB 435 TGAATAGTATCTATCTATCTATCTTTTCTTATATATGACATATATAGAGAGAT 376
 QY 2096 TGTTCTTGTATATGATGTATACAAATAGCCCAATATATAGATCTATAGATTA 2155
 DB 375 TGTTCTTGTATATGATGTATACAAATAGCCCAATATATAGATCTATAGATTA 316
 QY 2156 TCTAGATGAATGTTTGAAGATGCTATTTGATATCACTGGCCATGACTGAGAGAAAG 2215
 DB 315 TCTAGATGAATGTTTGAAGATGCTATTTGATATCACTGGCCATGACTGAGAGAAAG 256
 QY 2216 GCTACGCCCAAGAGACTGGGCTGCTCCCGAGGCAACCCCAAGAGGCTGAGAAAG 2275
 DB 255 GCTACGCCCAAGAGACTGGGCTGCTCCCGAGGCAACCCCAAGAGGCTGAGAAAG 196
 QY 2276 TCAGGCTCAGGAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2335
 DB 195 TCAGGCTCAGGAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 136
 QY 2336 CTCTCTTGAAGAGAGGAGTCTCAAGACATTTCTGCTTATAGCTTTCTTTAT 2395
 DB 135 CTCTCTTGAAGAGAGGAGTCTCAAGACATTTCTGCTTATAGCTTTCTTTAT 76
 QY 2396 TTTTAACTTTTGGGGGAGAAAGATTTTGAAGATTGCTTGAATGATTTTAA 2455
 DB 75 TTTTAACTTTTGGGGGAGAAAGATTTTGAAGATTGCTTGAATGATTTTAA 16
 QY 2456 ATAGTAATTAAGTT 2470
 DB 15 WTAGTAATTAAGTT 1

RESULT 7

AL551293 1106 bp mRNA linear EST 31-MAY-2003
 LOCUS AL551293 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
 DEFINITION clone CS0D1041Y019 5-PRIME, mRNA sequence.

ACCESSION AL551293
 VERSION AL551293.2 GI:31273109
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 1106)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12889101.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 4009.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1041AH10QPI&cluster=4009.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1041AH10QPI.
 FEATURES
 Location/Qualifiers
 1..1106
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1041Y019"
 /tissue="types=PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoRV
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Query Match 41.5%; Score 1035.6; DB 9; Length 1106;
 Best Local Similarity 99.4%; Pred. No. 1.2e-177;
 Matches 1038; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 2y 13 AGCCGCTTCTGCTGATTCACAGCTTGGCGCGTGTACTGTCGCCCATCCCTGCGC 72
 Db 63 ATCCGCTTCTGCTGATTCACAGCTTGGCGCGTGTACTGTCGCCCATCCCTGCGC 122
 Qy 73 GCCCAGCTGCAAGCAGCGTGGCGCGTGTACTGTCGCCCATCCCTGCGC 132
 Db 123 GCCCAGCTGCAAGCAGCGTGGCGCGTGTACTGTCGCCCATCCCTGCGC 182
 Qy 133 CTCTGGCGCGTGGCGTGTACTGTCGCCCATCCCTGCGC 192
 Db 183 CTCTGGCGCGTGGCGTGTACTGTCGCCCATCCCTGCGC 242
 Qy 193 GGCGCAGCTGGCGCGTGGCGTGTACTGTCGCCCATCCCTGCGC 252
 Db 243 GGCGCAGCTGGCGCGTGGCGTGTACTGTCGCCCATCCCTGCGC 302
 Qy 253 CTGCGCCAGTGGCGCGTGGCGTGTACTGTCGCCCATCCCTGCGC 312
 Db 303 CTGCGCCAGTGGCGCGTGGCGTGTACTGTCGCCCATCCCTGCGC 362
 Qy 313 GGCGCAGCTGGCGCGTGGCGTGTACTGTCGCCCATCCCTGCGC 372
 Db 363 GGCGCAGCTGGCGCGTGGCGTGTACTGTCGCCCATCCCTGCGC 422
 Qy 373 TGTGGCTCCGCGCTTGGCGTGTACTGTCGCCCATCCCTGCGC 432
 Db 423 TGTGGCTCCGCGCTTGGCGTGTACTGTCGCCCATCCCTGCGC 482
 Qy 433 CTGACCGCGCGCGCTTGGCGTGTACTGTCGCCCATCCCTGCGC 492
 Db 483 CTGACCGCGCGCGCTTGGCGTGTACTGTCGCCCATCCCTGCGC 542

QY 1518 AACCAAGAAGATGTTATGCTTCAAGTACCTGTACTGCTGGGAGACTATGGAGAA 1577
 Db 925 AACCAAGAAGATGTTATGCTTCAAGTACCTGTACTGCTGGGAGACTATGGAGAA 866
 QY 1578 ATAAAGTGGAGTCTTACTGTTTAAATAATGATCTAAGATGTTCTAGGGCACTCTG 1637
 Db 865 ATAAAGTGGAGTCTTACTGTTTAAATAATGATCTAAGATGTTCTAGGGCACTCTG 806
 QY 1538 GGAACCTATAAGGACGATATTTGGGAGCCCTCTCTCAAGAACTCTCTGAAGACATGG 1697
 Db 805 GGAACCTATAAGGACGATATTTGGGAGCCCTCTCTCAAGAACTCTCTGAAGACATGG 746
 QY 1698 CCCAGTCGAAGGCCAGAGATGGCTTTGCTGGGAGCCCTGGGGTAGAGGACAGAGAG 1757
 Db 745 CCCAGTCGAAGGCCAGAGATGGCTTTGCTGGGAGCCCTGGGGTAGAGGACAGAGAG 686
 QY 1758 ACAGGAGAGTCAAGCTCCACATTCAGAGGATCAGAGTAATGACAAATCTTGGAT 1817
 Db 685 ACAGGAGAGTCAAGCTCCACATTCAGAGGATCAGAGTAATGACAAATCTTGGAT 626
 QY 1818 GACTGCAGAAAATAGTGTGTTGATGTTCAACTCAAGACGAAGCTTATTTCTGAGGAT 1877
 Db 625 GACTGCAGAAAATAGTGTGTTGATGTTCAACTCAAGACGAAGCTTATTTCTGAGGAT 566
 QY 1878 AAGCTCTTTAAGGCAAAAGCTTTATTTTCACTCTCACTCTTCTCTTGGACAAAT 1937
 Db 565 AAGCTCTTTAAGGCAAAAGCTTTATTTTCACTCTCTCACTCTTCTCTTGGACAAAT 506
 QY 1938 GTAAAAAAGATAGTAATATCAGAAACAGAAAGAGATGGCTTCTGGGAGGCCATCC 1997
 Db 505 GTAAAAAAGATAGTAATATCAGAAACAGAAAGAGATGGCTTCTGGGAGGCCATCC 446
 QY 1998 AGGACACTGGAGACATAGAGATTCACCCATGTTTGTGAACCTTAGAGTCTCTGATG 2057
 Db 445 AGGACACTGGAGACATAGAGATTCACCCATGTTTGTGAACCTTAGAGTCTCTGATG 386
 QY 2058 CTTTCTTTTATATTCACACATATATGAGAGAAATATGTTCTTTTAACTATGTATAC 2117
 Db 385 CTTTCTTTTATATTCACACATATATGAGAGAAATATGTTCTTTTAACTATGTATAC 326
 QY 2118 AACATAGCCCAATATATGTAAGTCTTACTATGATATCTTAAATGTAATGTAAGAT 2177
 Db 325 AACATAGCCCAATATATGTAAGTCTTACTATGATATCTTAAATGTAATGTAAGAT 266
 QY 2178 GCTATTGATACACTGTGGCCATGACTGAGAAAGAGCTCAGGCCAGAGACTGGGCT 2237
 Db 265 GCTATTGATACACTGTGGCCATGACTGAGAAAGAGCTCAGGCCAGAGACTGGGCT 206
 QY 2238 GCTCTCCCGAGGCCAAACCAAGAGGTCTGGCAAGTCAAGGCTCAGGGAGACTGGCC 2297
 Db 205 GCTCTCCCGAGGCCAAACCAAGAGGTCTGGCAAGTCAAGGCTCAGGGAGACTGGCC 146
 QY 2298 CTGCTGAGAGCCTGGTGGGACACAGCTCATAGAGCTCTCTGTAAGAAACAGAGGGT 2357
 Db 145 CTGCTGAGAGCCTGGTGGGACACAGCTCATAGAGCTCTCTGTAAGAAACAGAGGGT 86
 QY 2358 CTCAAGACATTTCTGCTACTTATGCTTTTCTTTATTTTAACTTTTGGGGGAAA 2417
 Db 85 CTCAAGACATTTCTGCTACTTATGCTTTTCTTTATTTTAACTTTTGGGGGAAA 26
 QY 2418 AGTATTTTGAAGATTTGCTGTCG 2442
 Db 25 AGTATTTTGAAGATTTGCTGTCG 1

RESULT 10
 AL553323/c 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL553323 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1075YA18 3-PRIME, mRNA sequence.
 ACCESSION AL553323
 VERSION AL553323.2 GI:31275137

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12893051.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 4009.r for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1075BA09NPLcluster=4009.r. Contact :
 Feng Liang Email: fliang@life.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1075BA09NPL.
 Location/Qualifiers
 source
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1075YA18"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 41.2%; Score 1027.4; DB 9; Length 1201;
 Best Local Similarity 94.7%; Pred. No. 3.7e-176;
 Matches 1064; Conservative 16; Mismatches 41; Indels 2; Gaps 2;
 1345 CTGTGTGCTTATGATGAGAAACAGCTTACACCCCATCCCGGTACAGTGCACAGGCT 1404
 Db 1122 CTTTGGGATGKKTCTTATGAGACAGCTCMCCACCCCGGTACAGGAGACAGG 1063
 QY 1405 TTATCGAAGATAGAAAACCTTTAAACCCCGGTATCCGAGATCCCAACGATCTCT 1464
 Db 1062 TTATCGAAGATAGAAAACCTTTAAACCCCGGTATCCGAGATCCCAACGATCTCT 1004
 QY 1465 GGAAGTCAAGGCTTGTGTGATTTCTGAAACAGAGGGGTGATCCCT-CAACCA 1523
 Db 1003 GGAAGTCAAGGCTTGTGTGATTTCTGAAACAGAGGGGTGATCCCT-CAACCA 944
 QY 1524 GAAGATGTTTATGCTTCAAGTGAACCTGATGCTTGGGACTATTTGGAGAAATAAG 1583
 Db 943 GAAGATGTTTATGCTTCAAGTGAACCTGATGCTTGGGACTATTTGGAGAAATAAG 884
 QY 1584 TGAAGTCCACTGTTTAAATAATGATCTAAGATGTTCTAGGGCACTCTGGAAACC 1643
 Db 883 TGAAGTCCACTGTTTAAATAATGATCTAAGATGTTCTAGGGCACTCTGGAAACC 824
 QY 1644 TATAAAGGAGATATTTGGGAGCCCTCTCTTCAAGATCTTCTGAAGCATGGCCAGT 1703
 Db 823 TATAAAGGAGATATTTGGGAGCCCTCTCTTCAAGATCTTCTGAAGCATGGCCAGT 764
 QY 1704 CGAAGGCCAGAGATGCTTTTGTCTGGGAGCCCGGTGGGAGAGAGAGAGAGAGAG 1763
 Db 763 CGAAGGCCAGAGATGCTTTTGTCTGGGAGCCCGGTGGGAGAGAGAGAGAGAGAG 704
 QY 1764 AGAGTCAAGCTCACAATTCAGAGGATCAACAAGTATGACAAATTTCTGGATGACTGC 1823
 Db 703 AGAGTCAAGCTCACAATTCAGAGGATCAACAAGTATGACAAATTTCTGGATGACTGC 644
 QY 1824 AGAAATAGTGTGTTGATGTTCAACAACCTCAAGAGAGAGAGAGAGAGAGAGAG 1883

```

Db 643 AGAAAAAGTGTGTTTGTAGTTCACAACTCAAGACGAAGCTTATTTCTGAGGATAAGCTC 584
2y TTTAAAGGCAAGCTTTATTTCTATCTCTCATCTTTGTCTCTTGTAGACATGTAATAA 1943
3b TTTAAAGGCAAGCTTTATTTCTATCTCTCATCTTTGTCTCTTGTAGACATGTAATAA 524
1944 AAGAAATAGTATATCAGAACAGGAAGAGGAATGGCTTGTGGGAGCCCATCCAGGACA 2003
523 AAGAAATAGTATATCAGAACAGGAAGAGGAATGGCTTGTGGGAGCCCATCCAGGACA 464
2004 CTGGAGACATAGAGATTACCCATGTTTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2063
463 CTGGAGACATAGAGATTACCCATGTTTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 404
2064 TTTTATAATTCACATATATGCGAGAGAGATATGTTCTTCTTAACTATGTTATACACATA 2123
403 TTTTATAATTCACATATATGCGAGAGAGATATGTTCTTCTTAACTATGTTATACACATA 344
2124 GCCCAATATAGTAAGATCTATATCTAGTAATCTAGATGAATGTTAGAGATGCTATT 2183
343 GCCCAATATAGTAAGATCTATATCTAGTAATCTAGATGAATGTTAGAGATGCTATA 284
2184 TGATACAACTGTGCGCATGACTGAGGAGAAAGAGCTCACGCCAGAGACTGGGCTGCTC 2243
283 TGATACAACTGTGCGCATGACTGAGGAGAAAGAGCTCACGCCAGAGACTGGGCTGCTC 224
2244 CCGAGAGCCAAACCAAGAGGCTGTGCAAGTCTGAGGAGAGCTCAGGAGAGCTGCTGCTG 2303
223 CCGAGAGCCAAACCAAGAGGCTGTGCAAGTCTGAGGAGAGCTCAGGAGAGCTGCTGCTG 164
2304 CAGACCTCGGTGTGACACACGCTGCATAGAGCTCTCTTGAAGAGAGAGGCTCTCAAG 2363
163 CAGACCTCGGTGTGACACACGCTGCATAGAGCTCTCTTGAAGAGAGAGGCTCTCAAG 104
2364 ACATTCGCTTACCTATAGCTTTCTTATTTTAACTTTTGGGGGAAAAAGTATT 2423
103 ACATTCGCTTACCTATAGCTTTCTTATTTTAACTTTTGGGGGAAAAAGTATT 44
2424 TTTGAGAGTTTGTCTGCAATGATTATTAATAAGTAATAA 2466
43 TTTGAGAGTTTGTCTGCAATGATTATTAATAAGTAATAA 1

```

```

RESULT 11
AL575300/c 1182 bp mRNA linear EST 01-JUN-2003
LOCUS AL575300 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI061YB17 3-PRIME, mRNA sequence.
ACCESSION AL575300
VERSION AL575300.2 GI:31313608
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1182)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12936333.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4009.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI061CA09NPI&cluster=4009.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI061CA09NPI.

```

```

FEATURES
source
Location/Qualifiers
1..1182
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI061YB17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 41.2%; Score 1026.6; DB 9; Length 1182;
Best Local Similarity 96.4%; Pred. No. 5.1e-176;
Matches 1036; Conservative 21; Mismatches 16; Indels 2; Gaps 1;

QY 1372 TCACCCCCACATCCCGTACAGTGGCGACAGGCTTTATCGAGAAATAGGAAAACCTTTAAAC 1431
Db 1073 KYTCCCCCCCACCCCKTACATTCGBACRAGYTTTATCKAGAWRK--AAACCTTTAAAC 1016
QY 1432 CCGGTCTATCCGGACATCCCAACGATCTCTCTGGAGCTCACAGCCTTCTGTGTGTCAT 1491
Db 1015 CCGGTCTATCCGGACATCCCAACGATCTCTCTGGAGCTCACAGCCTTCTGTGTGTCAT 956
QY 1492 TTCTGAACAAAGGGGCTGATCCCTCAACCAAGAGATGTTTATGCTTCAAGTGACCT 1551
Db 955 TTCTGAACAAAGGGGCTGATCCCTCAACCAAGAGATGTTTATGCTTCAAGTGACCT 896
QY 1552 GTACTGCTTGGGACTATTGGAGAAATAAGGTGGAGTCTTACTTTTAAAAAATATGT 1611
Db 895 GTACTGCTTGGGACTATTGGAGAAATAAGGTGGAGTCTTACTTTTAAAAAATATGT 836
QY 1612 ATCTAAGATGTTCTAGGGCACTCTGGGAACCTATAAGGAGGATTTTCGGGCCCTCT 1671
Db 835 ATCTAAGATGTTCTAGGGCACTCTGGGAACCTATAAGGAGGATTTTCGGGCCCTCT 776
QY 1672 CTTCAAGGATCTTCTGGAAGACATGGCCCACTCGAAGCCCAAGGATGGCTTTTCTCGG 1731
Db 775 CTTCAAGGATCTTCTGGAAGACATGGCCCACTCGAAGCCCAAGGATGGCTTTTCTCGG 716
QY 1732 CCCCCTGGGTAGGAGGACAGAGACAGAGAGAGTCCAGCTCCACATTCAGAGGATC 1791
Db 715 CCCCCTGGGTAGGAGGACAGAGACAGAGAGAGTCCAGCTCCACATTCAGAGGATC 656
QY 1792 ACAAGTAATGGCAACAATCTCTCGATGACTCGAAGAAATAGTGTGTTGTAGTTCACAAAC 1851
Db 655 ACAAGTAATGGCAACAATCTCTCGATGACTCGAAGAAATAGTGTGTTGTAGTTCACAAAC 596
QY 1852 TCAGACGAAGCTTATTTCTGAGGATAGCTCTTTAAGGCAAGCTTTATTTTCATCTC 1911
Db 595 TCAGACGAAGCTTATTTCTGAGGATAGCTCTTTAAGGCAAGCTTTATTTTCATCTC 536
QY 1912 TCATCTTTTGTCTCTCTTAGCACATGTAAAAAAGAAATAGTAATATCAGAACAGGAAGA 1971
Db 535 TCATCTTTTGTCTCTCTTAGCACATGTAAAAAAGAAATAGTAATATCAGAACAGGAAGA 476
QY 1972 GGAATGGCTTGTGGGAGCCCATCCAGACACTGGGAGGACATAGAGATTCACCCATGT 2031
Db 475 GGAATGGCTTGTGGGAGCCCATCCAGACACTGGGAGGACATAGAGATTCACCCATGT 416
QY 2032 TTGTTGAATCTAGAGTCAATCTCATGCTTTTCTTTTAAATTCACACATATATGAGAGAA 2091
Db 415 TTGTTGAATCTAGAGTCAATCTCATGCTTTTCTTTTAAATTCACACATATATGAGAGAA 356
QY 2092 GATATGTTCTGTTAACTATGTTATACAACTAGGCCCAATATAGTAAGATCTATCTAG 2151
Db 355 GATATGTTCTGTTAACTATGTTATACAACTAGGCCCAATATAGTAAGATCTATCTAG 296
QY 2152 ATAACTCTAGATGAATCTGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAA 2211
Db 295 ATAACTCTAGATGAATCTGAGATGCTATTGATACAACTGTGGCCATGACTGAGGAA 236

```


clone CSOD1074YB01 3-PRIME, mRNA sequence.

ACCESSION BX402691
VERSION BX402691.1 GI:30618891

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1201)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 4009.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS1A10192D01NP1&cluster=4009.r. Contact :

Feng Liang Email : fliang@lifetech.com URL : Corporation 1600

http://fulllength.invitrogen.com/ invitrogen

Faraday Avenue Genoscope sequence ID : CS1A10192D01NP1.

Location/Qualifiers

1. 1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="CSOD1074YB01"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

Query Match 40.6%; Score 1012.2; DB 13; Length 1201;

Best Local Similarity 94.1%; Pred. No. 2.1e-173;

Matches 1082; Conservative 17; Mismatches 45; Indels 6; Gaps 5;

1316 GCCGACCACTGCTTGACCTTAGCGGCTGCTGCTATGAGACACGCTTCAC 1375

1145 GTCGAGCGCCGCAATATATATATATATATATATATATATATATATAT 1086

1376 CCCCACTCCCGTACAGTGCACAGGCTTTATCAGAAATAGGAAACCTTTAAACCCCG 1435

1085 CCCCACTCCCGTACAGTGCACAGGCTTTATCAGAAATAGGAAACCTTTAAACCCCG 1030

1436 GTCATCGGACATCCACGCTATGCTGAGCTCAGGCTTCTGCTGCTATTTCT 1495

1029 GTCATCGGACATCCACGCTATGCTGAGCTCAGGCTTCTGCTGCTATTTCT 970

1496 GAAACAAGGGGTGGATCCCTCAACC-AAGAAAGATGTTATGCTTCAAGTGACCTGTA 1554

969 GAAACAAGGGGTGGATCCCTCAACC-AAGAAAGATGTTATGCTTCAAGTGACCTGTA 910

1555 CTGCTGGGACTATGAGAAATAGTGGAGTCTCTTGTAAATAATGTATC 1614

909 CTGCTGGGACTATGAGAAATAGTGGAGTCTCTTGTAAATAATGTATC 850

1615 TAAGAAATGTTAGGGACTCTGGGAACTATAAGGAGGATTTTCGGCCCTCTCTT 1674

849 TAAGAAATGTTAGGGACTCTGGGAACTATAAGGAGGATTTTCGGCCCTCTCTT 790

1675 CAGGAATCTTCTGAGACATGCGCCAGTGAAGCCAGGATGGCTTTTGTGCGGCC 1734

789 CAGGAATCTTCTGAGACATGCGCCAGTGAAGCCAGGATGGCTTTTGTGCGGCC 730

1735 CGTGGGTAGAGGACAGAGACAGGAGGAGTCCAGCTCCATTCAGAGGATCACA 1794

729 CGTGGGTAGAGGACAGAGACAGGAGGAGTCCAGCTCCATTCAGAGGATCACA 670

ORIGIN

1795 AGTAATGCCACAATTTCTTGGATGACATGCGAATAAATAGTGTGTTAGTCAACAATCA 1854

669 AGTAATGCCACAATTTCTTGGATGACATGCGAATAAATAGTGTGTTAGTCAACAATCA 610

1855 AGACGAAGCTATTCTTGGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCTCA 1914

609 AGACGAAGCTATTCTTGGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCTCA 550

1915 TCTTTTTCCTCTTCTTGGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCTCA 1974

549 TCTTTTTCCTCTTCTTGGAGGATAAGCTCTTTAAAGGCAAGCTTTATTTTCATCTCTCA 490

1975 ATGGCTTCTCTGGGAGCCCATCCAGGACATGCGGAGCAGACATAGAGATTCCACCATGTTTG 2034

489 ATGGCTTCTCTGGGAGCCCATCCAGGACATGCGGAGCAGACATAGAGATTCCACCATGTTTG 430

2035 TTGAACCTTAGAGTCAATCTCATGCTTTTCTTTTAAATTCACACATATATGAGAGAGAT 2094

429 TTGAACCTTAGAGTCAATCTCATGCTTTTCTTTTAAATTCACACATATATGAGAGAGAT 370

2095 ATGTTTCTTTTAAACATGTTATACACATAGCCCAATATATAGTAAATCTATCTAGATA 2154

369 ATGTTTCTTTTAAACATGTTATACACATAGCCCAATATATAGTAAATCTATCTAGATA 310

2155 ATCTAGATGAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGG 2214

309 ATCTAGATGAAATGTTAGAGATGCTATTTGATACAACTGTGGCCATGACTGAGGAAAGG 250

2215 AGCTCAGCCCGAGAGACTGGCTGCTCTCCGGAGGCCAACCAGAGAGCTCTGGCAAA 2274

249 RG-TSACGCCCGAGAGACTGGGCGGCTCTCCGGAGGCCAACCAGAGAGCTCTGGCAAA 191

2275 GTCAGGCTCAGGAGACACTGCTCCCTGCTGCGAGACCTCGGTGGACACACGCTGCATAGA 2334

190 GTCAGGCTCAGGAGACACTGCTCCCTGCTGCGAGACCTCGGTGGACACACGCTGCATAGA 131

2335 GCTCTCTTGAACAGAGAGGCTCTCAAGACATCTGCTACCTATTAGCTTTCTTTAT 2394

130 GCTCTCTTGAACAGAGAGGCTCTCAAGACATCTGCTACCTATTAGCTTTCTTTAT 71

2395 TTTTAACTTTTGGGGGAAAAGTATTTTGGAGAGTTTGTCTTGAATGTATTATA 2454

70 TTTTAACTTTTGGGGGAAAAGTATTTTGGAGAGTTTGTCTTGAATGTATTATTWN 11

2455 AATAGTAAAT 2464

10 AATAGTAAAK 1

RESULT 14

LOCUS BX377586

DEFINITION BX377586 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CSOD1008YF01 5-PRIME, mRNA sequence.

ACCESSION BX377586

VERSION BX377586.1 GI:30450584

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1183)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 4009.r For

more information about this cluster, see

http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSOD1008CC01Q1P1&cluster=4009.r. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSOD1008CC01Q1P1.

FEATURES

Source

Location/Qualifiers
 1..1183
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSOD1008YF01"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /note="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 40.3%; Score 1004.6; DB 13; Length 1183;
 Best Local Similarity 97.6%; Pred. No. 5e-172; Indels 7; Gaps 7;
 Matches 1084; Conservative 8; Mismatches 12;

14 GCCGCTTCTGCTGATTCACAGCTTCGCGCTGATGTCGCCCATCTCTGCGCG 73
 48 GCGGCTTCTGCTGATTCACAGCTTCGCGCTGATGTCGCCCATCTCTGCGCG 107

74 CCCAGCTGCCAAGAGAGCTGCGCGCTGATGTCGCCCATCTCTGCGCG 133
 108 CCCAGCTGCCAAGAGAGCTGCGCGCTGATGTCGCCCATCTCTGCGCG 167

134 TCTGGGCGCGCTGCTGATGTCGCTGCTGCGCGCGCGCGCGCGCGCGCTG 193
 168 TCTGGGCGCGCTGCTGATGTCGCTGCTGCGCGCGCGCGCGCGCGCGCTG 227

194 GCGGAGCTCGGCGCGCTGCGCGCTGCTGCTGCGCGCGCGCGCGCGCTG 253
 228 GCGGAGCTCGGCGCGCTGCGCGCTGCTGCTGCGCGCGCGCGCGCGCTG 287

254 TGGCCAGTGCAGCGCTGCGCGCGCTGCTGCTGCGCGCGCGCGCGCGCTG 313
 288 TGGCCAGTGCAGCGCTGCGCGCGCTGCTGCTGCGCGCGCGCGCGCGCTG 345

314 GCTGCTGCTGAGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCGCTG 373
 346 GCTGCTGCTGAGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCGCTG 405

374 GTGGCTCGGCGCTGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCTG 433
 406 GTGGCTCGGCGCTGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCTG 465

434 TGGAGCGCGCGCGCTGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCTG 493
 466 TGGAGCGCGCGCGCTGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCTG 525

494 TGGAGCGCGCGCGCTGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCTG 553
 526 TGGAGCGCGCGCGCTGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCTG 585

554 GTGGAGAGCGCGCTGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCTG 613
 586 GTGGAGAGCGCGCTGCTGCGCGCTGCGCGCGCTGCTGCTGCGCGCGCTG 645

614 TCCATTCAAAGATATCATCAAGAAAGGCGATGCAAGAGAGCGCGCTGCAAG 673
 646 TCCATTCAAAGATATCATCAAGAAAGGCGATGCAAGAGAGCGCGCTGCAAG 705

674 TTGACTACAGAGTCTCAGAGCAGATACCGAGAACTTCTCTCGAGTCAAGCGGAGA 733
 706 TTGACTACAGAGTCTCAGAGCAGATACCGAGAACTTCTCTCGAGTCAAGCGGAGA 765

734 CAGAAATATGTCCTCGCGCTGAGAGAAATGAGAGACACTGAACTACTGAACTTCTCA 793

Db 766 CAGAAATATGTCCTCGCGCTGAGAGAAATGAGAGACACTGAACTACTGCTCA 825
 794 ATGTGCTAGTCCCGAGGGGTGTACACATTCACATGTCAGCAAGAGGATTTATAGA 853
 826 ATGTGCTAGTCCCGAGGGGTGTACACATTCACATGTCAGCAAGAGGATTTATAGA 885

854 AAAAGCAGTGTGCGCGCTTCCAAAGCGAGAG-CCGCGCTTGTGCTGTGTGATAG 912
 886 AAAAGCAGTGTGCGCGCTTCCAAAGCGAGAG-CCGCGCTTGTGCTGTGTGATAG 945

913 TATGGGCGAGCTCTCCCGAGGCTACACACC-AGGGGAGAGAGAGCGTCACTAG 971
 946 TATGGGCGAGCTCTCCCGAGGCTACACACC-AGGGGAGAGAGAGCGTCACTAG 1005

972 CATGACAGCAAG-TAGAGCGCTGCGCAAGGTT-AATGTGAGCTCAAAATATGCTTAT 1029
 1006 CATGACAGCAAGTATAGAGCGCTGCGCAAGGTTAAATGTGAGCTCAAAATATGCTTAT 1065

1030 TTTCGACAAAGACAGCGCAAGAGCATGACACAGAGCTGCTACGCTGATATATTT 1089
 1066 TTTCGACAAAGACAGCGCAAGAGCATGACACAGAGCTGCTACG-CTGATTTATATTT 1124

1090 CTGTTTGTGTGACTGATTTTATTAAC 1120
 1125 CTGTTTGTGTGACTGATTTTATTAAC 1155

RESULT 15
 BX364743/c 1201 bp mRNA linear EST 05-MAY-2003
 LOCUS BX364743 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CSOD1010YA21 3-PRIME, mRNA sequence.
 ACCESSION BX364743
 VERSION BX364743.1 GI:30378851
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 4009.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS1A1003ZC1NP1&cluster=4009.r. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS1A1003ZC1NP1.

FEATURES

Source

Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSOD1010YA21"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /note="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 40.2%; Score 1001.8; DB 13; Length 1201;
 Best Local Similarity 95.1%; Pred. No. 1.6e-171; Indels 2; Gaps 2;
 Matches 1026; Conservative 24; Mismatches 27;

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

M nucleic - nucleic search, using sw model

un on: March 10, 2004, 08:38:17 ; Search time 9409.41 Seconds
(without alignments)
17011.249 Million cell updates/sec

title: US-10-084-817-20

effect score: 3693
sequence: 1 cgaatgggggactccacact.....ttaagtgaataaaaaaa 3693

coring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

searched: 3470272 seqs, 21671516995 residues

total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sta:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sta:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pin:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3670.8	99.4	3742	9	HSM807566
2	3663	99.2	3705	9	BC000055
3	3190.6	86.4	5688	9	AB039661
4	2715.2	73.4	152024	9	AC063952
5	2710.4	73.4	170233	2	AC068844
6	2089	56.6	2180	9	AF288537
7	1940	52.5	1987	6	AX410641
8	1940	52.5	1987	9	HSU06863
9	1729.8	46.8	2538	6	AX577955
10	1729.8	46.8	2538	9	D89937
11	1639.8	44.4	1694	9	AK025860
12	1565.2	42.4	1587	9	BC017413
13	1049	28.4	2851	10	BC028921
14	1025.4	27.8	2823	10	MUSRSC36A
15	1008.4	27.3	1010	9	HSM800525
16	924.2	25.0	1017	6	BD079574
17	892.8	24.2	896	6	AR423658
18	892.8	24.2	896	6	BD119211
19	850.2	23.0	1370	10	RNU06864
20	844	22.9	879	6	BD091087
21	757.2	20.5	861	6	BD079576
22	729.4	19.8	930	6	AX577880
23	729.2	19.7	810	6	BD079577
24	674.8	18.3	808	6	BD079578
25	658.4	17.8	879	6	BD079541
26	657.2	17.8	705	6	BD091079
27	657	17.8	719	6	BD079537
28	630.4	17.1	634	6	AX322009
29	629.4	17.0	708	6	BD079539
30	619.4	16.8	621	6	BD275800
31	619.4	16.8	621	6	AR220585
32	619.4	16.8	621	6	AR255579
33	619.4	16.8	621	6	AR281149
34	619.4	16.8	621	6	AX365816
35	578.2	15.7	782	6	BD079538
36	558.4	15.1	1072	5	GGA328977
37	543.2	14.7	589	6	AX322015
38	520.4	14.1	652	6	BD079540
39	493.8	13.4	664	6	BD079536
40	477.2	12.9	708	6	AR146594
41	477.2	12.9	708	6	BD079843
42	461.6	12.5	2496	5	BC043983
43	460	12.5	2510	5	AB049354
44	439.6	11.9	793	6	BD079585
45	385.2	10.4	398	6	AX895678

ALIGNMENTS

RESULT 1
HSM807566
LOCUS HSM807566 3742 bp mRNA linear PRI 30-AUG-2003
DEFINITION Homo sapiens mRNA; cDNA DKFZp686F1144 (from clone DKFZp686F1144).
ACCESSION BX647421
VERSION BX647421.1 GI:34366578
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3742)
AUTHORS Wambutt, R., Heubner, D., Mewes, H.W., Weill, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
The German Human cDNA Consortium
CONSTRM

TITLE Direct Submission
 JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
 COMMENT Neuhuber, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing
 consortium of the German Genome Project.
 This clone (DKFZ686F1144) is available at the RPD in Berlin.
 Please contact the RPD: Ressourcenzentrum, Heubergweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rpz.de Further
 information about the clone and the sequencing project is available
 at <http://mips.gsf.de/proj/cdna/>.
 Location/Qualifiers
 1..3742
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZ686F1144"
 /tissue_type="human colon endothel primary cell culture"
 /clone_lib="686 (synonym: hicc3). Vector pSPORT1_Sfi; host
 DH10B; sites SfiI + SfiIb"
 /dev_stage="adult"
 polyA_signal
 polyA_site
 3691..3696
 ORIGIN
 Query Match 99.4%; Score 3670.8; DB 9; Length 3742;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3675; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

672 GTGTGATGCTCTCATTGAACTGTCTGATGAAATGCTGATTGGAACTCAGCTTCCAG 731
 690 GTGTATGCTCTCATTGAACTGTCTGATGAAATGCTGATTGGAACTCAGCTTCCAG 749
 732 AGTTTCTCAAGTCCCTCAACCCATCTTTCACCTCTGAGAAAGATGTGCTCGAGG 791
 750 AGTTTCTCAAGTCCCTCAACCCATCTTTCACCTCTGAGAAAGATGTGCTCGAGG 809
 792 ATGAACGATGATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 851
 810 ATGAACGATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 869
 852 GTGAATTTGGTCTGTACAGCATGACCTGTGACGGAATGATGAGAGGAGGAGCCAGA 911
 870 GTGAATTTGGTCTGTACAGCATGACCTGTGACGGAATGATGAGAGGAGGAGCCAGA 929
 912 CCCAGACAGAGAGAGATGACCAATATGTGTCAGAGGCTCCAAAGCATTCAGAAACAG 971
 930 CCCAGACAGAGAGAGATGACCAATATGTGTCAGAGAGCTCCAAAGCATTCAGAAACAG 989
 972 CTGAAGAAGCAAGAGAGATGACCAATATGTGTCAGAGAGCTCCAAAGCATTCAGAAACAG 1031
 990 CTGAAGAAGCAAGAGAGATGACCAATATGTGTCAGAGAGCTCCAAAGCATTCAGAAACAG 1049
 1032 TGGATCCAGACATCTTCTCAGCTTCCAGCTGAGTGAATGATGATGATGATGATGATG 1091
 1050 TGGATCCAGACATCTTCTCAGCTTCCAGCTGAGTGAATGATGATGATGATGATGATG 1109
 1092 GTGCAAAATCAGCAATATTTGCTATATGAAATGAGTTTATTTGTTATTTGTTT 1151
 1110 GTGCAAAATCAGCAATATTTGCTATATGAAATGAGTTTATTTGTTATTTGTTT 1169
 1152 GCAATTAAGATATGAAAGTGTGCTATGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1211
 1170 GCAATTAAGATATGAAAGTGTGCTATGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1229
 1212 GAGTGTATTAAGAACTGTAATGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1271
 1230 GAGTGTATTAAGAACTGTAATGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1289
 1272 ATCAGATTAAGAACTGTAATGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1331
 1290 ATCAGATTAAGAACTGTAATGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1349
 1332 CAGCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1391
 1350 CAGCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1409
 1392 AGAGTTTGGAGAGCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1451
 1410 AGAGTTTGGAGAGCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1469
 1452 GTGAGATGACAGAGCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1511
 1470 GTGAGATGACAGAGCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1529
 1512 ACATAGCAATCTGCTAGTTAAACCAAGTGTCTTCCAGATTTGATGAGATTTCTGAGAG 1571
 1530 ACATAGCAATCTGCTAGTTAAACCAAGTGTCTTCCAGATTTGATGAGATTTCTGAGAG 1589
 1572 GTACACCCCAATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1631
 1590 GTACACCCCAATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1649
 1632 TTAATAATCTTTTTCACCAAGGAGTATTTCTGTAATAACATTTTTCGCAAGTT 1691
 1650 TTAATAATCTTTTTCACCAAGGAGTATTTCTGTAATAACATTTTTCGCAAGTT 1709
 1692 GACTTATTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1751
 1710 GACTTATTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1769

1752 TAGGTATTAAGCTTTTGTAAATATTTTTCAGTAGTCCACCACTCTCATAGGTGGAAGG 1811
1770 TAGGTATTAAGCTTTTGTAAATATTTTTCAGTAGTCCACCACTCTCATAGGTGGAAGG 1829
1812 TTTGGGGTTCTTCTGGTGCAGGGGTGAAATAACCCAGATGCTCCACCTTGCACATA 1871
1830 TTTGGGGTTCTTCTGGTGCAGGGGTGAAATAACCCAGATGCTCCACCTTGCACATA 1889
1872 CTAGATGACGCCCATAGTTGGCCCCCTAGCTTCCAGCAGTCCACTATCTGCGCAGAGG 1931
1890 CTAGATGACGCCCATAGTTGGCCCCCTAGCTTCCAGCAGTCCACTATCTGCGCAGAGG 1949
1932 CAAGGTGCTTAGACCTTAAGCCAGGGGAAGAGCATCTTCTATAAAACTTTCAAGATC 1991
1950 CAAGGTGCTTAGACCCAGGAGCCAGGGGAAGAGCATCTTCTATAAAACTTTCAAGATC 2009
1992 CAAACATTAATTTGTTTTTATTTATTTCTGAGAGTTGAGGCAAACTCAGTATCCCAAGG 2051
2010 CAAACATTAATTTGTTTTTATTTATTTCTGAGAGTTGAGGCAAACTCAGTATCCCAAGG 2069
2052 TGCGCAAGGGCAGCCAAAGCAGGGCTTAGGATATCCAGCCTACCAATATGCTCATTCG 2111
2070 TGCGCAAGGGCAGCCAAAGCAGGGCTTAGGATATCCAGCCTACCAATATGCTCATTCG 2129
2112 ACTAATAGAGGGTCAAGTTGGCCCTGCTCTCTTTTCTGGAAGCTCAGTTTCTCAG 2171
2130 ACTAATAGAGGGTCAAGTTGGCCCTGCTCTCTTTTCTGGAAGCTCAGTTTCTCAG 2189
2172 TGAGCTGGTAAGAAATGCACTAACCTTTGATTTGATTAAGTATAAACTCTGTTCTGA 2231
2190 TGAGCTGGTAAGAAATGCACTAACCTTTGATTTGATTAAGTATAAACTCTGTTCTGA 2249
2232 TCATTGGTCCAGGGGAGATAGTTTCTGTGATTTTCTCTTCTCTATAGATAAAT 2291
2250 TCATTGGTCCAGGGGAGATAGTTTCTGTGATTTTCTCTTCTCTATAGATAAAT 2309
2292 GAAATCTTGTGTTAGAAAGAAATGTCAGATGGCCAAAGAAACAGATGACCAAGATTTGA 2351
2310 GAAATCTTGTGTTAGAAAGAAATGTCAGATGGCCAAAGAAACAGATGACCAAGATTTGA 2369
2352 TCTCAGCTGATGACCTTACAGTCTGCTATGATATGAGTCTCATGGTAAAGCAGG 2411
2370 TCTCAGCTGATGACCTTACAGTCTGCTATGATATGAGTCTCATGGTAAAGCAGG 2429
2412 AAGAGAGTGGAAAGAGAACCCACCTCTGCTTCATTTGATTTGATTTGATTTTAAACC 2471
2430 AAGAGAGTGGAAAGAGAACCCACCTCTGCTTCATTTGATTTGATTTTAAACC 2489
2472 TCCGGCTGGAAATAGAAAGCATTTCCCTTAGAGATGAGGATAAAAGATTTGAGATCA 2531
2490 TCCGGCTGGAAATAGAAAGCATTTCCCTTAGAGATGAGGATAAAAGATTTGAGATCA 2549
2532 ACAGGGGGAAGAAATGGAGATTTAATCTTAAACTGTGACTTGGGAGGTGAGTCATTT 2591
2550 ACAGGGGGAAGAAATGGAGATTTAATCTTAAACTGTGACTTGGGAGGTGAGTCATTT 2609
2592 ACAGTTAGTCTGTGCTTTTCGACTTCTGTGATTAATTAACCCACTACCTGTTTC 2651
2610 ACAGTTAGTCTGTGCTTTTCGACTTCTGTGATTAATTAACCCACTACCTGTTTC 2669
2652 AGATGCAATTTGGATACCAAGATTAATCTTGTGATATGATATGATATGATATGATATGAT 2711
2670 AGATGCAATTTGGATACCAAGATTAATCTTGTGATATGATATGATATGATATGATATGAT 2729
2712 GATTAAAGCATTAGAGGAAATTTAGTGTGTAATGCAAGCACTGTCGAGAAAC 2771
2730 GATTAAAGCATTAGAGGAAATTTAGTGTGTAATGCAAGCACTGTCGAGAAAC 2789
2772 TGTGTGCCAAATATAGATTTCTTCTAGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 2831
2790 TGTGTGCCAAATATAGATTTCTTCTAGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 2849
2832 TCCACTTTGTTAGCATTTCAAGCTTTTATGATATCCACTATCCACTTAAAACTCTTCAAAC 2891

2850 TCACACTTTGTTAGCATTTCAAGCTTTTATGATCCATCCATCTAAAACTCTCTCAAC 2909
2892 TCACACTTTGTTAGCATTTCAAGCTTTTATGATCCATCCATCTAAAACTCTCTCAAC 2951
2910 TCACACTTTGTTAGCATTTCAAGCTTTTATGATCCATCCATCTAAAACTCTCTCAAC 2969
2952 CACGCCCTTAATCAAAAGGTTTTTACAGCCCTTGGACACTATGAGGAGGAGGCAAGATACA 3011
2970 CACGCCCTTAATCAAAAGGTTTTTACAGCCCTTGGACACTATGAGGAGGAGGCAAGATACA 3029
3012 CCAATTTGTTAAAGCAAGAAACCAAGCTGCTCTTCTACCTAGTCACTTTAGAAATGTTA 3071
3030 CCAATTTGTTAAAGCAAGAAACCAAGCTGCTCTTCTACCTAGTCACTTTAGAAATGTTA 3089
3072 TCATCCAAAGCACTACTCTACCTTGCACATTTGAATCTCCAAAGAGCAAAATCCACATTCCTCT 3131
3090 TCATCCAAAGCACTACTCTACCTTGCACATTTGAATCTCCAAAGAGCAAAATCCACATTCCTCT 3149
3132 TGAGTTCTGAGCTTCTGTGTAAATAGGGCAGCTGCTCTATGCTGCTAGTAAATCACAATGA 3191
3150 TGAGTTCTGAGCTTCTGTGTAAATAGGGCAGCTGCTCTATGCTGCTAGTAAATCACAATGA 3209
3192 TCTGAGCACCATTCTGGAAGCTGCTAAATAGCTAGTCTGCGGAGTCTTCCATAAAGTT 3251
3210 TCTGAGCACCATTCTGGAAGCTGCTAAATAGCTAGTCTGCGGAGTCTTCCATAAAGTT 3269
3252 TTGCATGGAGCAAAACCAAGGATTAATAGTTTGGTTTCTTACGCCCTCTTAAAGCA 3311
3270 TTGCATGGAGCAAAACCAAGGATTAATAGTTTGGTTTCTTACGCCCTCTTAAAGCA 3329
3312 TAGGGCTTAGCCTGCGGCTTCTTGGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3371
3330 TAGGGCTTAGCCTGCGGCTTCTTGGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3389
3372 TAGCATCTGTTAAGATCCAGTGTCCATGGAACCTTCCACATGCCCTGCTCTGGAATA 3431
3390 TAGCATCTGTTAAGATCCAGTGTCCATGGAACCTTCCACATGCCCTGCTCTGGAATA 3449
3432 TATCAGTTTTTGGAAAGCAGGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3491
3450 TATCAGTTTTTGGAAAGCAGGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3509
3492 AATGCTTCTTCTTACACCTATGTTTTTAAAGTAGTCAAACTTCAAGAAACAACTTAAACA 3551
3510 AATGCTTCTTCTTACACCTATGTTTTTAAAGTAGTCAAACTTCAAGAAACAACTTAAACA 3569
3552 AGTTTCTGTTGCATATGTTTGTGAACCTTGTATTTGTATTTAGTAGGCTTCTATATGC 3611
3570 AGTTTCTGTTGCATATGTTTGTGAACCTTGTATTTGTATTTAGTAGGCTTCTATATGC 3629
3612 ATTTAACTGTTTTTGTAACTCCTGATTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3671
3630 ATTTAACTGTTTTTGTAACTCCTGATTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3689
3672 AATTAAGTGAAAAA 3693
3690 AATTAAGTGAAAAA 3711

RESULT 2
BC000055
LOCUS BC000055
DEFINITION Homo sapiens follistatin-like 1, mRNA (cdna clone MGC:1993
IMAGE:3505833), complete cds.
ACCESSION BC000055
VERSION BC000055.2 GI:33990756
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3705)

QY 3131 TTGAAGTCTGCAGCTTCTGTGTAATAGGCGAGCTGTGCTATGCGGTAGATACATG 3190
 DB 3132 TTGAAGTCTGCAGCTTCTGTGTAATAGGCGAGCTGTGCTATGCGGTAGATACATG 3191
 QY 3191 ATCTAGGACCATTCATGAGAGCTGCTAATATAGCTAGCTGGGAGCTCTCCATAAGT 3250
 DB 3192 ATCTAGGACCATTCATGAGAGCTGCTAATATAGCTAGCTGGGAGCTCTCCATAAGT 3251
 QY 3251 TTTCATGAGCAAAACAAACAGGATTAAGTGTGTTGCTTCAAGCTCTAAGAC 3310
 DB 3252 TTTCATGAGCAAAACAAACAGGATTAAGTGTGTTGCTTCAAGCTCTAAGAC 3311
 QY 3311 ATAGGAGCTAGGCTGAGCTCTGCTGGGCTTCTGCTGTGTAGTGTGTTGTAACACT 3370
 DB 3312 ATAGGAGCTAGGCTGAGCTCTGCTGGGCTTCTGCTGTGTAGTGTGTTGTAACACT 3371
 QY 3371 ATAGCATCTGTAAAGATCCAGTGTCCATGAGAAACCTTCCACATGCGCTGACT 3430
 DB 3372 ATAGCATCTGTAAAGATCCAGTGTCCATGAGAAACCTTCCACATGCGCTGACT 3431
 QY 3431 ATATGAGTTTGGAAAGAGGCTTCTGCTGCTGCTAACAAGCCACGAGCAAGTCT 3490
 DB 3432 ATATGAGTTTGGAAAGAGGCTTCTGCTGCTGCTAACAAGCCACGAGCAAGTCT 3491
 QY 3491 GAATGCTTCTTCCCTTAACACCTATGTTTAAAGTAACTTCAAGAAACATCTAAG 3550
 DB 3492 GAATGCTTCTTCCCTTAACACCTATGTTTAAAGTAACTTCAAGAAACATCTAAG 3551
 QY 3551 AAGTTCTGTCATATGATGTTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTG 3610
 DB 3552 AAGTTCTGTCATATGATGTTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTG 3611
 QY 3611 CATTTAACTGTTTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTG 3670
 DB 3612 CATTTAACTGTTTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTG 3671
 QY 3671 AATTTAAAGTGAAGAAAAA 3693
 DB 3672 AATTTAAAGTGAAGAAAAA 3694

RESULT 3
 AB039661
 LOCUS 5688 bp mRNA linear PRI 10-APR-2001
 DEFINITION Macaca fascicularis mRNA for OCCL, complete cds.
 ACCESSION AB039661 GI:12082112
 VERSION AB039661.1 GI:12082112
 KEYWORDS OCCL.
 SOURCE Macaca fascicularis (crab-eating macaque)
 ORGANISM Macaca fascicularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 1 (sites)
 Tochtiani, S., Liang, F., Watakabe, A., Hashikawa, T. and Yamamori, T.
 The OCCL gene is preferentially expressed in the primary visual
 cortex in an activity-dependent manner: a pattern of gene
 expression related to the cytoarchitectonic area in adult macaque
 neocortex
 Eur. J. Neurosci. 13 (2), 297-307 (2001)
 JOURNAL MEDLINE 21097300
 PUBMED 11168534
 2 (bases 1 to 5688)
 Tochtiani, S. and Yamamori, T.
 Direct Submission
 Submitted (29-FEB-2000) Shiro Tochtiani, National Institute for
 Basic Biology, Division of Speciation Mechanisms I, Nishigonaka 36,
 Myodaiji, Okazaki, Aichi 444-8585, Japan (E-mail: tochtian@nibb.ac.jp,
 Tel:+81-564-55-7616, Fax:+81-564-55-7617)
 Location/Qualifiers
 1..5688
 /organism="Macaca fascicularis"

/mol_type="mRNA"
 /db_xref="taxon:9541"
 /sex="male"
 /tissue_type="brain"
 /dev_stage="adult"
 1..5688
 /gene="occl"
 75..1001
 /gene="occl1"
 /codon_start=1
 /product="OCCL"
 /protein_id="BAB20770.1"
 /db_xref="GI:12082113"
 /translation="MKKWLALALAVAVVAREEELRSKXICANVFCGAGRECAV
 TEKEPTCLICBOCKPHKRPVCSNGKTYLNHCELDHAPDLGSKIQVDYDGHCKEK
 STSPASPVVCKYQSNRDELRRILIQMLEAEIIPDMFSGSVSEILKVFNPNGD
 SLDSSEPLKPVQWETALNTTVPDOENKLLRGLCYDALIELSDMAWMLSPFQF
 LKCLNPSRNPPEKCALDEFTYADAEIEVDNRCVCAAGNVCATMTCDGNQKQAO
 TQTEEMTRIVVELQKHDTAKTRVSTKEI"

Query Match 86.4%; Score 3190.6; DB 9; Length 5688;
 Best Local Similarity 94.7%; Pred. No. 0;
 Matches 3498; Conservative 0; Mismatches 149; Indels 48; Gaps 17;

QY 12 CTCCACCTCCGCTTACAGCTGCTGCGCGCTCTGCTGCGCGCGCGCGCGCGCGCGCGCG 71
 DB 5 CTCCAACCTCCGCTTACAGCTGCTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCG 63
 QY 72 ACCAGACCGATGAGGAAAGCTGAGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 131
 DB 64 ACCGTCACAGATGAGGAAAGCTGAGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 123
 QY 132 GGGTCGCGCGCGCGGAAAGCTGAGGAGGAAATCCAAAGTCTGTGCGAAATGTTGTTGTG 191
 DB 124 GGGTCGCGCGCGCGGAAAGCTGAGGAGGAAATCCAAAGTCTGTGCGAAATGTTGTTGTG 183
 QY 192 GAGCGCGCGCGGAAATGAGGAGTCAAGGAAAGGGAACCCACCTGTCTGTGATGAGC 251
 DB 184 GAGCTGCGCGGAAATGAGGAGTCAAGGAAAGGGAACCCACCTGTCTGTGATGAGC 243
 QY 252 AATGCAACCTCAAGAGAGGCTGTGTGTGAGATATGAGCAAGCTTACCTCAACACT 311
 DB 244 AATGCAACCTCAAGAGAGGCTGTGTGTGAGATATGAGCAAGCTTACCTCAACACT 303
 QY 312 GTGAATGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
 DB 304 GTGAATGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
 QY 372 ACTGCAAGAGAAATCCGTAAGTCAATCTGCCAGGCCAGTTGTTGCTATCACTGCA 431
 DB 364 ACTGCAAGAGAAATCCATTAAGTCAATCTGCCAGGCCAGTTGTTGCTATCACTGCA 423
 QY 432 ACCGTATGAGCTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
 DB 424 ACCGTATGAGCTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
 QY 492 GCTGTTCTGTAAGGAGCACTACAGTGAATCTCTAGCAAGATTTTAAAGACTTTG 551
 DB 484 GCTGTTCTGTAAGGAGCACTACAGTGAATCTCTAGCAAGATTTTAAAGACTTTG 543
 QY 552 ATATGATGATTTTCCGCTGAGATCCAGAGATTTCTGGAAGTTTGTGGAACGAATGAA 611
 DB 544 ATATGATGATTTTCCGCTGAGATCCAGAGATTTCTGGAAGTTTGTGGAACGAATGAA 603
 QY 612 CTGCCATCATATTAAACGTATCCAGAGAGAGAAACAAGTTGCTTAAAGGAGCTCT 671
 DB 604 CTGCCATCATATTAAACGTATCCAGAGAGAGAAACAAGTTGCTTAAAGGAGCTCT 663
 QY 672 GTGTGATGCTTCAATTGAAGTCTGATGAGAAATCTGATGAGAACTCAGCTTCCAG 731
 DB 664 GTGTGATGCTTCAATTGAAGTCTGATGAGAAATCTGATGAGAACTCAGCTTCCAG 723

732 AGTTCTCAAGTGCCTCAACCCATCTTTCAACCCCTCTCAGAGAGAGTGTGCTCGAGG 791
724 AGTTCTCAAGTGCCTCAACCCATCTTTCAACCCCTCTCAGAGAGAGTGTGCTCGAGG 783
792 ATGAAACGATATGAGATGAGCTGAGACCGAGTGTGACTGTAAACGCTGTGCTGTGCT 851
784 ATGAAACGATATGAGATGAGCTGAGACCGAGTGTGACTGTAAACGCTGTGCTGTGCT 843
852 GTGAAATTTGGGTCTGTACAGCCATACCTGTGACCGAAAGAAATCAGAAAGGGGGCCAGA 911
844 GTGAAATTTGGGTCTGTACAGCCATACCTGTGACCGAAAGAAATCAGAAAGGGGGCCAGA 903
912 CCAGACAGAGGAGGATGACAGATATGTCCAGAGCTCCAAAGCATCAGGAAACAG 971
904 CTGAGACAGAGGAGGATGACAGATATGTCCAGAGCTCCAAAGCATCAGGAAACAG 963
972 CTGAAAGACCAAGAGATGAGCACCACCAAGAGATCTAATGAGAGGACACAGACCAAGTGC 1031
964 CTGAAAGACCAAGAGATGAGCACCACCAAGAGATCTAATGAGAGGACACAGGATGTC 1023
1032 TGGATCCAGCATCTTC---TCCACTTACGCTGAGTTCAGTATACACAGTGTGCT 1088
1024 TGGAGCCAGCATCTCTCTCTTCCACTTCCAGCTGAGTCCAGTATACACAGTGTGCT 1083
1089 ACAGTGCCTCAATACACAGTATTTGCTTATATAGCAATGAGTATTTTGTATTGT 1148
1084 ACAGTGCCTCAATACACAGTATTTGCTTATATAGCAATGAGTATTTTGTATTGT 1143
1149 TTTGCAATAAGAGATGAAGGTGGTGGTGTGAGAGGAGGACACAGCTTCATTTTC 1208
1144 TTTGCAATAAGAGATGAAGGTGGTGGTGTGAGAGGAGGACACAGCTTCATTTTC 1203
1209 TAGAGTGTCTTTAAGAGAACTGTAAATGTGCTCTGGGGCTGAGGCTAGTAAGAAAC 1268
1204 TAGAGTGTCTTTAAGAGAACTGTAAATGTGCTCTGGGGCTGAGGCTAGTAAGAAAC 1260
1269 TGCATCACGATGAAAGAGAAACAGACCCAAATCTGAACTCTTTTGTAGTTACTGCATC 1328
1261 TGCATCACGATGAAAGAGAAACAGACCCAAATCTGAACTCTTTTGTAGTTACTGCATC 1320
1329 TGTACAGAGCTCGAGGAGTGCACAGATGCGAGAGAGAACTTACAGAGTGTGCTCGCG 1388
1321 TGTACAGAGTTCAGGAGTGCACATGCGAGAGAACTTACAGAGTGTGCTCGCG 1380
1389 AGGAGAGTTTGGGAGCTCCAGAGAGAAACGCTCTCTGTTCCAGCTCTTTCCATT 1448
1381 AGGAGAGTTTGGGAGTTCACAGAGAGAAACGCTCTCTGTTCCAGCTCTTTCCATT 1440
1449 GCGTACAGATGACAGATCCAGCATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1508
1441 GCGTACAGATGACAGATCCAGCATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1509 GATACATAGCCATCTGCTAGTTAAACCCAGTGTCCCTCAGACTTGTGATGGAGTTTCTGGG 1568
1501 GATACATAGCCATCTGCTAGTTAAACCCAGTGTCCCTCAGACTTGTGATGGAGTTTCTGGG 1560
1569 AGGTACACCCAAATGATGAGATCTGATGATGATGATGATGATGATGATGATGATGAT 1628
1561 AGGTACACCCAAATGATGAGATCTGATGATGATGATGATGATGATGATGATGATGAT 1620
1629 ATTTTAAATATCTTTTACCAAGTGTCTTCTCTGTAACAC---TTTTTTTTT 1684
1621 ATTTTAAATATCTTTTACCAAGTGTCTTCTCTGTAACACACTTTTTTTTTT 1680
1685 GCAAGTGTGATTTCTTCAATATTTATCATATATATATATATATATATATATATATAT 1744
1681 GCAAGTGTGATTTCTTCAATATTTATCATATATATATATATATATATATATATATAT 1740
1745 TCTTGTAGTATTAAGTCTTTGTAATATTTTTCAGTGTGCTGCTGCTGCTGCTGCTGCT 1804
1741 TCTTGTAGTATTAAGTCTTTTATATATTTTCAATAGTGTGCTGCTGCTGCTGCTGCT 1800
1805 GAAGGAGTTTGGGGTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1864

1801 GAAGGAGTCTGGGGTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
1865 CCACATATAGATGACAGCCATAGTTGGCCCCCTAGCTTCCAGCAGTCCACTATCTGCC 1924
1861 CCACATATAGATGACAGCCATAGTTGGCCCCCTAGCTTCCAGCAGTCCACTATCTGCC 1919
1925 AGAGGAGCAA-GGGTGCTTAGACCTAAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1983
1920 AGAGGAGCAAAGGGTGTCTTAGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1979
1984 TCAAGATCCAAACATTAATTTGTTTTTATTTATTTCTGAGAGTTCAGGCAAACTCAGTAT 2043
1980 TCGAGATCCAAACATTAATTTGTTTTTATTTCTGAGAGTTCAGGCAAACTCAGTAT 2039
2044 CCCAAGATGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2103
2040 CCCAAGATGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2098
2104 CTCATT-----CGACTAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2155
2099 CTCATTGCGCTACCACTAATCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2158
2156 ACCTCAGTTCTCTCAGTGTGCTGTAAAGATGCACTAACTTTGATTTGATTAAGTTATA 2215
2159 ACCTCAGTTCTCTCAGTGTGCTGTAAAGATGCACTAACTTTGATTTGATTAAGTTATA 2217
2216 AATTCGTGTTCTGATCATTTGTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2275
2218 AATTCGTGTTCTGATCATTTGTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2277
2276 TCTCTATAGATAAATGAAATCTTTGTACTAGAACAAAGAAATGTGATGAGGAGGAGGAGGAGGAGGAG 2335
2278 TCTCTATAGATAAATGAAATCTTTGTTAGAACAAAGAAATGTGATGAGGAGGAGGAGGAGGAGGAG 2337
2336 AGATGACAGATTTGATCTCAGCTGTATGACCTTACAGCTGTGCTGTATGATGAGGAGGAGGAGGAG 2395
2338 AGATGACAGATTTGATCTCAGCTGTATGACCTTACAGCTGTGCTGTATGATGAGGAGGAGGAGGAG 2397
2396 TCATGGGTAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2455
2398 TCATGGGTAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2457
2456 CATTTGATTTTAACTTCCGCTGGAATAGAAAGCATTCCTTAGAGATGAGGAGGAGGAGGAGGAGGAG 2515
2458 CATTTGATTTTAACTTCCGCTGGAATAGAAAGCATTCCTTAGAGATGAGGAGGAGGAGGAGGAGGAG 2517
2516 GAAAGTTTTCAGATTCAACAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2575
2518 GAAAGTTTGTAAATTCACAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2577
2576 GGGAGTTCAGTCAATTTACAGTTAGTCTGTGCTCTTTCGACTTCTGTGATTTAAACCCCA 2635
2578 GGGAGTTCAGTCAATTTACAGTTAGTCTGTGCTCTTTCGACTTCTGTGATTTAAACCCCA 2637
2636 CTCACCTCCCTGTTTCAGATGCAATTTGGAATACCAAGATTTAAATCTTGTGATTAAGATC 2695
2638 CTCACCTCCCTGTTTCAGATGCAATTTGGAATACCAAGATTTAAAGCTTGTGATTAAGATC 2697
2696 TCATTTGAGAAAGCAGATTAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2755
2698 TCATTTGAGAAAGCAGATTAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2757
2756 GGCACCTGTGAGAACTGTTGTCGCAAAATAGAAATTCCTTCTAGTTTCTTCTGTTCTCA 2815
2758 AGCACTGTGAGAACTGTTGTCGCAAAATATTAATTCCTTCTAGTTTCTTCTGTTCTCA 2817
2816 TTTGAAAGGAG 2875
2818 TTTGAAAGGAG 2877
2876 TAAAAA---CTCTTCAAACTCCACTTGTTCAGTGTGAAATGACAGCTCCCTGTCAGGAGGAGGAGGAG 2933

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT.

Location/Qualifiers

1. 152024
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-17403"
1. 1989
/notes="overlaps bases 125039..127026 of clone AC092897"
/functions="clone overlap"
complement(715..903)
/rpt_family="MER5A"

misc_feature

1333..1632
/rpt_family="AluSx"
1869..2174
/rpt_family="AluSx"
2175..2469
/rpt_family="AluSg"
complement(2490..2594)
/rpt_family="L1M4"
complement(2583..3057)
/rpt_family="L1MEC"
complement(3058..3341)
/rpt_family="AluJo"
complement(3342..3457)
/rpt_family="L1MEC"
complement(3458..3742)
/rpt_family="AluJo"
complement(3743..4307)
/rpt_family="L1MEC"
complement(4309..4810)
/rpt_family="L1MEC"
7165..7485
/rpt_family="L1ME1"
7535..7778
/rpt_family="AluUb"
complement(7797..8080)
/rpt_family="AluUb"
complement(8145..8327)
/rpt_family="AluSx"
complement(8328..8620)
/rpt_family="AluSx"
complement(8623..8923)
/rpt_family="AluSg"
complement(8924..9050)
/rpt_family="AluSx"

repeat_region complement(10590..12443)
repeat_region /rpt_family="L1PA16"
repeat_region 12444..13788
repeat_region /rpt_family="L1PA16"
repeat_region 16327..16697
repeat_region /rpt_family="L1ME2"
repeat_region complement(16905..17393)
repeat_region /rpt_family="L2"
repeat_region 19621..19661
repeat_region /rpt_family="(CGGG)n"
repeat_region 21150..21379
repeat_region /rpt_family="L2"
repeat_region 23893..24046
repeat_region /rpt_family="AluSg"
repeat_region 24047..25562
repeat_region /rpt_family="pTR5"
repeat_region 25563..25719
repeat_region /rpt_family="AluSg/x"
repeat_region 25722..26043
repeat_region /rpt_family="AluSx"
repeat_region 26044..26555
repeat_region /rpt_family="L1PA12"
repeat_region complement(26556..26766)
repeat_region /rpt_family="AluSg/x"
repeat_region 26767..27745
repeat_region /rpt_family="L1PA12"
repeat_region 27746..28039
repeat_region /rpt_family="AluSg"
repeat_region 28040..28357
repeat_region /rpt_family="L1PA12"
repeat_region 28358..28443
repeat_region /rpt_family="AluS"
repeat_region 28444..28845
repeat_region /rpt_family="L1PA14"
repeat_region 29846..29951
repeat_region /rpt_family="L1PA5"
repeat_region 29952..31071
repeat_region /rpt_family="L1PA14"

Query Match 73.5%; Score 2715.2; DB 9; Length 152024;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2717; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	963	AGGAACAGCTGAAAGACCAAGAGAGTGAGCAGCAAGAGATCTAATGAGGAGGCACAG	1022
Db	131507	AGGAACAGCTGAAAGACCAAGAGAGTGAGCAGCAAGAGATCTAATGAGGAGGCACAG	131448
QY	1023	ACCACTGTCTGGATCCCAAGCATCTTCCACTTCAGCGCTGAGTTCAGTATACACAGTG	1082
Db	131447	ACCACTGTCTGGATCCCAAGCATCTTCCACTTCAGCGCTGAGTTCAGTATACACAGTG	131388
QY	1083	TCTGCTCAGTCGCCAATCACCAGTATTTGCTTATATAGCAATGAGTTTATTTTGT	1142
Db	131387	TCTGCTCAGTCGCCAATCACCAGTATTTGCTTATATAGCAATGAGTTTATTTTGT	131328
QY	1143	ATTCTTTTGAATTAAGGATATGAAGTGTCTGGCTAGGAAGGAGGAGGCACAGCCTT	1202
Db	131327	ATTCTTTTGAATTAAGGATATGAAGTGTCTGGCTAGGAAGGAGGAGGCACAGCCTT	131268
QY	1203	CATTCTTAGGAGTCTTTTAAGAGAACTGTAAATGGTCTCTGGGCTGGAGGCTAGTAA	1262
Db	131267	CATTCTTAGGAGTCTTTTAAGAGAACTGTAAATGGTCTCTGGGCTGGAGGCTAGTAA	131208
QY	1263	GGAACTGCATCAGATTGAAGAGGAAACAGACCCAAATCTGAACCTCTTTTGTAGTTTAC	1322
Db	131207	GGAACTGCATCAGATTGAAGAGGAAACAGACCCAAATCTGAACCTCTTTTGTAGTTTAC	131148
QY	1323	TGCATCTGTAGCAGGCTGCAGGGAGTGCACCATGCCAGAGAGAACTTAGCAGGGTGT	1382
Db	131147	TGCATCTGTAGCAGGCTGCAGGGAGTGCACCATGCCAGAGAGAACTTAGCAGGGTGT	131088
QY	1383	CCCCGAGGAGAGGTTTGGGAAGCTCCACGAGGAGGAACGCTCTCTGCTCCAGCCTTT	1442

Db 131087 CCCCCGAGAGAGTTGGGAAAGCTCCACGGAGAGAAAGCTCTCTGCTTCACGCTCTT 131028
Qy 1443 TCCATGCGCGTACAGATAGACAGCTCCAGCATCCAGCATCTCTGCTGCCAATACAGT 1502
Db 131027 TCCATGCGCGTACAGATAGACAGCTCCAGCATCCAGCATCTCTGCTGCCAATACAGT 130968
Qy 1503 CCTCTAGATACATAGCCATCTACTGCTAGTTAAACCCAGTGTCCCTCAGACTTGGATGAGTT 1562
Db 130967 CCTCTAGATACATAGCCATCTACTGCTAGTTAAACCCAGTGTCCCTCAGACTTGGATGAGTT 130908
Qy 1563 TCTGGAGAGGTACACCCAAAGATAGCAATCTGTATATCTTGAAGCCCCCTTAGCGACT 1622
Db 130907 TCTGGAGAGGTACACCCAAAGATAGCAATCTGTATATCTTGAAGCCCCCTTAGCGACT 130848
Qy 1623 AACCAATTTTAAAAATCTTTTACCAAGGTGCTATTTCTGTAAACACTTTT 1682
Db 130847 AACCAATTTTAAAAATCTTTTACCAAGGTGCTATTTCTGTAAACACTTTT 130788
Qy 1683 TGGCAAGTTGACTTTATTTCTCAATTAATTAATTAATTAATTTTATTTTAT 1742
Db 130787 TGGCAAGTTGACTTTATTTCTCAATTAATTAATTAATTAATTTTATTTTAT 130728
Qy 1743 TTTCTTGACTAGTATTAAGCTTTTGTATTAATTTTTCAGTAGTCCACCACTTCATAGG 1802
Db 130727 TTTCTTGACTAGTATTAAGCTTTTGTATTAATTTTTCAGTAGTCCACCACTTCATAGG 130668
Qy 1803 TGGAAAGAGTTGGGGGTTCTTCTGTGTGAGGGGCTGAAATTAACCAATGCTCCACCC 1862
Db 130667 TGGAAAGAGTTGGGGGTTCTTCTGTGTGAGGGGCTGAAATTAACCAATGCTCCACCC 130608
Qy 1863 TSCCAATCTAGTATGACAGCCATAGTTGGCCCCCTTCCAGAGTCCAGTATATGTG 1922
Db 130607 TSCCAATCTAGTATGACAGCCATAGTTGGCCCCCTTCCAGAGTCCAGTATATGTG 130548
Qy 1923 CCAGAGAGCAAGGGTGCCTTAGACCTTAAGCCAGGGGAAAGAGCATTTTCAATAAAAACT 1982
Db 130547 CCAGAGAGCAAGGGTGCCTTAGACCCGAAAGCCAGGGGAAAGAGCATTTTCAATAAAAACT 130488
Qy 1983 TTTCAAGATCCAAACATTAATTTGTTTTTATTTATCTGAGAAAGTTGAGGCAATACAGAT 2042
Db 130487 TTTCAAGATCCAAACATTAATTTGTTTTTATTTATCTGAGAAAGTTGAGGCAATACAGAT 130428
Qy 2043 TCCCAAGAGTGGCGACCAAGGGGAGCCCAAGCAGGCTTAGAATATCCAGCTTACCAATAT 2102
Db 130427 TCCCAAGAGTGGCGACCAAGGGGAGCCCAAGCAGGCTTAGAATATCCAGCTTACCAATAT 130368
Qy 2103 GGTCAATTCGACTTAAGAGAGGTGAGTTGGCCCTGCTCTTTTCTTGGAGCTGAG 2162
Db 130367 GGTCAATTCGACTTAAGAGAGGTGAGTTGGCCCTGCTCTTTTCTTGGAGCTGAG 130308
Qy 2163 TTTCTCAGTGAAGCTGTGTAGAAATGCACTAACCTTTTGAATTTGATTAATTTCTG 2222
Db 130307 TTTCTCAGTGAAGCTGTGTAGAAATGCACTAACCTTTTGAATTTGATTAATTTCTG 130248
Qy 2223 TGGTCTGTGATTTGGTCCAGAGGGGAGATAGGTTCCGTGATTTTCTCTCTCTAT 2282
Db 130247 TGGTCTGTGATTTGGTCCAGAGGGGAGATAGGTTCCGTGATTTTCTCTCTCTAT 130188
Qy 2283 AGAATTAATGAATCTTTGTACTAGAACAGAAATGTCAATGAGCCAAACCAAGATGAC 2342
Db 130187 AGAATTAATGAATCTTTGTACTAGAACAGAAATGTCAATGAGCCAAACCAAGATGAC 130128
Qy 2343 CAGATTTGATTTTCAGGCTGATGACCTTAAGGTGTGTGATTAATTAAGAGTCCATAGG 2402
Db 130127 CAGATTTGATTTTCAGGCTGATGACCTTAAGGTGTGTGATTAATTAAGAGTCCATAGG 130068
Qy 2403 TAAAGCAGAGAGAGTGGGAAAGAGAACCAACCCCACTGTCTTCAATTTGCAATTTCA 2462
Db 130067 TAAAGCAGAGAGAGTGGGAAAGAGAACCAACCCCACTGTCTTCAATTTGCAATTTCA 130008
Qy 2463 TGTTTAACTCCGCGCTGGAATTAAGAAAGATTCCTCTAGAGATGAGATTAAGAAAGATT 2522
Db 130007 TGTTTAACTCCGCGCTGGAATTAAGAAAGATTCCTCTAGAGATGAGATTAAGAAAGATT 129948

Qy 2523 TCAGATTTCAACAGGGGAAAGAAATGAGATTTAATCCATAAACTGTGACTTTGGGAGGT 2582
Db 129947 TCAGATTTCAACAGGGGAAAGAAATGAGATTTAATCCATAAACTGTGACTTTGGGAGGT 129888
Qy 2583 CAGTCAATTTACAGTTAGTCTGTGTCTTTCAGACTTCTGTGATTAATTAACCCCACTACAT 2642
Db 129887 CAGTCAATTTACAGTTAGTCTGTGTCTTTCAGACTTCTGTGATTAATTAACCCCACTACAT 129828
Qy 2643 CCTGTGATGAGATTTGAAATACCAAGATTAATTCCTTGAATTAAGATCTCATTTG 2702
Db 129827 CCTGTGATGAGATTTGAAATACCAAGATTAATTCCTTGAATTAAGATCTCATTTG 129768
Qy 2703 CAGAAAGCAGATTTAAAGACATCAGAGAAATTTATTTAGTGTAAATGCAAGGCACT 2762
Db 129767 CAGAAAGCAGATTTAAAGACATCAGAGAAATTTATTTAGTGTAAATGCAAGGCACT 129708
Qy 2763 GTGAGAACTGTGTGCCCCAAATTAATTCCTTCACTTTTCTTGTCTCATTTGAA 2822
Db 129707 GTGAGAACTGTGTGCCCCAAATTAATTCCTTCACTTTTCTTGTCTCATTTGAA 129648
Qy 2823 GAGAAATTTCCACTTTGTTTATGATTCAGCTTTATATATTCATCCATCTAATAAC 2882
Db 129647 GAGAAATTTCCACTTTGTTTATGATTCAGCTTTATATATTCATCCATCTAATAAC 129588
Qy 2883 TCTTCAACTCCACTTGTCAAGTGAATGAGAGCTCCCTGCCAAGTCCCTTGAGAAC 2942
Db 129587 TCTTCAACTCCACTTGTCAAGTGAATGAGAGCTCCCTGCCAAGTCCCTTGAGAAC 129528
Qy 2943 TCACAGCAGACGCTTAAATCAAGGTTTTCAGAGCTTTCAGACATATGAGAGAGG 3002
Db 129527 TCACAGCAGACGCTTAAATCAAGGTTTTCAGAGCTTTCAGACATATGAGAGAGG 129468
Qy 3003 AAGATGACCAATTTGTTAAAGCAAGAAACCAAGTGTCTCTTCACTAGTCAATTA 3062
Db 129467 AAGATGACCAATTTGTTAAAGCAAGAAACCAAGTGTCTCTTCACTAGTCAATTA 129408
Qy 3063 ACATGTTATCATCCAAAGACTACTACCTGCAATTTGAATCCCAAGAGAAATCCA 3122
Db 129407 ACATGTTATCATCCAAAGACTACTACCTGCAATTTGAATCCCAAGAGAAATCCA 129348
Qy 3123 CATTCCTGTTAGTGTGAGCTCTGTGTAAATAGGGAGCTGTGTATAGCCGTAGA 3182
Db 129347 CATTCCTGTTAGTGTGAGCTCTGTGTAAATAGGGAGCTGTGTATAGCCGTAGA 129288
Qy 3183 ATCAGATGATCTGAGACCATTCATGAAAGCTCTAAATAGCTTCTGAGGAGTCTTC 3242
Db 129287 ATCAGATGATCTGAGACCATTCATGAAAGCTCTAAATAGCTTCTGAGGAGTCTTC 129228
Qy 3243 CATTAAGTTTGTGATGAGCAACCAACAGATTAACATAGTTGGTCCCTTCAAGCCCT 3302
Db 129227 CATTAAGTTTGTGATGAGCAACCAACAGATTAACATAGTTGGTCCCTTCAAGCCCT 129168
Qy 3303 CTAAAGCATAGGCTTAGCTGACAGCTTCTTGGGCTTCTGTGTGTGTAGTTTG 3362
Db 129167 CTAAAGCATAGGCTTAGCTGACAGCTTCTTGGGCTTCTGTGTGTGTAGTTTG 129108
Qy 3363 TAAACATTAAGATCTGTAAATCCAGTGTCCATGAAACCTTCCCAAGTCCGTGAC 3422
Db 129107 TAAACATTAAGATCTGTAAATCCAGTGTCCATGAAACCTTCCCAAGTCCGTGAC 129048
Qy 3423 TCTGAGCTATATCAGTTTGTGAAACAGGCTTCTCTGCTGCTTCAACAGCCACGTGG 3482
Db 129047 TCTGAGCTATATCAGTTTGTGAAACAGGCTTCTCTGCTGCTTCAACAGCCACGTGG 128988
Qy 3483 ACCAGTCTGAATGCTTTCTTCAACCTATGTTTAAAGTATGCAAACTTCAAGAAACA 3542
Db 128987 ACCAGTCTGAATGCTTTCTTCAACCTATGTTTAAAGTATGCAAACTTCAAGAAACA 128928
Qy 3543 ATCTAAACAGTTCTGTGATGATGTTGTGAACCTTGATTTGATTTAGTAGCTT 3602
Db 128927 ATCTAAACAGTTCTGTGATGATGTTGTGAACCTTGATTTGATTTAGTAGCTT 128868


```

cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match      24.5%; Score 905.6; DB 13; Length 1201;
Best Local Similarity 97.1%; Pred. No. 1.4e-171;
Matches 913; Conservative 16; Mismatches 10; Indels 1; Gaps 1;

QY 1 CGATCGGGGACTCCACCTCCGCTTACAGCTCGCTCGCGCGCTCCGCGCGCCCC 60
DB 71 CGATCGGGGACTCCACCTCCGCTTACAGCTCGCTCGCGCGCTCCGCGCGCCCC 130
QY 61 AGGAGACTGGACACAGACACAGATGTGGAACGCTGCTCGCTCGCTCGCGCTGGT 120
DB 131 AGGAGACTGGACACAGACACAGATGTGGAACGCTGCTCGCTCGCTCGCGCTGGT 190
QY 121 GCGGTGCTGCTGGTTCGCGCGCGGAGAGCTAAGAGCAATCCCAAGATCTGTGCAA 180
DB 191 GCGGTGCTGCTGGTTCGCGCGCGGAGAGCTAAGAGCAATCCCAAGATCTGTGCAA 250
QY 181 TGTGTTTTGTGAGCGCGCGCGGAGATGTGCAATGTGCAAGAGAGAGAGAGAGAGAG 240
DB 251 TGTGTTTTGTGAGCGCGCGCGGAGATGTGCAATGTGCAAGAGAGAGAGAGAGAG 310
QY 241 CTGCATTGAGCAATGCAAACTCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 311 CTGCATTGAGCAATGCAAACTCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 370
QY 301 CTTCAACCACTGTGAACGTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 360
DB 371 CTTCAACCACTGTGAACGTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 430
QY 361 TTACGATGGACACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 431 TTACGATGGACACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 490
QY 421 CTATCAGTCCAACTGATGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAG 480
DB 491 CTATCAGTCCAACTGATGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAG 550
QY 481 CATCTCAGATGGCTGGTTCCTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 551 CATCTCAGATGGCTGGTTCCTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 610
QY 541 TAAGAACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 611 TAAGAACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 670
QY 601 ACAGAAATGAATGCTGATCAATATTAACAGTATTAACAGTATTAACAGTATTAAC 660
DB 671 ACAGAAATGAATGCTGATCAATATTAACAGTATTAACAGTATTAACAGTATTAAC 730
QY 661 TAGGGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 731 TAGGGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
QY 721 CAGCTTCCAGAGAGTTCCTCAAGTGCCTCAACCCATCTTCAACCCCTCTCGAGAGAG 780
DB 791 CAGCTTCCAGAGAGTTCCTCAAGTGCCTCAACCCATCTTCAACCCCTCTCGAGAGAG 850
QY 781 TGCCCTGGAGGATGAACGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 840
DB 851 TGCCCTGGAGGATGAACGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 910
QY 841 TGTCTGTGCTGTGGAATTTGGGCTGTACAGGCAATGACCTGTGACCGGAAAGATCAGAA 900
DB 911 TGTCTGTGCTGTGGAATTTGGGCTGTACAGGCAATGACCTGTGACCGGAAAGATCAGAA 970
QY 901 GGGGGCCAGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAT 940
DB 971 GGGGGCCC -GNCMGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAT 1009

```

```

RESULT 10
AL544661
LOCUS
DEFINITION
AL544661 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI022YC11 5-PRIME, mRNA sequence.
AL544661
VERSION
AL544661.2 GI:31266502
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 995)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12877141.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1910.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI022AB06QP1&cluster=1910.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DI022AB06QP1.
FEATURES
Location/Qualifiers
1..995
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI022YC11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      23.8%; Score 879.6; DB 9; Length 995;
Best Local Similarity 98.2%; Pred. No. 2.4e-166;
Matches 890; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 CGATCGGGGACTCCACCTCCGCTTACAGCTCGCTCGCGCGCTCCGCGCGCCCC 50
DB 69 CGATCGGGGACTCCACCTCCGCTTACAGCTCGCTCGCGCGCTCCGCGCGCCCC 128
QY 61 AGGAGACTGGACACAGACACAGATGTGGAACGCTGCTCGCGCTCGCGCTGGT 120
DB 129 AGGAGACTGGACACAGACACAGATGTGGAACGCTGCTCGCGCTCGCGCTGGT 188
QY 121 GCGGTGCTGCTGGTTCGCGCGCGGAGAGCTAAGAGCAATCCAGATCTGTGCCAA 180
DB 189 GCGGTGCTGCTGGTTCGCGCGCGGAGAGCTAAGAGCAATCCAGATCTGTGCCAA 248
QY 181 TGTGTTTTGTGAGCGCGCGCGGAGATGTGCAATGTGCAAGAGAGAGAGAGAGAG 240
DB 249 TGTGTTTTGTGAGCGCGCGCGGAGATGTGCAATGTGCAAGAGAGAGAGAGAG 308
QY 241 CTGCATTGAGCAATGCAAACTCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 309 CTGCATTGAGCAATGCAAACTCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
QY 301 CTTCAACCACTGTGAACGTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 360
DB 369 CTTCAACCACTGTGAACGTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 428
QY 361 TTACGATGGACACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 420

```



```
Db 429 TTACGATGCACACTGCAAGAGAGAAATCCGTAAGTCCATCTGCCAGCCAGTTGTTG 488
Qy 421 CTATCAGTCCCAACCTGATGAGCTCCGACCTCGCATCATCCAGTGGCTGAGAGTGAT 480
Db 489 CTATCAGTCCCAACCTGATGAGCTCCGACCTCGCATCATCCAGTGGCTGAGAGTGAT 548
Qy 481 CATCTCAGATGCTGGTCTCTTAAGGAGGAGCAACTACAGTGAATCCCTAGACAAAGTATTT 540
Db 549 CATTCAGATGCTGGTCTCTTAAGGAGGAGCAACTACAGTGAATCCCTAGACAAAGTATTT 608
Qy 541 TAAGAACTTTGATATGATGATTTCTCGCTGAGCTCCAGTGAATCTCTGAAGTTTGGGA 600
Db 609 TAAGAACTTTGATATGATGATTTCTCGCTGAGCTCCAGTGAATCTCTGAAGTTTGGGA 668
Qy 601 ACAGAAATGAATGCAATCAATATTACAACTGATCCAGACAGAGCAACAACAAGTTGCT 660
Db 669 ACAGAAATGAATGCAATCAATATTACAACTGATCCAGACAGAGCAACAACAAGTTGCT 728
Qy 661 TAGGGGACTCTGTGTTGATGCTCTCATTTGAATGCTGATGAATGCTGATGGAAACT 720
Db 729 TAGGGGACTCTGTGTTGATGCTCTCATTTGAATGCTGATGAATGCTGATGGAAACT 788
Qy 721 CAGCTTCAAGAGTTTCTCAAGTGGCTCAACCCATCTTTCAACCTCTCTGAGAGAAAGTG 780
Db 789 CAGCTTCAAGAGTTTCTCAAGTGGCTCAACCCATCTTTCAACCTCTCTGAGAGAAAGTG 848
Qy 781 TGCCCTGAGGATGAACCTGATGAGATGAGAGTGGAGCTGAGACCGAGTGAACCGCTG 840
Db 849 TGCCCTGAGGATGAACCTGATGAGATGAGAGTGGAGCTGAGACCGAGTGAACCGCTG 908
Qy 841 TGCTGTGCTGCTGGAATTTGGTCTGTACAGCCATGCTGACGGAAGAAATCAGAA 900
Db 909 TGCTGTGCTGCTGGAATTTGGTCTGTACAGCCATGCTGACGGAAGAAATCAGAA 967
Qy 901 GGGGCC 906
Db 968 GGGGCC 973

RESULT 11
BX395667
LOCUS
DEFINITION
BX395667 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1003YH20 5-PRIME, mRNA sequence.
ACCESSION
BX395667
KEYWORDS
BX395667.1 GI:30624642
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 987)
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1910.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1003D100Pl&cluster=1910.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1003D100Pl.
FEATURES
Location/Qualifiers
1..987
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1003YH20"
```

```
ORIGIN
Query Match 23.7%; Score 875.6; DB 13; Length 987;
Best Local Similarity 94.8%; Pred. No. 1.5e-165;
Matches 884; Conservative 26; Mismatches 21; Indels 1; Gaps 1;
Qy 862 GGTCTCTA CAGCATGACCTGTGACGAAAGAAATCAGAAGGGGGCCAGACCCAGACAGA 921
Db 47 GGTCCGGAATTCCTGGGATTGTGACGAAAGAAATCAGAAGGGGGCCAGACCCAGACAGA 106
Qy 922 GGAGGAGATGACAGATATGTCCAGAGCTCCAAAGAGCATCAGGAAACAGCTGAAAGAC 981
Db 107 GGAGGAGATGACAGATATGTCCAGAGCTCCAAAGAGCATCAGGAAACAGCTGAAAGAC 166
Qy 982 CAAGAGAGTGAACACAAAGAGATCTAATGAGAGGACAGACACAGTGTGATCCCCAG 1041
Db 167 CAAGAGAGTGAACACAAAGAGATCTAATGAGAGGACAGACACAGTGTGATCCCCAG 226
Qy 1042 CATCTTCTCCATTCAGCGCTGAGTTCACTATACAAAGTGTCTGACAGTCGCAAT 1101
Db 227 CATCTTCTCCATTCAGCGCTGAGTTCACTATACAAAGTGTCTGACAGTCGCAAT 286
Qy 1102 CACCAGTATTTGCTTATATAGCAATGAGTTTATTTGTTATTTGTTTGAATAAAGG 1161
Db 287 CACCAGTATTTGCTTATATAGCAATGAGTTTATTTGTTATTTGTTTGAATAAAGG 346
Qy 1162 ATATGAGTGTGCTGGCTAGGAGGAGGAGGACAGAGCTTCATTTCTAGGAGTCTTTA 1221
Db 347 ATATGAGTGTGCTGGCTAGGAGGAGGAGGACAGAGCTTCATTTCTAGGAGTCTTTA 406
Qy 1222 AGAGAACTGTAAATGCTCTCTGGGGCTGGAGGCTAGTAAGGAAACATGCATCAGGATTG 1281
Db 407 AGAGAACTGTAAATGCTCTCTGGGGCTGGAGGCTAGTAAGGAAACATGCATCAGGATTG 466
Qy 1282 AAAGAGAAACAGACCCCAATCTGAACCTCTTTGAGTTTACTGATCTGTGAGGCTG 1341
Db 467 AAAGAGAAACAGACCCCAATCTGAACCTCTTTGAGTTTACTGATCTGTGAGGCTG 526
Qy 1342 CAGGGAGTGCACACGATGCCAGAGAGAACTTAGCAGGGTGTCCCGGAGGAGAGGTTGG 1401
Db 527 CAGGGAGTGCACACGATGCCAGAGAGAACTTAGCAGGGTGTCCCGGAGGAGAGGTTGG 586
Qy 1402 GAAGCTCCAGGAGAGAAACGCTCTCTGCTTCCAGCTTTTCCATTTGCCGTGAGCATGA 1461
Db 587 GAAGCTCCAGGAGAGAAACGCTCTCTGCTTCCAGCTTTTCCATTTGCCGTGAGCATGA 646
Qy 1462 CAGACCTCCAGCATCCACGCATCTCTTGGTCCCAATACTGCTCTAGATACATAGCCAT 1521
Db 647 CAGACCTCCAGCATCCACGCATCTCTTGGTCCCAATACTGCTCTAGATACATAGCCAT 706
Qy 1522 ACTGCTAGTAAACCCAGTGTCCCTCAGACTTGGATGGAGTTTCT -GGGAGGTTACACCA 1580
Db 707 ACTGCTAGTAAACCCAGTGTCCCTCAGACTTGGATGGAGTTTCTGGGAGGTTACACCA 766
Qy 1581 AATGATGAGATACTTGTATACTTTGAGCCCTTAGCGACCTAAACCAATTTTAAATA 1640
Db 767 AATGATGAGATACTTGTATATTTGAGCCCTTAGCGACCTAAACCAATTTTBBCTT 826
Qy 1641 CTTTTTACAAAGGTGCTATTTCTCTGTAACCACTTTTTTTTGGCAAGTCACTTAT 1700
Db 827 CTTTTTACAAAGGTGCTATTTCTCTGTAACCACTTTTTTTTGGCAAGTCACTTAT 886
Qy 1701 CTTCAATATATCATATATATTTTATTTTAAATATTTTATTTCTGACTAGTATTA 1760
Db 887 CTTCAATATTTATTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTA 946
Qy 1761 AGCTTTTGTAAATTTATTTTTCAGTAGTCCCAACC 1792
```

/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."


```
FEATURES
  source
    Location/Qualifiers
      1..916
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:6275533"
        /tissue_type="epidermoid carcinoma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_102"
        /notes="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
        Site_2: EcoRI; CDNA made by oligo-dT priming.
        Directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGCACGAG(G). Library constructed
        by Ling Hong in the laboratory of Gerald M. Rubin
        (University of California, Berkeley) using ZAP-CDNA
        synthesis kit (Stratagene) and Superscript II RT (Life
        Technologies). Note: this is a NIH_MGC Library."
      ORIGIN
        Query Match      22.9%; Score 845.8; DB 13; Length 916;
        Best Local Similarity 97.3%; Pred. No. 1.5e-159;
        Matches 870; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
      QY 1956 GGGGAAGAGCATCTTCATATAAAACCTTCAGATCCAAACATTAATTTCTTTTATTTA 2015
      DB 23 GGGGAAGAGCATCTTCATATAAAACCTTCAGATCCAAACATTAATTTCTTTTATTTA 82
      QY 2016 TTCTGAGAAGTTGAGGCAATCAGTATTCCTCAAGGATGGGCAAGGCGCAAGCAGG 2075
      DB 83 TTCTGAGAAGTTGAGGCAATCAGTATTCCTCAAGGATGGGCAAGGCGCAAGCAGG 142
      QY 2076 GCTTAGGATATCCAGCCTACCAATATGCTCATTCGACTAAGTAGGAGGTAGTTGGCC 2135
      DB 143 GCTTAGGATATCCAGCCTACCAATATGCTCATTCGACTAAGTAGGAGGTAGTTGGCC 202
      QY 2136 CTGCTCTCTTTCTTTCTGGACCTCAGTTTCTCAGTGAGCTGTAAGATGCACTAAC 2195
      DB 203 CTGCTCTCTTTCTTTCTGGACCTCAGTTTCTCAGTGAGCTGTAAGATGCACTAAC 262
      QY 2196 TTTTGATTTGATTAAGTTATAAATCTGTGGTCTTGATCATTTGTCAGAGGGAGATAGG 2255
      DB 263 TTTTGATTTGATTAAGTTATAAATCTGTGGTCTTGATCATTTGTCAGAGGGAGATAGG 322
      QY 2256 TTCCTGTGATTTTCTTTCTCTATAGATAAATGAATCTTTGTTACTAGAACAGAA 2315
      DB 323 TTCCTGTGATTTTCTTTCTCTATAGATAAATGAATCTTTGTTACTAGAACAGAA 382
      QY 2316 ATGTCAGATGGCCAAAACAAAGATGACAGATTTGATCTCAGCCTGATGACCCCTACAGGT 2375
      DB 383 ATGTCAGATGGCCAAAACAAAGATGACAGATTTGATCTCAGCCTGATGACCCCTACAGGT 442
      QY 2376 CGTGTATGATGAGTCCCTCATGGTAAAGCAGGAGAGAGTGGGAAGAGAACCCACC 2435
      DB 443 CGTGTATGATGAGTCCCTCATGGTAAAGCAGGAGAGAGTGGGAAGAGAACCCACC 502
      QY 2436 CCACCTCTGCTTCATATTTGCAATTTCACTGTTTAACTCCGCTCGAAATAGAAAGCATTC 2495
      DB 503 CCACCTCTGCTTCATATTTGCAATTTCACTGTTTAACTCCGCTCGAAATAGAAAGCATTC 562
      QY 2496 CCTTAGATGAGGATAAAGAAAGTTTCAGATTCACAGGGGGAAGAAATGGAGATTT 2555
      DB 563 CCTTAGATGAGGATAAAGAAAGTTTCAGATTCACAGGGGGAAGAAATGGAGATTT 622
      QY 2556 AATCCTAAATCTGACCTTGGGAGGTGAGTCATTTACAGTTAGTCTGCTCTTTTCGAC 2615
      DB 623 AATCCTAAATCTGACCTTGGGAGGTGAGTCATTTACAGTTAGTCTGCTCTTTTCGAC 682
      QY 2616 TTCCTGTATTTAATACCCCACTCACTACCTGTTTCAGATGCATTTGGAATACCAAGAT 2675
      DB 683 TTCCTGTATTTAATACCCCACTCACTACCTGTTTCAGATGCATTTGGAATACCAAGAT 742
      QY 2676 TAAATCCTTGATCATAGATCTCATTTTGAGAAAGCAGATTAAGACCATCAGAGGAAAT 2735
      DB 743 TANATCCTTGACATAAGATCTCATTTGCAGAAAGCAGATTAAGA-CATCAGAAAGAAAT 801
      QY 2736 TATTAGGTTTGAATGCACAGCACTGTGAGAACTGTGTGCAAAATAGATTCCT 2795
      DB 802 TATTAGGTTTGAATGCACAGCACTGTGAGAACTGTGTGCAAAATAGATTCCT 861
      QY 2796 TCTAGTCTTTCTTTCTTCATTTGAAAGGAGAAATTCACATTTGTTTAGCAT 2849
      DB 862 TCTAGTCTTTCTTTCTTCATTTGAAAGGAGAAATTCACATTTGTTTAGCAT 915
      RESULT 14
      LOCUS AB045227
      DEFINITION AB045227 Homo sapiens HeLa (Suzuki,T.) Homo sapiens cDNA clone E81,
      mRNA sequence.
      ACCESSION AB045227
      VERSION AB045227.1 GI:12404605
      KEYWORDS EST.
      ORGANISM Homo sapiens (human)
      SOURCE Homo sapiens
      ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      REFERENCE 1 (bases 1 to 879)
      AUTHORS Suzuki,T., Minagawa,S., Michishita,E., Ogino,H., Fujii,M.,
      Mitui,Y. and Ayusawa,D.
      TITLE Induction of senescence-associated genes by 5-bromodeoxyuridine in
      HeLa cells
      JOURNAL Exp. Gerontol. 36 (3), 465 (2001)
      MEDLINE 21147913
      PUBMED 11250118
      COMMENT Contact: Toshikazu Suzuki
      Kihara Institute for Biological Research
      Yokohama City University, Division of Biochemistr
      Maioha-cho 641-12, Totsuka-ku, Yokohama, Kanagawa 244-0813, Japan
      Tel: 81-45-820-1906
      Fax: 81-45-820-1901
      Email: piseuke@yokohama-cu.ac.jp.
      FEATURES
        source
          1..879
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="E81"
            /cell_line="HeLa"
            /clone_lib="Homo sapiens HeLa (Suzuki,T.)"
          ORIGIN
            Query Match      22.9%; Score 844; DB 9; Length 879;
            Best Local Similarity 98.7%; Pred. No. 3.6e-159;
            Matches 861; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
            QY 1719 TATTATTGTTTTTAAATATTTTCTTCTGACTAGGTATTAAAGCTTTTGAATTTT 1778
            DB 8 TTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTCTGACTAGGTATTAAAGCTTTTGAATTTT 67
            QY 1779 TCAGTAGTCCCACTTCATAGTGGAGGAGTTTGGGTTTCTTCCTGGTACAGGGCT 1838
            DB 68 TCAGTAGTCCCACTTCATAGTGGAGGAGTTTGGGTTTCTTCCTGGTACAGGGCT 127
            QY 1839 GAAATTAACCAATGCTCCACCTGCCACATACACTAGATGAGCCCATAGTTGGCCCCC 1898
            DB 128 GAAATTAACCAATGCTCCACCTGCCACATACACTAGATGAGCCCATAGTTGGCCCCC 187
            QY 1899 TAGCTTCCAGCAGTCCACTATCTGCGCAGAGGAGCAAGGTTGCTTTAGACCTTAAGCAGG 1958
            DB 188 TAGCTTCCAGCAGTCCACTATCTGCGCAGAGGAGCAAGGTTGCTTTAGACCTTAAGCAGG 247
            QY 1959 GAAGAAGCATCTTCTATAAAACCTTTCAAGATCCAAACATTAATTTGTTTATTATTC 2018
            DB 248 GAAGAAGCATCTTCTATAAAACCTTTCAAGATCCAAACATTAATTTGTTTATTATTC 307
            QY 2019 TGAGAAGTTGAGGCAATCAGTATTTCCTCAAGGATGGGCAAGGCGCAGCAGGAGGCT 2078
```

```

Db      308 TGAAGAGTGGAGCAAAATCAGTATTCCTCAAGATGCGACAGAGGACCCAGACGGGCT 367
Qy      2079 TGAAGATATCCAGCCACCAATATGCTCATTCGACCTAACTAGAGAGGTGAGTGGCCCTG 2138
Db      368 TAGAGATATCCAGCCACCAATATGCTCATTCGACCTAACTAGAGAGGTGAGTGGCCCTG 427
Qy      2139 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2138
Db      428 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 487
Qy      2199 TGAATTTGATAGTATTAATTTCTGTGTCTGATGATGATGATGATGATGATGATGATGATGAT 2258
Db      488 TGAATTTGATAGTATTAATTTCTGTGTCTGATGATGATGATGATGATGATGATGATGATGAT 547
Qy      2259 CTGTGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2318
Db      548 CTGTGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 607
Qy      2319 TCAGATGGCCAAAACAGATGACAGATTTGATCTGACGCTGATGACGCTGATGACGCTGAT 2378
Db      608 TCAGATGGCCAAAACAGATGACAGATTTGATCTGACGCTGATGACGCTGATGACGCTGAT 667
Qy      2379 GCTATGATATGAGATCTCTCATGGTAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2438
Db      668 GCTATGATATGAGATCTCTCATGGTAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
Qy      2439 CTCTGCTTCATATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGAT 2498
Db      728 CTCTGCTTCATATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGAT 787
Qy      2499 TAGAGATGAGATTAAGAAAGTTTCAGATTCAGAGGGGGGAA-GAAATGAGATTTTAA 2557
Db      788 TAGAGATGAGATTAAGAAAGTTTCAGATTCAGAGGGGGGAAAGAAATGAGATTTTAA 847
Qy      2558 TCTTAAACTGTGACTTGGGAGGTGATCAT 2589
Db      848 TCTTAAACTGTGACTTGGGAGGTGATCAT 879

```

```

RESULT 15
BOJ18886 927 bp mRNA linear EST 20-AUG-2002
LOCUS BOJ18886
DEFINITION AGENCOURT_8779335 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6372787
5', mRNA sequence.
ACCESSION BOJ18886
VERSION BOJ18886.1 GI:22333584
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 927)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csabds-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LDCW549 row: b column: 20
High quality sequence stop: 529.
Location/Qualifiers
1..927
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6372787"

```

```

/issue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistance)"
/clone_id="NIH_MGC_18"
/notes="Organ: Lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
SuperScript II RT (Life technologies). Note: this is a
NIH_MGC Library."

```

ORIGIN

Query Match 22.9%; Score 844; DB 13; Length 927;

Best Local Similarity 97.3%; Pred. No. 3.5e-159;

Matches 890; Conservative 0; Mismatches 21; Indels 4; Gaps 3;

```

Qy      672 GTGTGATGCTCTCATTTGAACCTGCTGATGAAAATGCTGATGAAAATCTGACCTTCCAG 731
Db      1 GTGTGATGCTCTCATTTGAACCTGCTGATGAAAATGCTGATGAAAATCTGACCTTCCAG 60
Qy      732 AGTTTCTCAAGTCCCTCAACCCACTTTTGAACCTCTGAGAGAGAGTGGCCCTGGAG 791
Db      61 AGTTTCTCAAGTCCCTCAACCTACTCTTTCAACCTCTGAGAGAGAGTGGCCCTGGAG 120
Qy      792 ATGAAACGTATGAGATGAGAGTGAAGCCAGAGTGAAGTGAACCGCTGTCTGTCT 851
Db      121 ATGAAACGTATGAGATGAGAGTGAAGCCAGAGTGAAGTGAACCGCTGTCTGTCT 180
Qy      852 GTGAAATTTGGTCTGTATACGCTATGACCTGTGACCGAAGAAATCAAGAGGGGGCCCA 911
Db      181 GTGAAATTTGGTCTGTATACGCTATGACCTGTGACCGAAGAAATCAAGAGGGGGCCCA 240
Qy      912 CCCAGACAGAGAGAGATGACAGATATGTCAGAGAGCTCCAAAAGCATCAGAAAACAG 971
Db      241 CCCAGACAGAGAGAGATGACAGATATGTCAGAGAGCTCCAAAAGCATCAGAAAACAG 300
Qy      972 CTGAAAAGACCAAGAGAGTGAAGCCAAAGATCTTAAGAGAGGACACAGACCAATGTC 1031
Db      301 CTGAAAAGACCAAGAGAGTGAAGCCAAAGATCTTAAGAGAGGACACAGACCAATGTC 360
Qy      1032 TGAATCCAGACATCTTCTCACTTCCAGCGCTGAGTTCAGATATCACAGAGTCTGTAC 1091
Db      361 TGAATCCAGACATCTTCTCACTTCCAGCGCTGAGTTCAGATATCACAGAGTCTGTAC 420
Qy      1092 GTGCCCAATACCAAGTATTTGCTTAATATGCAATGATGTTATTTTGTATTTGTTT 1151
Db      421 GTGCCCAATACCAAGTATTTGCTTAATATGCAATGATGTTATTTTGTATTTGTTT 480
Qy      1152 GCAATTAAGATTAAGAGAGTGGCTGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1211
Db      481 GCAATTAAGATTAAGAGAGTGGCTGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy      1212 GAGTCTTTAAGAGAACTGTAATATGAGTCTCTGAGAGCTGAGAGCTGATAGAGAACTGC 1271
Db      541 GAGTCTTTAAGAGAACTGTAATATGAGTCTCTGAGAGCTGAGAGCTGATAGAGAACTGC 600
Qy      1272 ATTCAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1331
Db      601 ATTCAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy      1332 CAGCAGGCTCAGAGAGTGAAGAGATGCAAGATGCAAGAGAGAGAGAGAGAGAGAGAGAG 1390
Db      661 CAGCAGGCTCAGAGAGTGAAGAGATGCAAGATGCAAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy      1391 GAGAGCTTTGGAGAGAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1450
Db      721 GAGAGCTTTGGAGAGAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy      1451 CGTCAGATGACAGAGAGCTCCAGAGATCCAGAGATCTTGTGTCCTTCAATGCTCTTGA 1510
Db      781 CGTCAGATGACAGAGAGCTCCAGAGATCCAGAGATCTTGTGTCCTTCAATGCTCTTGA 840

```

Qy	1511	TACATAGCCATACTGCTAGTTAA-CCAGTGTCCCTCAGACTT--GGATGGAGTTTCTGG	1567
Db	841	TACATAGCCATACTGCTAGTTAAACCCAGGGTCCCTCCGAATTTGGATGGAGTTTCTGG	900
Qy	1568	GAGGTTACACCCAAA	1582
Db	901	GAAGGGACCCCAA	915

Search completed: March 11, 2004, 14:23:18
Job time : 6123.39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2004, 08:38:17 ; Search time 14512.9 Seconds
(without alignments)
17011.249 Million cell updates/sec

Title: US-10-084-817-25

Perfect score: 5696
Sequence: I gactacgtgactgcaggg.....ggttttcaaaaaaaaaa 5696

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sv.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	5576.6	97.9	5784	6	AX330488	AX330488 Sequence
2	5576.6	97.9	5784	6	AX375587	AX375587 Sequence
3	5576.6	97.9	5784	6	AX409513	AX409513 Sequence
4	5576.6	97.9	5784	6	AX480837	AX480837 Sequence
5	5576.6	97.9	5784	6	AX774982	AX774982 Sequence
6	5576.6	97.9	5784	9	HUMTHSPD	L12350 Human throm
7	3319.8	58.3	3339	9	HSMB07201	EX641023 Homo sapi
8	2845.2	50.0	4697	4	BTTHROM2	X96540 B.taurus mR
9	2780.2	48.8	4125	10	BC053702	BC053702 Mus muscu
10	2763.6	48.5	2780	9	HUMTHRSPD	M81339 Human throm
11	2753.2	48.3	4108	6	BD129562	BD129562 Polynucle
12	2753.2	48.3	4108	10	MUSTSP2B	L07803 Mus musculu
13	2036.2	35.7	159175	9	EX322234	EX322234 Human DNA
14	2036	35.7	3537	5	CHKTHBSA	M60853 Chicken thr
15	1912.8	33.6	2026	11	G06722	G06722 human STS W
16	1881.6	33.0	2837	6	BD129561	BD129561 Polynucle
17	1881.6	33.0	2837	10	MUSTHBS2	M64866 Mouse throm
18	1612.2	28.3	5369	4	AB005287	AB005287 Bos tauru
19	1612.2	28.3	5369	6	BD129598	BD129598 Polynucle
20	1552	27.2	5722	6	AX094823	AX094823 Sequence
21	1552	27.2	5722	6	AX411057	AX411057 Sequence
22	1552	27.2	5722	6	AX587747	AX587747 Sequence
23	1552	27.2	5722	6	AX663627	AX663627 Sequence
24	1552	27.2	5722	6	BD094089	BD094089 Shear str
25	1552	27.2	5722	6	BD129558	BD129558 Polynucle
26	1552	27.2	5722	9	HSTS	X14787 Human mRNA
27	1552	27.2	5724	6	AX480835	AX480835 Sequence
28	1550.4	27.2	4434	6	BD129560	BD129560 Polynucle
29	1550.4	27.2	4434	9	HSTHROMR	X04665 Human mRNA
30	1550.4	27.2	7232	6	AX281758	AX281758 Sequence
31	1533.6	26.9	2154	10	BC031843	BC031843 Mus muscu
32	1531.2	26.9	3734	10	AF309630	AF309630 Rattus no
33	1526.6	26.8	5819	10	BC050917	BC050917 Mus muscu
34	1525	26.8	5812	10	BC042422	BC042422 Mus muscu
35	1523.8	26.8	4339	6	BD129600	BD129600 Polynucle
36	1523.8	26.8	4339	10	MUSTSP1A	M87276 Mouse throm
37	1340.2	23.5	3522	5	XELSTAGE	L04278 Xenopus lae
38	1144.2	20.1	1559	4	BTRNAT3	X87620 B.taurus mR
39	905.6	15.9	2162	4	BTRNAT1	X87618 B.taurus mR
40	687.8	12.1	2468	6	AX147459	AX147459 Sequence
41	617.6	10.8	2302	4	AF325902	AF325902 Equus cab
42	605.4	10.6	2438	10	AF033530	AF033530 Mus muscu
43	601.6	10.6	2274	9	AB086984	AB086984 Homo sapi
44	601.6	10.6	2439	6	AR380910	AR380910 Sequence
45	601.6	10.6	2439	6	AX329932	AX329932 Sequence

ALIGNMENTS

RESULT 1	AX330488	AX330488	5784 bp	DNA	linear	PAT 09-JAN-2002
LOCUS	Sequence	997 from Patent WO0194629.				
DEFINITION	AX330488					
ACCESSION	AX330488.1	GI:18103466				
VERSION						
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,					
	Horrigan, S., Soppet, D.R. and Weaver, Z.					
TITLE	Cancer gene determination and therapeutic screening using signature					

1981	2Y	TCAC	TGCCTG	CCCTGCCG	CCCGCCG	GATACAG	AGGGAAC	CCAG	CCCGT	TGCGGGT	CGGCTGG	2040				
2089	3b	TCAC	TGCCTG	CCCTGCCG	CCCGCCG	GATACAG	AGGGAAC	CCAG	CCCGT	TGCGGGT	CGGCTGG	2148				
2041	2Y	AGAC	GCCAAG	ACGGA	AAAGCA	AGTGT	GAGCC	CGAA	ACCCAT	CNAGGA	CAAGACAC	2100				
2149	3b	AGAC	GCCAAG	ACGGA	AAAGCA	AGTGT	GAGCC	CGAA	ACCCAT	CNAGGA	CAAGACAC	2208				
2101	2Y	ACAA	CTGCCA	AGCAG	CGGAGT	GCATCT	CACTG	GGCCA	CTTCAG	CGAC	CCCCATGTACA	2160				
2209	3b	ACAA	CTGCCA	AGCAG	CGGAGT	GCATCT	CACTG	GGCCA	CTTCAG	CGAC	CCCCATGTACA	2268				
2161	2Y	AGTG	CGNGT	CCAGAC	CAGGCT	ACGCGG	CGCAG	CGGCT	CACTCT	CGGGG	AGGACTCGGAC	2220				
2269	Db	AGTG	CGAGT	CCAGAC	CAGGCT	ACGCGG	CGCAG	CGGCT	CACTCT	CGGGG	AGGACTCGGAC	2328				
2221	2Y	TGAC	CGGCT	GGCCAA	CACTCA	ATCTGG	CTGCC	CAAC	AGCCCA	CTACCA	CTGCATCA	2280				
2329	Db	TGAC	CGGCT	GGCCAA	CACTCA	ATCTGG	CTGCC	CAAC	AGCCCA	CTACCA	CTGCATCA	2388				
2281	2Y	AGGAT	AACTG	CCCCC	CACTG	CCAAA	TTCTGG	GAGG	AAGACT	TTTGAC	AGGACGGGATTG	2340				
2389	3b	AGGAT	AACTG	CCCCC	CACTG	CCAAA	TTCTGG	GAGG	AAGACT	TTTGAC	AGGACGGGATTG	2448				
2341	2Y	GCAT	CGCTGT	GATGAT	GACGAT	GCAAT	CACCGT	GTG	ACCGAT	GAGAG	AGGACCACTGCC	2400				
2449	Db	GCAT	CGCTGT	GATGAT	GACGAT	GCAAT	CACCGT	GTG	ACCGAT	GAGAG	AGGACCACTGCC	2508				
2401	2Y	AGTC	CTCTTT	CAATCC	CGCC	CAAGCT	GATCAT	GAC	CAAGAT	AGTTGG	GGGACCGCTGTG	2460				
2509	Db	AGTC	CTCTTT	CAATCC	CGCC	CAAGCT	GATCAT	GAC	CAAGAT	AGTTGG	GGGACCGCTGTG	2568				
2461	2Y	ACAAC	TGCCCTT	ACGTG	CACAA	CCCTGCC	CAGAT	CGAC	ACACAA	CAAT	TGGAGAGGGTG	2520				
2569	Db	ACAAC	TGCCCTT	ACGTG	CACAA	CCCTGCC	CAGAT	CGAC	ACACAA	CAAT	TGGAGAGGGTG	2628				
2521	2Y	AGC	CTGCTC	GTGG	GCAATT	GATGGG	AGATG	CTTCA	ATGAAC	GAGACA	CAATGTGCCCT	2580				
2629	Db	AGC	CTGCTC	GTGG	GCAATT	GATGGG	AGATG	CTTCA	ATGAAC	GAGACA	CAATGTGCCCT	2688				
2581	2Y	ACGT	CTTAC	ACACT	GACG	AGGAG	GACG	GATG	TCGCGT	GTGGG	ATCACTGTGACA	2640				
2689	Db	ACGT	CTTAC	ACACT	GACG	AGGAG	GACG	GATG	TCGCGT	GTGGG	ATCACTGTGACA	2748				
2641	2Y	ACTG	CCCTCT	GGTGTG	CAAC	CCCTTG	ACAG	ACCG	ACGTG	GACA	CAATGTGGGGACC	2700				
2749	Db	ACTG	CCCTCT	GGTGTG	CAAC	CCCTTG	ACAG	ACCG	ACGTG	GACA	CAATGTGGGGACC	2808				
2701	QY	AGTG	TGAC	AAAC	AC	AGGAG	CAT	AGAT	GACG	CGCC	ACACAG	CAACTGCC	2760			
2809	Db	AGTG	TGAC	AAAC	AC	AGGAG	CAT	AGAT	GACG	CGCC	ACACAG	CAACTGCC	2868			
2761	2Y	CTTAC	ATCT	CCAA	CGCC	CAAC	AGGCTG	ACCAT	CACAG	ACGCG	CGACGCGCTGTG	2820				
2869	Db	CTTAC	ATCT	CCAA	CGCC	CAAC	AGGCTG	ACCAT	CACAG	ACGCG	CGACGCGCTGTG	2928				
2821	2Y	ACCT	GATG	ATG	AC	ACGAT	TGG	CGTCCC	CGAT	GAC	AGGGA	CAACTCGCGGCTGTGTTCA	2880			
2929	Db	ACCT	GATG	ATG	AC	ACGAT	TGG	CGTCCC	CGAT	GAC	AGGGA	CAACTCGCGGCTGTGTTCA	2988			
2881	QY	ACCC	AGAC	CCAG	GAGG	ACTT	CGAC	CGGTG	ATG	TG	AGAG	TGATTTTG	2940			
2989	Db	ACCC	AGAC	CCAG	GAGG	ACTT	CGAC	CGGTG	ATG	TG	AGAG	TGATTTTG	3048			
2941	QY	ACAAT	GAC	AACT	CCCC	GATAT	TGAT	GATGT	GTCT	TG	AAAA	CAATG	CCCAT	CAGTGAGA	3000	
3049	Db	ACAAT	GAC	AACT	CCCC	GATAT	TGAT	GATGT	GTCT	TG	AAAA	CAATG	CCCAT	CAGTGAGA	3108	
3001	QY	CAG	ACTT	CAG	AACT	CCCC	TGAT	CCCA	AGGGA	CCAC	CCAA	TATG	ATC		3060	
3109	Db	CAG	ACTT	CAG	AACT	CCCC	TGAT	CCCA	AGGGA	CCAC	CCAA	TATG	ATC		3168	
3061	QY	CCAA	CTGGGT	CA	TTTCG	CCAT	CA	AGGCA	AGGAG	CTGG	TT	CAG	ACAG	CGAC	CACTCGGAC	3120

[illegible]

ORIGIN

Db 2089 TCCATGCGCTGCGCTGCGCGCGCGGATACAGAGGGAACCAAGCGGTGCGGCTGG 2148
Qy 2041 AAGCAGCCAAAGACGAAAGCAAGTGTGTGAGCCCGGAAAGCCCATGCAAGACAAAGACAC 2100
Db 2149 AAGCAGCCAAAGACGAAAGCAAGTGTGTGAGCCCGGAAAGCCCATGCAAGACAAAGACAC 2208
Qy 2101 ACAACTGCCAAGACAGCGGAGTGCATCTACCTGGGCCACTTCAGCGACCCCATGTACA 2160
Db 2209 ACAACTGCCAAGACAGCGGAGTGCATCTACCTGGGTCACTTCAGCGACCCCATGTACA 2268
Qy 2161 AGTGGAGTGGCCAGACAGCTACCGGGGCGACGGGCTCATCTGGGGGAGGACTCGGACC 2220
Db 2269 AGTGGAGTGGCCAGACAGCTACCGGGGCGACGGGCTCATCTGGGGGAGGACTCGGACC 2328
Qy 2221 TGGAGCGCTGGCCCAACCTCAATCTGTGTGGCCACCAAGCCCACTACCACTGCATCA 2280
Db 2329 TGGAGCGCTGGCCCAACCTCAATCTGTGTGGCCACCAAGCCCACTACCACTGCATCA 2388
Qy 2281 AGGATAACTGCCCCCATCTGCCAAATCTGGGCGAGGAAGACTTTGACAAAGACGGGATTG 2340
Db 2389 AGGATAACTGCCCCCATCTGCCAAATCTGGGCGAGGAAGACTTTGACAAAGACGGGATTG 2448
Qy 2341 GCGATGCTGTGATGATGACGATGACATGACGCTGTGACCGATGAGAAAGACAACTGCC 2400
Db 2449 GCGATGCTGTGATGATGACGATGACATGACGCTGTGACCGATGAGAAAGACAACTGCC 2508
Qy 2401 AGCTCTCTTCAATCCCGCCAGGCTGACTATGACAAAGATGAGGTGGGACCGCTGTG 2460
Db 2509 AGCTCTCTTCAATCCCGCCAGGCTGACTATGACAAAGATGAGGTGGGACCGCTGTG 2568
Qy 2461 ACAATGCCCTTACGTGCAAAACCTGCCAGATCGACACAGACAAATGAGAGGGTG 2520
Db 2569 ACAATGCCCTTACGTGCAAAACCTGCCAGATCGACACAGACAAATGAGAGGGTG 2628
Qy 2521 AGCGCTGCTCCGTGACATTTGATGGGCGAGTCTTCAATGAAAGACAAATGTCCCT 2580
Db 2629 AGCGCTGCTCCGTGACATTTGATGGGCGAGTCTTCAATGAAAGACAAATGTCCCT 2688
Qy 2581 AGCTGTACAACACTGACAGAGGACACGGATGGTGACGGTGTGGGGATCACTGTGACA 2640
Db 2689 AGCTGTACAACACTGACAGAGGACACGGATGGTGACGGTGTGGGGATCACTGTGACA 2748
Qy 2641 AGTGGCCCTGTGACACACCTGACCGAGCGAGCTGGACAAATGACCTGTGTGGGACC 2700
Db 2749 AGTGGCCCTGTGACACACCTGACCGAGCGAGCTGGACAAATGACCTGTGTGGGACC 2808
Qy 2701 AGTGTGACAAACAGAGGACATAGATGACGACGGCCACAGACAAACAGGACAACTGCC 2760
Db 2809 AGTGTGACAAACAGAGGACATAGATGACGACGGCCACAGACAAACAGGACAACTGCC 2868
Qy 2761 CCTAGATCTCCAGCCCAACGAGCTGACCATGACAGAGCGGCCAGGCGACGCTGTG 2820
Db 2869 CCTAGATCTCCAGCCCAACGAGCTGACCATGACAGAGCGGCCAGGCGACGCTGTG 2928
Qy 2821 ACCCTGATGATGACAAACGATGGCGTCCCGATGACAGGGAACAACCTGCGGCTGTGTTC 2880
Db 2929 ACCCTGATGATGACAAACGATGGCGTCCCGATGACAGGGAACAACCTGCGGCTGTGTTC 2988
Qy 2881 ACCAGACAGAGGACTTGGACGCTGTGAGAGGGGTGATATTTGAAAGATGATTTTG 2940
Db 2989 ACCAGACAGAGGACTTGGACGCTGTGAGAGGGGTGATATTTGAAAGATGATTTTG 3048
Qy 2941 ACAATGACAAACATCCAGATATTTGATGATGTGTCTGAAACAAATGCCATCAGTGAGA 3000
Db 3049 ACAATGACAAACATCCAGATATTTGATGATGTGTCTGAAACAAATGCCATCAGTGAGA 3108
Qy 3001 CAGACTTCAGGAATCTTCAGATGGTCCCTTGGATGCCAAAGGACCAACCAATGTATC 3060
Db 3109 CAGACTTCAGGAATCTTCAGATGGTCCCTTGGATGCCAAAGGACCAACCAATGTATC 3168
Qy 3061 CCAACTGGGTCTTTCGCCATCAAGGCAAGAGCTGTTTCCAGACGCAACTCGGACCCCG 3120
Db 3169 CCAACTGGGTCTTTCGCCATCAAGGCAAGAGCTGTTTCCAGACGCAACTCGGACCCCG 3228

Qy 3121 GCATCCTCTAGGTTTTCAGAGTTTGGTCTGTGGACTTCAGTGGCACTTCTACGTAA 3180
Db 3229 GCATCCTCTAGGTTTTCAGAGTTTGGTCTGTGGACTTCAGTGGCACTTCTACGTAA 3288
Qy 3181 ACATCTACCGGAGCAGACTATCGCGCTTCGTCTTTGGTTACAGTCAAGCAGCGCT 3240
Db 3289 ACATCTACCGGAGCAGACTATCGCGCTTCGTCTTTGGTTACAGTCAAGCAGCGCT 3348
Qy 3241 TCTATCTGTGTGTGAGAGCAGGTGACGACACCTTCTGGGAGGACCAAGCCACGCGGG 3300
Db 3349 TCTATCTGTGTGTGAGAGCAGGTGACGACACCTTCTGGGAGGACCAAGCCACGCGGG 3408
Qy 3301 CCTATGGCTACTCCGCGGTGCTCCCTCAAGGTGTGAATCTCCACACGCGGAGCGGCGAGC 3360
Db 3409 CCTATGGCTACTCCGCGGTGCTCCCTCAAGGTGTGAATCTCCACACGCGGAGCGGCGAGC 3468
Qy 3361 ACCTGAGGAACCGCTGTGTGCAACGCGGAAACACGCGGGGAGGTGGAACTTATGGC 3420
Db 3469 ACCTGAGGAACCGCTGTGTGCAACGCGGAAACACGCGGGGAGGTGGAACTTATGGC 3528
Qy 3421 AGACCCAGGACATTTGGCTGGAGGACTACAGGCTTATAGGTGGACCTGACTCACA 3480
Db 3529 AGACCCAGGACATTTGGCTGGAGGACTACAGGCTTATAGGTGGACCTGACTCACA 3588
Qy 3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAACAGGTCTATGGCAGACT 3540
Db 3589 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAACAGGTCTATGGCAGACT 3648
Qy 3541 CAGGACTTATCTATGACCAAACTAGCTGGCGGGGCGGTGGTCTATTTGCTCTCTC 3600
Db 3649 CAGGACTTATCTATGACCAAACTAGCTGGCGGGGCGGTGGTCTATTTGCTCTCTC 3708
Qy 3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGATGACAGAGATATTTAAACAAGATTG 3660
Db 3709 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGATGACAGAGATATTTAAACAAGATTG 3768
Qy 3661 CTGCATTTCCGGAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTGTGG 3720
Db 3769 CTGCATTTCCGGAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTGTGG 3828
Qy 3721 TCCTTGTGGCTTCTCTCTAGCAGCACCTCTGTGCTCCCTTGACCTTAACTCTGATGGTTC 3780
Db 3829 TCCTTGTGGCTTCTCTCTAGCAGCACCTCTGTGCTCCCTTGACCTTAACTCTGATGGTTC 3888
Qy 3781 TTCACCTCTGCGAGCAACCCCAAGCCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
Db 3889 TTCACCTCTGCGAGCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948
Qy 3841 GCAGAGATGAACATCTAACCCCTAGAGGAACCCAGTTTGGTGATATAGACCTTTATG 3900
Db 3949 TCAGAGATGAACATCTAACCCCTAGAGGAACCCAGTTTGGTGATATAGACCTTTATG 4008
Qy 3901 TGGAGTGAATAATTTGGGATGCCATTCATTCGTTTCTTTGTTTGTAAAGAAATGAC 3960
Db 4009 TGGAGTGAATAATTTGGGATGCCATTCATTCGTTTCTTTCTTTGTTTGTAAAGAAATGAC 4068
Qy 3961 GTTTACATATAAATCTTAATCTTATTTATTTATGTATGTATGTAGTTGAAGGAATA 4020
Db 4069 GTTTACATATAAATCTTAATCTTATTTATTTATGTATGTATGTAGTTGAAGGAATA 4128
Qy 4021 CTGTGCATAGCCATTTATGATAAATTAAGCATGAATAAATTTGCTGAACTACTTTTGGTG 4080
Db 4129 CTGTGCATAGCCATTTATGATAAATTAAGCATGAATAAATTTGCTGAACTACTTTTGGTG 4188
Qy 4081 CTTTAAAGTTGTCACTATTTCTTGAATTTAGAGTTGCTCTCAATGACACACAAATCCCGCTA 4140
Db 4189 CTTTAAAGTTGTCACTATTTCTTGAATTTAGAGTTGCTCTCAATGACACACAAATCCCGCTA 4248
Qy 4141 AATAAATTAATAACAGGGTCAATTCAAATTTGAAGTAATGTTTAAAGGAGAGATTA 4200
Db 4249 AATAAATTAATAACAGGGTCAATTCAAATTTGAAGTAATGTTTAAAGGAGAGATTA 4308

4201	GAAGACAACAGG	CATAGCAAAATGACATACGCTACCGATTAACTAAATCGNAACATGTAAAA	4266
4309	GAAGACAACAGG	CATAGCAAAATGACATACGCTACCGATTAACTAAATCGGNAACATGTAAAA	4368
4261	CAGTTACAAAAA	TAAAGCAAACTCTCTCTTTGTCTCTACAAATGAAAGCCCTCATGTGCAGTA	4320
4369	CAGTTACAAAAA	TAAAGCAAACTCTCTCTTTGTCTCTACAAATGAAAGCCCTCATGTGCAGTA	4428
4321	GAGATGCGAGTTT	CATCAAAGAAACAAACATCCTTTGCAAAATGGGTGTGATCGGTTCCAGAT	4380
4429	GAGATGCGAGTTT	CATCAAAGAAACAAACATCCTTTGCAAAATGGGTGTGATCGGTTCCAGAT	4488
4381	GTGGATTGGCAAAA	CCCTCATTTTAAGTAAAGGTTAGCAGAGCAAAAGTGGGTGCTTTTAG	4440
4489	GTGGATTGGCAAAA	CCCTCATTTTAAGTAAAGGTTAGCAGAGCAAAAGTGGGTGCTTTTAG	4548
4441	CTGCTGCTTTG	CGCGCTGTGGTGTGGGGAGGCTCTGCTCTGAGCTTCCTTCCCGACGCTT	4500
4549	CTGCTGCTTTG	CGCGCTGTGGTGTGGGGAGGCTCTGCTCTGAGCTTCCTTCCCGACGCTT	4608
4501	TGCTGCTGAGAGAA	CCAGAGCAGACGCAAGCCGGAAGAGCGGCATCTAACCGGTAT	4560
4609	TGCTGCTGAGAGAA	CCAGAGCAGACGCAAGCCGGAAGAGCGGCATCTAACCGGTAT	4668
4561	CTAGGCTTTGGT	TAACCTGGACAGAGTTGCTTTTACCTGATTGATGATACATTTTCATTA	4620
4669	CTAGGCTTTGGT	TAACCTGGACAGAGTTGCTTTTACCTGATTGATGATACATTTTCATTA	4728
4621	GGTTCAGTTATA	AAATAATTTTGTTPAATAATTTAATTAAGTGAATAGAAATGCAACTCCATT	4680
4729	GGTTCAGTTATA	AAATAATTTTGTTPAATAATTTAATTAAGTGAATAGAAATGCAACTCCATT	4788
4681	TACAGTAACCTAT	TTTAAATATGCCCTAGTAAACACATATGTAGTATATAATTTCTAGAAACA	4740
4789	TACAGTAACCTAT	TTTAAATATGCCCTAGTAAACACATATGTAGTATATAATTTCTAGAAACA	4848
4741	AACATCTAAATAG	TAATAATCTCTGAAATAATAGAGCTGTATAATTTAGGTTGTGCAC	4800
4849	AACATCTAAATAG	TAATAATCTCTGAAATAATAGAGCTGTATAATTTAGGTTGTGCAC	4908
4801	GATGAACATGCT	AGAGCTGTACACAAATACATAGAGAATATAGAGAGTTTATGATGG	4860
4909	GATGAACATGCT	AGAGCTGTACACAAATACATAGAGAATATAGAGAGTTTATGATGG	4968
4861	AACCTTAAATATA	TAATAGTTGCCAGGATTTAGTTCAAATTTGTTACTGTTATCTATC	4920
4969	AACCTTAAATATA	TAATAGTTGCCAGGATTTAGTTCAAATTTGTTACTGTTATCTATC	5027
4921	TGCTGTATATGGA	ATCTTTTAAATCAAAACGCTCAAAA-GAATCAGCATTTAGCTTGTGCC	4979
5028	TGCTGTATATGGA	ATCTTTTAAATCAAAACGCTCAAAAACGAAATAGCTTGTGCC	5087
4980	AGGCACACCCAA	TAAATCAGTCATGTGTAAATAGCACAAGTTGTTTGTGTTTGTGTTTT	5039
5088	AGGCACACCCAA	TAAATCAGTCATGTGTAAATAGCACAAGTTGTTTGTGTTTGTGTTTT	5147
5040	TTTCTGTGTTGGT	TTTGTGTTTTCCTTTTAAAGTTGCATGATCTTTCTGCAGGAAATAGTCA	5099
5148	TTTGTGTTGGT	TTTGTGTTTTCCTTTTAAAGTTGCATGATCTTTCTGCAGGAAATAGTCA	5203
5100	CTCATCCCACTCC	ACATAAAGGGTTTAGTAAGAGAAGCTGTCTGTCTGATGATGGATAG	5159
5204	CTCATCCCACTCC	ACATAAAGGGTTTAGTAAGAGAAGCTGTCTGTCTGATGATGGATAG	5263
5160	GGGGCAAAATCT	TTTTTCCCTTTCTGTTTAAATAGTCATCACATTTCTATGCCAAACAGGAAC	5219
5264	GGGGCAAAATCT	TTTTTCCCTTTCTGTTTAAATAGTCATCACATTTCTATGCCAAACAGGAAC	5323
5220	AATCCATAACCTT	AGTCTTAATGTACACATGCAATTTGATAAATAATTTGTTGCTGTTT	5279
5324	GATCCATAACCTT	AGTCTTAATGTACACATGCAATTTGATAAATAATTTGTTGCTGTTT	5383
5280	CCTTTGAGGTTG	ATGCTGTGTTGTTGCTGCACTTTTACTTTTTTGGCGTGTGGA	5339

[illegible]

Db 769 AGCCCTTCTACAGACACTGTCAGGCGGAAAGAGCCGGATGTACGTGGCCAAAGGCTCTG 828
Qy 721 CCAGAGAGTCACTTTCAGGGGTTTGTCTCAGAACGTCCTAGTCTTGTGAAACTCTG 780
Db 829 CCAGAGAGTCACTTTCAGGGGTTTGTCTCAGAACGTCCTAGTCTTGTGAAACTCTG 888
Qy 781 TGGAGATATTTAAGCAGAGAGGTTGCCAGCAAGGCCAGGGAGCTGAGTCAAGCCCA 840
Db 889 TGGAGATATTTAAGCAGAGAGGTTGCCAGCAAGGCCAGGGAGCTGAGTCAAGCCCA 948
Qy 841 TCAGTGAGAACACAGAGACGCTGGCCCTGGGTCCGCAATGTCAACACCGAGTACGTGGGCC 900
Db 949 TCAGTGAGAACACAGAGACGCTGGCCCTGGGTCCGCAATGTCAACACCGAGTACGTGGGCC 1008
Qy 901 CCAGCTCAGAGAGAGGCCCGAGAGTGTGCGAACCTGTGCGAGGAGCTGGGAAACATGG 960
Db 1009 CCAGCTCGAGAGAGGCCCGAGAGTGTGCGAACCTGTGCGAGGAGCTGGGAAACATGG 1068
Qy 961 TCCAGGAGCTCTCGGGGCTCCACAGCTCTCTGTGAACCAAGCTCAGCGAGAACTCAAGAGAG 1020
Db 1069 TCCAGGAGCTCTCGGGGCTCCACAGCTCTCTGTGAACCAAGCTCAGCGAGAACTCAAGAGAG 1128
Qy 1021 TGTGGAATGATAACAGATTTCTTGGAGTCTATGTGGCCCTCTTAAGACAGGAACA 1080
Db 1129 TGTGGAATGATAACAGATTTCTTGGAGTCTATGTGGCCCTCTTAAGACAGGAACA 1188
Qy 1081 TGTGAGCTTGTGCGAGATGGCCGCTTCTTTCGGAAATGAACCTGGTGGTGGACA 1140
Db 1189 TGTGAGCTTGTGCGAGATGGCCGCTTCTTTCGGAAATGAACCTGGTGGTGGACA 1248
Qy 1141 GCTGACCACTGTACTCTGCAAGAAATTTAAACATTTGCGACCAAAATCACTGGCCCGC 1200
Db 1249 GCTGACCACTGTACTCTGCAAGAAATTTAAACATTTGCGACCAAAATCACTGGCCCGC 1308
Qy 1201 CTGCAACCTGGCCAGTCCATCTCTTGGGAAGCGAATGTGCGCTTCTGCTGCCACT 1260
Db 1309 CTGCAACCTGGCCAGTCCATCTCTTGGGAAGCGAATGTGCGCTTCTGCTGCCACT 1368
Qy 1261 CGGTGACGCTGAGAGGCTTGGTCTCGGTGGGAGAGTGAAACCAAGTGTCTCGTGACGT 1320
Db 1369 CGGTGACGCTGAGAGGCTTGGTCTCGGTGGGAGAGTGAAACCAAGTGTCTCGTGACGT 1428
Qy 1321 GTGGCTCTGGACCCAGAGAGGCGGCTCTGTAGCGTCAACAGCAACACCTGCTTGG 1380
Db 1429 GTGGCTCTGGACCCAGAGAGGCGGCTCTGTAGCGTCAACAGCAACACCTGCTTGG 1488
Qy 1381 GGCCTTCATCCAGACAGGCTTGCAGTCTGAGCAAGTGTGACACCGCATCCGGCAGG 1440
Db 1489 GGCCTTCATCCAGACAGGCTTGCAGTCTGAGCAAGTGTGACACCGCATCCGGCAGG 1548
Qy 1441 ACGGCGCTGGAGCCACTGCTTGGTCTTCACTGTCTGACCTGTGGAGTTGGCA 1500
Db 1549 ACGGCGCTGGAGCCACTGCTTGGTCTTCACTGTCTGACCTGTGGAGTTGGCA 1608
Qy 1501 ATATCACACGATCCGTCTCTGCAACTCCCAAGTCCCAAGTGGGGGCAAGAATTGCA 1560
Db 1609 ATATCACACGATCCGTCTCTGCAACTCCCAAGTCCCAAGTGGGGGCAAGAATTGCA 1668
Qy 1561 AAGGAGTGGCGGAGACCAAGCCTGCGCAGGGGCCCCATGCCAATCGATGGCCGT 1620
Db 1669 AAGGAGTGGCGGAGACCAAGCCTGCGCAGGGGCCCCATGCCAATCGATGGCCGT 1728
Qy 1621 GGAGCCCTGGTCCCGTGGTGGGCTGCACTGTCACTGTGCGGTGGGATCCGGGAGC 1680
Db 1729 GGAGCCCTGGTCCCGTGGTGGGCTGCACTGTCACTGTGCGGTGGGATCCGGGAGC 1788
Qy 1681 GCACCCGGTCTGCAACAGCCCTGAGCTCAGTACGAGAGGAAGGCTGCTGGGGGATG 1740
Db 1789 GCACCCGGTCTGCAACAGCCCTGAGCTCAGTACGAGAGGAAGGCTGCTGGGGGATG 1848
Qy 1741 TGCAGAGCGTTCAGATGTGCAACAGAGAGGCTGCCCGTGGATGGCTTTTCCAAACC 1800
Db 1849 TGCAGAGCGTTCAGATGTGCAACAGAGAGGCTGCCCGTGGATGGCTTTTCCAAACC 1908

Qy 1801 CTGTCTTCCCGGAGCCAGTGCAGAGCTTCCCGATGGGTCTTGGTCACTGCGGCTCT 1860
Db 1909 CTGTCTTCCCGGAGCCAGTGCAGAGCTTCCCGATGGGTCTTGGTCACTGCGGCTCT 1968
Qy 1861 GCCCTGTGGGCTTCTTGGSCAATGACCCACTGTGAGGACCTGAGTGTGCGCTGG 1920
Db 1969 GCCCTGTGGGCTTCTTGGSCAATGACCCACTGTGAGGACCTGAGTGTGCGCTGG 2028
Qy 1921 TCCCGACATCTGCTTCTCCACAGAGGTGCTTGGTGTGTCAACACTCAGCCTGGCT 1980
Db 2029 TCCCGACATCTGCTTCTCCACAGAGGTGCTTGGTGTGTCAACACTCAGCCTGGCT 2088
Qy 1981 TCCACTGCTGCTGCTGCGGCCCATACAGAGGAACACAGCCCGTGGGGTGGCCCTGG 2040
Db 2089 TCCACTGCTGCTGCTGCGGCCCATACAGAGGAACACAGCCCGTGGGGTGGCCCTGG 2148
Qy 2041 AAGCAGCCAAAGCAGAAAGAAAGTGTGTGAGCCCGGAAACCCATGCAAGGACAAGAC 2100
Db 2149 AAGCAGCCAAAGCAGAAAGAAAGTGTGTGAGCCCGGAAACCCATGCAAGGACAAGAC 2208
Qy 2101 ACAACTGCCACAAAGCAGCGGAGTGCATCTACTGGGCCACTTCAGCGACCCCATGTACA 2160
Db 2209 ACAACTGCCACAAAGCAGCGGAGTGCATCTACTGGGTCACTTCAGCGACCCCATGTACA 2268
Qy 2161 AGTGGAGTGCACAGACAGGCTACGCGGGCGACGGGCTCATCTGCGGGAGGACTCGGACC 2220
Db 2269 AGTGGAGTGCACAGACAGGCTACGCGGGCGACGGGCTCATCTGCGGGAGGACTCGGACC 2328
Qy 2221 TGGACGGCTGGCCCAACCTCAATCTGGTCTGGGCCACCAACGCCACCTACCACTGCATCA 2280
Db 2329 TGGACGGCTGGCCCAACCTCAATCTGGTCTGGGCCACCAACGCCACCTACCACTGCATCA 2388
Qy 2281 AGGATAAATCTGCCCCCATCTGCCAAAATTTGGGCGAGAAAGACTTTGACAAGGACGGGATTG 2340
Db 2389 AGGATAAATCTGCCCCCATCTGCCAAAATTTGGGCGAGAAAGACTTTGACAAGGACGGGATTG 2448
Qy 2341 GGAATGCTGTGATGATGACGATGACATGACGGTGTGACCGATGAGAAAGACAATGCC 2400
Db 2449 GGAATGCTGTGATGATGACGATGACATGACGGTGTGACCGATGAGAAAGACAATGCC 2508
Qy 2401 AGTCTCTTCAATCCCGCCAGGCTGACTATGACAAGATGAGGTGGGGACCGCTGTG 2460
Db 2509 AGTCTCTTCAATCCCGCCAGGCTGACTATGACAAGATGAGGTGGGGACCGCTGTG 2568
Qy 2461 ACAATGCTCTTACGTGCAACACCTGCGCCAGATCGACACAGACAACAAATGGAGAGGTG 2520
Db 2569 ACAATGCTCTTACGTGCAACACCTGCGCCAGATCGACACAGACAACAAATGGAGAGGTG 2628
Qy 2521 ACGCCTGCTCCGTGGACATTTGATGGGACGATGCTTCAATGAAAGAGACAATTTGCCCT 2580
Db 2629 ACGCCTGCTCCGTGGACATTTGATGGGACGATGCTTCAATGAAAGAGACAATTTGCCCT 2688
Qy 2581 ACGTCTAACAACTGACCAAGAGGACACCGATGGTGCAGGCTGGGGGATCACTGTGACA 2640
Db 2689 ACGTCTAACAACTGACCAAGAGGACACCGATGGTGCAGGCTGGGGGATCACTGTGACA 2748
Qy 2641 ACTGCCCTCTGCTGCACACCTGACCGACGCGATGACCAATGACCTTGTGGGGACC 2700
Db 2749 ACTGCCCTCTGCTGCACACCTGACCGACGCGATGACCAATGACCTTGTGGGGACC 2808
Qy 2701 AGTGTGACAAACCAAGGACATAGATGACGACCGGCAACAGAAACCAACAGGACAATGCC 2760
Db 2809 AGTGTGACAAACCAAGGACATAGATGACGACCGGCAACAGAAACCAACAGGACAATGCC 2868
Qy 2761 CTTAGATCTCCAAAGCCCAACAGGCTGACCATGACAGAGCGGCCAGGGCGGCTGTG 2820
Db 2869 CTTAGATCTCCAAAGCCCAACAGGCTGACCATGACAGAGCGGCCAGGGCGGCTGTG 2928
Qy 2821 ACCCTGATGATCAACACGATGGCGTCCCGATGACAGGAGACAATCTGCCGGCTTGTGTCA 2880
Db 2929 ACCCTGATGATGACACGATGGCGTCCCGATGACAGGAGACAATCTGCCGGCTTGTGTCA 2988

Db 5148 TTGTGGTGTG---GTTTTTTGCTTAAAGTTCATGATCTTTCTGCAGAAATAGTCA 5203
 QY 5100 CTCATCCCACTCCACATTAAGGGGTTAGTAAGAGAGTCTGTCTGTATGATGATGATG 5159
 Db 5204 CTCATCCCACTCCACATTAAGGGGTTAGTAAGAGAGTCTGTCTGTATGATGATG 5263
 QY 5160 GGGGCAATCTTTTCCCTTTCTGTAAATAGTCATCATTTCTATGCCAAACGGAAC 5219
 Db 5264 GGGGCAATCTTTTCCCTTTCTGTAAATAGTCATCATTTCTATGCCAAACGGAAC 5323
 QY 5220 AATCCATTAATCTTATGCTTAAATGATACATGTCATTTGATTAATTTTGTGTTT 5279
 Db 5324 GATCCATTAATCTTATGCTTAAATGATACATGTCATTTGATTAATTTTGTGTTT 5383
 QY 5280 CTTTGAAGTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5339
 Db 5384 CTTTGAAGTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5440
 QY 5340 GCTGTATTCGCCAGACCAAGAGCGTTGGGATCTTCAATTAATGATGACGATGCAAC 5399
 Db 5441 GCTGTATTCGCCAGACCAAGAGCGTTGGGATCTTCAATTAATGATGACGATGCAAC 5499
 QY 5400 AGCGTCAGGTTTCTGT 5459
 Db 5500 AGCGTCAGGTTTCTGT 5559
 QY 5460 GATGATGCAATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 5519
 Db 5560 GATGATGCAATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 5619
 QY 5520 AAATTTATCGTATAGGTTGATGAAAGTCATGTGTGTGTGTGTGTGTGTGTGTGTGT 5579
 Db 5620 AAATTTATCGTATAGGTTGATGAAAGTCATGTGTGTGTGTGTGTGTGTGTGTGTGT 5679
 QY 5580 TTATGTGTTCACATGCTCAAAATTTTCAACCATGAAACCTGCACTTAAAGTCAAT 5639
 Db 5680 TTATGTGTTCACATGCTCAAAATTTTCAACCATGAAACCTGCACTTAAAGTCAAT 5739
 QY 5640 TTTTAAAGATTAAACAAGGAATTAATTGTAAAAAGTTTCT 5684
 Db 5740 TTTTAAAGATTAAACAAGGAATTAATTGTAAAAAGTTTCT 5784
 RESULT 5
 AX774982 5784 bp DNA linear PAT 09-JUL-2003
 LOCUS AX774982
 DEFINITION Sequence 298 from Patent WO03038129.
 ACCESSION AX774982
 VERSION AX774982.1 GI:32486498
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1. Rapori, M.
 TITLE Methods for assessing and treating leukemia
 JOURNAL Patent: WO 03038129-A 298 08-MAY-2003;
 Ortho-Clinical Diagnostics, Inc. (US)
 FEATURES
 source 1..5784
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 97.9%; Score 5576.6; DB 6; Length 5784;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;
 QY 1 GACTAGCTGCACTGCAAGGCGGCTCTCGCTCCAGCAGAGAGCTGCGCTTCTGACTC 60
 Db 109 GAGCATCTGCACTGCAAGGCGGCTCTCTGCTCCAGCAGAGAGCTGCGCTTCTGACTC 168

QY 61 GGTCGGAGACCTGAAACAGAGTCATCTGCAATCTTTTGGCAACACAGAGCTCAGCTG 120
 Db 169 GGTCGGAGACCTGAAACAGAGTCATCTGCAATCTTTTGGCAACACAGAGCTCAGCTG 228
 QY 121 CAGAGGACAGATGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 Db 229 CAGAGGACAGATGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
 QY 181 AAGCTGTCAACAGAGCAAAAGACAGACCTTCAACCTTTTCAATATCAGCAATCAAC 240
 Db 289 AAGCTGTCAACAGAGCAAAAGACAGACCTTCAACCTTTTCAATATCAGCAATCAAC 348
 QY 241 GCAAGACCATTTGGGCCAAGACAGTCCGGGGGGCCGACCCCGGCGTCCGCTTACCGCT 300
 Db 349 GCAAGACCATTTGGGCCAAGACAGTCCGGGGGGCCGACCCCGGCGTCCGCTTACCGCT 408
 QY 301 TCGTGCCTTTGACTATCCACCGGTTGAACGAGATGACTCTCAGCAAGATCAACAGA 360
 Db 409 TCGTGCCTTTGACTATCCACCGGTTGAACGAGATGACTCTCAGCAAGATCAACAGA 468
 QY 361 TCATGCGGCAAGAGAGAGGCTTCTCTCTCAAGGCTCCAGCTCAAGAGAGAGGCAATCCA 420
 Db 469 TCATGCGGCAAGAGAGAGGCTTCTCTCTCAAGGCTCCAGCTCAAGAGAGAGGCAATCCA 528
 QY 421 GGGGCAAGCTGTTGGCTCTGGAAGGCCCCGGTCTCTCCAGAGGCAAGTTCAGATCGCT 480
 Db 529 GGGGCAAGCTGTTGGCTCTGGAAGGCCCCGGTCTCTCCAGAGGCAAGTTCAGATCGCT 588
 QY 481 CCAAGGCCCCGGGCAAGACGCTGATTTCACTTCACTGATTTGACGGCACCCGGCATGTG 540
 Db 589 CCAAGGCCCCGGGCAAGACGCTGATTTCACTTCACTGATTTGACGGCACCCGGCATGTG 648
 QY 541 TCTCCCTGGAAGAGTGTGGCTGTGCTGATGCTGAGTGAAGAAAGTCAACGCTGAGGTG 600
 Db 649 TCTCCCTGGAAGAGTGTGGCTGTGCTGATGCTGAGTGAAGAAAGTCAACGCTGAGGTG 708
 QY 601 CTGGCAGACCTTACAGCTTGCACGCTGGGCTGCGACTCATATGACAGGCTTGTGAGC 660
 Db 709 CTGGCAGACCTTACAGCTTGCACGCTGGGCTGCGACTCATATGAGCCAGTGTCTGAGC 768
 QY 661 AGCCCTCTCAAGACACCTGACAGCGGAAAGCGGAGTGTACGTGAGGCTGCTG 720
 Db 769 AGCCCTCTCAAGACACCTGACAGCGGAAAGCGGAGTGTACGTGAGGCTGCTG 828
 QY 721 CCAGAGAGTCACTTCAAGGAGTTTGTCTGAGACGTCACTAGTGTGAAACCTGTG 780
 Db 829 CCAGAGAGTCACTTCAAGGAGTTTGTCTGAGACGTCACTAGTGTGAAACCTGTG 888
 QY 781 TGAAGATATTTTAAGCAAGAGGTTGCCAGCAAGGCTCAGGAGCTGATCAACGCCA 840
 Db 889 TGAAGATATTTTAAGCAAGAGGTTGCCAGCAAGGCTCAGGAGCTGATCAACGCCA 948
 QY 841 TCACTGGAACACAGAGACCTGCGCTGAGTCCGATCTCAACACCGAGTACGTGGGCC 900
 Db 949 TCACTGGAACACAGAGACCTGCGCTGAGTCCGATCTCAACACCGAGTACGTGGGCC 1008
 QY 901 CCACTCAAGAGAGAGGCTCCGAGGTGTGCGAAGCTGTGTCGAGAGCTGGGAAACATGG 960
 Db 1009 CCACTCAAGAGAGAGGCTCCGAGGTGTGCGAAGCTGTGTCGAGAGCTGGGAAACATGG 1068
 QY 961 TCCAGAGAGCTCTCGGGGCTCCAGCTCTCTGTAACAGCTCAGGAGAACTCAAGAGAG 1020
 Db 1069 TCCAGAGAGCTCTCGGGGCTCCAGCTCTCTGTAACAGCTCAGGAGAACTCAAGAGAG 1128
 QY 1021 TGTGAATGATTAACAATTTCTCTGGAAGCTCATTTGTGGCTCTCTTAACAAGAGAA 1080
 Db 1129 TGTGAATGATTAACAATTTCTCTGGAAGCTCATTTGTGGCTCTCTTAACAAGAGAA 1188
 QY 1081 TGTGAGCTTGTGCAAGATGAGCGGCTTTCTTGGGAAATGAAACGTGGGTGTGAGCA 1140
 Db 1189 TGTGAGCTTGTGCAAGATGAGCGGCTTTCTTGGGAAATGAAACGTGGGTGTGAGCA 1248

Db 3409 CCTATGGCTACTCCGGGCTGTCCCTCAAGGTGTGTAATCTCAACGAGGGAAGGGGAGAC 3468
QY 3361 ACCTGAGGAACGGCTGTGTGCAACAGGGGAAACAGCGCGGGGAGGTCGCACTTATGGC 3420
Db 3469 ACCTGAGGAACGGCTGTGTGCAACAGGGGAAACAGCGCGGGGAGGTCGCACTTATGGC 3528
QY 3421 ACGACCCCAAGAAACATTTGGCTGGAAGACTTACAGCGGCTTATAGTGGCACTTACTCA 3480
Db 3529 ACGACCCCAAGAAACATTTGGCTGGAAGACTTACAGCGGCTTATAGTGGCACTTACTCA 3588
QY 3481 GGGCCCAAGACTGGCTCATCAGAGGTTGTGTGATAGAGAAACAGGTCAGTGGAGACT 3540
Db 3589 GGGCCCAAGACTGGCTCATCAGAGGTTGTGTGATAGAGAAACAGGTCAGTGGAGACT 3648
QY 3541 CAGAGCTATCTATGACCAAACTCAGCTGGCGGGGCGGTGGGTCTATTTGTCTCTC 3600
Db 3649 CAGAGCTATCTATGACCAAACTCAGCTGGCGGGGCGGTGGGTCTATTTGTCTCTC 3708
QY 3601 AAGAAATGGCTATTTCTCAGACCTCAAGTAAGAAATGAGAGATATTTAAAGAAATTTG 3660
Db 3709 AAGAAATGGCTATTTCTCAGACCTCAAGTAAGAAATGAGAGATATTTAAAGAAATTTG 3768
QY 3661 CTGCATTTCCGGCAATGCGCTGTGATGCCATGTGCTTACACCTCAGTTCATTTGG 3720
Db 3769 CTGCATTTCCGGCAATGCGCTGTGATGCCATGTGCTTACACCTCAGTTCATTTGG 3828
QY 3721 TCTTTGTGCTTCTCTCTCTCAGACGACCTCTCTCTCTTACCTTATCTGTAGTTC 3780
Db 3829 TCTTTGGGCTTCTCTCTCTCAGACGACCTCTCTCTCTTACCTTATCTGTAGTTC 3888
QY 3781 TTCACTTCCTGCGAGAACCCCAACCCCAAGTCCCTCAGAGATTAATCATATGAAAC 3840
Db 3889 TTCACTTCCTGCGAGAACCCCAACCCCAAGTCCCTCAGAGATTAATCATATGAAAC 3948
QY 3841 GCAGAGATGAACATCTTACCCTATGAGAAACCAAGTTGTGTATATATGAGACTTTATG 3900
Db 3949 TCGAGATGAACATCTTACCCTATGAGAAACCAAGTTGTGTATATATGAGACTTTATG 4008
QY 3901 TGGAGTGAATAATGGGCAATGCCATTCATTTGCTTTTCTGTTTAAAGATGAC 3960
Db 4009 TGGAGTGAATAATGGGCAATGCCATTCATTTGCTTTTCTGTTTAAAGATGAC 4068
QY 4021 CTGTGATGAACCATTAATGTAATTAAGCATGAATAATATGCTGAATCTATCTTTGGTG 4080
Db 4129 CTGTGATGAACCATTAATGTAATTAAGCATGAATAATATGCTGAATCTATCTTTGGTG 4188
QY 4081 CTTAAAGTGTCACTATTTCTTGAATTAAGTGTCTCTCAATGACACAAATCCCGCTA 4140
Db 4189 CTTAAAGTGTCACTATTTCTTGAATTAAGTGTCTCTCAATGACACAAATCCCGCTA 4248
QY 4141 AATTAATTAATAACAAGGCTCATTTGAATTAATTAATTAATTAATTAATTAATTAATTA 4200
Db 4249 AATTAATTAATAACAAGGCTCATTTGAATTAATTAATTAATTAATTAATTAATTAATTA 4308
QY 4201 GAAGACAAACAGGATAGCAAAATGACATTAAGCTACCGATTAATCTAATCGGAACATGTA 4260
Db 4309 GAAGACAAACAGGATAGCAAAATGACATTAAGCTACCGATTAATCTAATCGGAACATGTA 4368
QY 4261 CAGTTACAAATAATAAGAACTCTCTCTGTCTTACATGAAGCCCTCAGTGTGAGTA 4320
Db 4369 CAGTTACAAATAATAAGAACTCTCTCTGTCTTACATGAAGCCCTCAGTGTGAGTA 4428
QY 4321 GAGATGAGTTTCTATCAAAAGAACAAATCTCTGCAATGGGTGTGATCGGTTCCAGAT 4380
Db 4429 GAGATGAGTTTCTATCAAAAGAACAAATCTCTGCAATGGGTGTGATCGGTTCCAGAT 4488
QY 4381 GTGATTTGGCAAAACCTCAATTAAGTAAAGGTTGACAGAGCAAAAGTGGGTCTTATG 4440
Db 4489 GTGATTTGGCAAAACCTCAATTAAGTAAAGGTTGACAGAGCAAAAGTGGGTCTTATG 4548

QY 4441 CTGTGCTGTGACCGCTGT 4500
Db 4549 CTGTGCTGTGTGACCGCTGT 4608
QY 4501 TGTGCTGTGAGAGAACCAAGAGCAAGCAAGCGCGGAAAGGCGATTAACGGCTAT 4560
Db 4609 TGTGCTGTGAGAGAACCAAGAGCAAGCAAGCGCGGAAAGGCGATTAACGGCTAT 4668
QY 4561 CTAGGCTTGTGTACTCGGACAAAGTCTTTTACCTGATTTGATGATTAATTAATTAATTA 4620
Db 4669 CTAGGCTTGTGTACTCGGACAAAGTCTTTTACCTGATTTGATGATTAATTAATTAATTA 4728
QY 4621 GGTTCAGTTAAATAATTTTGTATATTTTATTAATTAATTAATTAATTAATTAATTAATTA 4680
Db 4729 GGTTCAGTTAAATAATTTTGTATATTTTATTAATTAATTAATTAATTAATTAATTAATTA 4788
QY 4681 TACAGATTAATTTTAAATATGCTAGTAACACATATGTATATTAATTTTGAAGAA 4740
Db 4789 TACAGATTAATTTTAAATATGCTAGTAACACATATGTATATTAATTTTGAAGAA 4848
QY 4741 AACATCTAATAGTAATAATCTGTGAAATAATGAGGCTTATATTAATTAATTAATTAATTA 4800
Db 4849 AACATCTAATAGTAATAATCTGTGAAATAATGAGGCTTATATTAATTAATTAATTAATTA 4908
QY 4801 GATAGACATGCTAGAGCTGTAAACAGATTAATAGAAATTAATGAGAGTTTATGATG 4860
Db 4909 GATAGACATGCTAGAGCTGTAAACAGATTAATAGAAATTAATGAGAGTTTATGATG 4968
QY 4861 AACCTTAAATATATATATTTTGTCCAGAGATTTTATGTTTATTTTACTGTATATATC 4920
Db 4969 AACCTT-AAATATATATTTTGTCCAGAGATTTTATGTTTATTTTACTGTATATATC 5027
QY 4921 TGTGCTATAGAGAACTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4979
Db 5028 TGTGCTATAGAGAACTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5087
QY 4980 AGGACACCAATATAGATATGTATATATGACAAAGTGTGTGTGTGTGTGTGTGTGTGT 5039
Db 5088 AGGACACCAATATAGATATGTATATATGACAAAGTGTGTGTGTGTGTGTGTGTGTGT 5147
QY 5040 TTTGT 5099
Db 5148 TTTGT 5203
QY 5100 CTCAATCCCACTCCACATAGAGGTTTATGTAAGAAAGTGTGTGTGTGTGTGTGTGTGTGT 5159
Db 5204 CTCAATCCCACTCCACATAGAGGTTTATGTAAGAAAGTGTGTGTGTGTGTGTGTGTGTGT 5263
QY 5160 GGGGCAATCTTTTCCCTTTCTGTATTAATGTATCAATTTCTATGCAACAGAAAC 5219
Db 5264 GGGGCAATCTTTTCCCTTTCTGTATTAATGTATCAATTTCTATGCAACAGAAAC 5323
QY 5220 AATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5279
Db 5324 GATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5383
QY 5280 CTTTGAAGTGTATGCTGT 5339
Db 5384 CTTTGAAGTGTATGCTGT 5440
QY 5340 GGTGATTTCCGAGAACCAAGAGCTTGGATTCCTCATTAATGTAAGGACGTGTGAC 5399
Db 5441 GGTGATTTCCGAGAACCAAGAGCTTGGATTCCTCATTAATGTAAGGACGTGTGAC 5499
QY 5400 AGCGTGAAGTTTCTGT 5459
Db 5500 AGCGTGAAGTTTCTGT 5559
QY 5460 GATGATGGAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5519
Db 5560 GATGATGGAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5619


```

QY 5520 AAATTTATCGTATAGTTGATGAACGTCATGTGTTTGGCCAAAGACTGTAAATATTAT 5579
Db 5620 AAATTTATCGTATAGTTGATGAACGTCATGTGTTTGGCCAAAGACTGTAAATATTAT 5679
QY 5580 TTATGTTTCACATGCTCAAAATTTACACATGAACCTGCACTAGCTAGAACCTCAT 5639
Db 5680 TTATGTTTCACATGCTCAAAATTTACACATGAACCTGCACTAGCTAGAACCTCAT 5739
QY 5640 TTTTAAAGATTAAACACAGCAATAAATTTGTAAGAAAGGTTTCT 5684
Db 5740 TTTTAAAGATTAAACACAGCAATAAATTTGTAAGAAAGGTTTCT 5784

RESULT 6
HUMTHRSPO 5784 bp mRNA linear PRI 30-DEC-1993
LOCUS Human thrombospondin 2 (THBS2) mRNA, complete cds.
DEFINITION L12350
ACCESSION L12350
VERSION L12350.1 GI:307505
KEYWORDS Thrombospondin 2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5784)
AUTHORS LaBell,T.L., Milewicz,D.J., Distche,C.M. and Byers,P.H.
TITLE Thrombospondin II: partial cDNA sequence, chromosome location, and
expression of a second member of the thrombospondin gene family in
humans
JOURNAL Genomics 12 (3), 421-429 (1992)
MEDLINE 92217961
PUBMED 1559694
REFERENCE 2 (bases 1 to 5784)
AUTHORS LaBell,T.L. and Byers,P.H.
TITLE Sequence and characterization of the complete human thrombospondin
2 cDNA: potential regulatory role for the 3' untranslated region
JOURNAL Genomics 17 (1), 225-229 (1993)
MEDLINE 94010892
PUBMED 8406456
COMMENT Original source text: Homo sapiens adult connective cDNA to mRNA.
FEATURES
source
1..5784
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="fibroblast"
/tissue_type="connective"
/dev_stage="adult"
1..5784
/genes="THBS2"
1..5784
/genes="THBS2"
/citation=[2]
/evidence=experimental
1..239
/genes="THBS2"
/notes="putative"
/citation=[2]
240..3758
/genes="THBS2"
/standard_name="TSP2"
/codon_start=1
/evidence=experimental
/product="thrombospondin 2"
/protein_id="AAA03703.1"
/db_xref="GI:307506"
/translations="MVRLVLLALWVPSIQAGHODKDTFDLFSINIRKTIKAKQ
FRGPDGVPAYRVRFDYTPPNADDLSKITMRQKEGFFLTALQKODGKSRGTLA
LEGPGSQRFELVSNGPADLDLTWIDGTRHVSLEVDGLADSKQKNVTYQVAGET
YSLHVGCDLIGPVALDEPFYHQAESRMVAKSARSHFRGLLQNVHLVFENSE
DILSKGQCOQGAENA-SENTETLRGLPHVTYEVGSSERRPEVRSCEEIENY
VQELSLGLHVLNQLSENLRVSNNDNQFLMELIGGPKTRNMGACQDGRFFAENETW

QY 5520 AAATTTATCGTATAGTTGATGAACGTCATGTGTTTGGCCAAAGACTGTAAATATTAT 5579
Db 5620 AAATTTATCGTATAGTTGATGAACGTCATGTGTTTGGCCAAAGACTGTAAATATTAT 5679
QY 5580 TTATGTTTCACATGCTCAAAATTTACACATGAACCTGCACTAGCTAGAACCTCAT 5639
Db 5680 TTATGTTTCACATGCTCAAAATTTACACATGAACCTGCACTAGCTAGAACCTCAT 5739
QY 5640 TTTTAAAGATTAAACACAGCAATAAATTTGTAAGAAAGGTTTCT 5684
Db 5740 TTTTAAAGATTAAACACAGCAATAAATTTGTAAGAAAGGTTTCT 5784

sig_peptide 240..293
/genes="THBS2"
/notes="putative"
/citation=[2]
mat_peptide 294..3755
/genes="THBS2"
/product="thrombospondin 2"
/citation=[2]
/evidence=experimental
3'UTR 3759..5784
/genes="THBS2"
/notes="putative"
/citation=[2]
polyA_signal 5761..5786
/genes="THBS2"
/notes="putative"
/citation=[2]
polyA_site 5784
/genes="THBS2"

ORIGIN
Query Match 97.9%; Score 5576.6; DB 9; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

QY 1 GACTACGCTCAGTCAGAGCGCGGTCTCTCGTCCAGCAGAGCGCTCGCGCTTCTGACTC 60
Db 109 GAGCATCTCTGATGACGGGCGGTCTCTCGTCCAGCAGAGCGCTCGCGCTTCTGACTC 168
QY 61 GGTCGGGAACACTGAAACCAAGTCATCATGTCATCTTTTGGGAAAACAGAGAGTCAGCTG 120
Db 169 GGTCGGGAACACTGAAACCAAGTCATCATGTCATCTTTTGGGAAAACAGAGAGTCAGCTG 228
QY 121 CAGGAGCAGAGTGGTCTGGAGGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 229 CAGGAGCAGAGTGGTCTGGAGGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
QY 181 AAGCTGGTCCACAGGACAAAGACACAGCACTTCGACCTTTTCAGTATCAGCAACATCAACC 240
Db 289 AAGCTGGTCCACAGGACAAAGACACAGCACTTCGACCTTTTCAGTATCAGCAACATCAACC 348
QY 241 GCAAGACATTTGGCCCAAGCAGTTCCGCGGGCCGACCCCGCGGCTGCGCGCTTACCGCT 300
Db 349 GCAAGACATTTGGCCCAAGCAGTTCCGCGGGCCGACCCCGCGGCTGCGCGCTTACCGCT 408
QY 301 TCGTGGCTTTGACTACATCCACCGGTGAACGAGATGACCTCAGCAAGATCACCAGA 360
Db 409 TCGTGGCTTTGACTACATCCACCGGTGAACGAGATGACCTCAGCAAGATCACCAGA 468
QY 361 TCATGGCGCAGAGGAGGGCTTTCTTCTCAGGCCCGAGCTCAAGCAGGAGCGGCAAGTCCA 420
Db 469 TCATGGCGCAGAGGAGGGCTTTCTTCTCAGGCCCGAGCTCAAGCAGGAGCGGCAAGTCCA 528
QY 421 GGGGCAAGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCAGAGGAGCTTCGAGATCGTCT 480
Db 529 GGGGCAAGCTGTTGGCTCTGGAGGGCCCCGGTCTCTCCAGAGGAGCTTCGAGATCGTCT 588
QY 481 CCAACGGCCCCCGGACACACGCTGGATCTCACCTACTGGATGACGGGACCCCGGATGCG 540

```

```

VDSCTTCTCKFKTKIHOITCPPTATCASPFEVEGCCFSCLSHSDVEEGWSPWAEWTQ
CSVTCGSGTQGRGSCDVTSNTCLGFSIQTRACSLSKCDTRIRQDGGWSPWSSCS
VTGNGNITRIRLCHNSPVPOMGKXKNGKRETKACQAPCPIDGRWSPWSPWACTV
TCAGGIRRETRVONSPPEYGGKACVGVQERQCMKNSCPVDGCLSNPCFPGAOCSS
PDGWSGCFPVGLKGTCHCEDLDBCALVPIICFSTKVPKVCVNTOPGFHCLPCPP
RINQPVGVGLERAAKTERKQVCEPENFCNDKTHNCHKHABCIYLGHFSIDPMYKCBQT
GYAGDGLICGEDSDLDGPNLNLVADYDKDEVDGDCNCPYVHNFAQIDTDNNGGDA
DDDDNDGVTDEKDNQCLLFNPRQADYDKDEVDGDCNCPYVHNFAQIDTDNNGGDA
DDDDNDGVTDEKDNQCLLFNPRQADYDKDEVDGDCNCPYVHNFAQIDTDNNGGDA
CSDVIDGDDVFNERNDCPVYVNTDQDITDGDGVDGDCNCPYVHNFAQIDTDNNGGDA
CQNNEDIDDDGHQNNQNCPIYSNANOQHDHDCGACDDDDNDGVDGDCNCPYVHNFAQIDTDNNGGDA
VFNDOEDLDGDRGDIKDDDFDNDNIPIDDVCPENNAISDTRFNFMVPLDPKGT
TOLDPNWIRHOGKELVOTANSDPGLAVGDFEFGVDFSGTFVYVNTDQDITDNDGAGVFG
YSSSRFVVMKQVTCYTWEDQPTFRAYGSGVSLKYVNSTGTGTEHLNLAHLNGNT
PGQVRLMHPDNKNIGWKDITAIRWHLTHRPKTIYIRLVHEGKQWADSGPIYDQTYA
GRLGLFVFSQEWYFSDLYKIECRDI"
240..293
/genes="THBS2"
/notes="putative"
/citation=[2]
mat_peptide 294..3755
/genes="THBS2"
/product="thrombospondin 2"
/citation=[2]
/evidence=experimental
3'UTR 3759..5784
/genes="THBS2"
/notes="putative"
/citation=[2]
polyA_signal 5761..5786
/genes="THBS2"
/notes="putative"
/citation=[2]
polyA_site 5784
/genes="THBS2"

```

Db ||||| 589 CCAAGGCCCCCGGCAAGCTGATCTCACTACTGATTCAGCGACCCGGCAATGGG 648
 Qy ||||| 541 TCTCCCTGAGAGACGCGGCTGGCTGACTCGCAGTGAAGAACTCAACCGTCAAGTGG 600
 Db ||||| 649 TCTCCCTGAGAGACGCGGCTGGCTGACTCGCAGTGAAGAACTCAACCGTCAAGTGG 708
 Qy ||||| 601 CTGGCGAGACTTAAGCTTTCAGCTGGGCTGCGACCTCATAGACAGCTTCGCTTGGACG 660
 Db ||||| 709 CTGGCGAGACTTAAGCTTTCAGCTGGGCTGCGACCTCATAGACAGCTTCGCTTGGACG 768
 Qy ||||| 661 AGCCCTTACAGAGCACTGCAAGGCGGAAAAGAGCGGAGTATAGCTGGCCAAAGGCTCTG 720
 Db ||||| 769 AGCCCTTACAGAGCACTGCAAGGCGGAAAAGAGCGGAGTATAGCTGGCCAAAGGCTCTG 828
 Qy ||||| 721 CCAGAGAGATCACTTCAGGGGTTTGCTTCAAGACGTCACCTAGTGTGAAAACCTGTG 780
 Db ||||| 829 CCAGAGAGATCACTTCAGGGGTTTGCTTCAAGACGTCACCTAGTGTGAAAACCTGTG 888
 Qy ||||| 781 TGGAGATATTTCTAAGCAAGAGGGTTGCGACAGAGGCGAGGAGTGAATCAAGCGCA 840
 Db ||||| 889 TGGAGATATTTCTAAGCAAGAGGGTTGCGACAGAGGCGAGGAGTGAATCAAGCGCA 948
 Qy ||||| 841 TCAGTAGAGACACAGAGAGCTGCGGCTGGGATCGGATGTCAACAACGATACGTGGGCG 900
 Db ||||| 949 TCAGTAGAGACACAGAGAGCTGCGGCTGGGATCGGATGTCAACAACGATACGTGGGCG 1008
 Qy ||||| 901 CCAGCTCAAGAGAGAGGCGCGAGGTGTGCGAAACGCTCTGCGAGAGAGCTGGGAAAACATGG 960
 Db ||||| 1009 CCAGCTCAAGAGAGAGGCGCGAGGTGTGCGAAACGCTCTGCGAGAGAGCTGGGAAAACATGG 1068
 Qy ||||| 961 TCCAGAGAGCTCTGGGGCTCCAAGTCTGTGAACAGCTCAGCGGAGAACTCAAGAGAG 1020
 Db ||||| 1069 TCCAGAGAGCTCTGGGGCTCCAAGTCTGTGAACAGCTCAGCGGAGAACTCAAGAGAG 1128
 Qy ||||| 1021 TGTGATATATTAACAGTTTCTGTGGAGCTCATTTGTGGCCCTCTTAAGACAAAGAAACA 1080
 Db ||||| 1129 TGTGATATATTAACAGTTTCTGTGGAGCTCATTTGTGGCCCTCTTAAGACAAAGAAACA 1188
 Qy ||||| 1081 TGTGATATATTAACAGTTTCTGTGGAGCTCATTTGTGGCCCTCTTAAGACAAAGAAACA 1140
 Db ||||| 1189 TGTGATATATTAACAGTTTCTGTGGAGCTCATTTGTGGCCCTCTTAAGACAAAGAAACA 1248
 Qy ||||| 1141 GCTGCAACCACTGTACTGTGCAAGAAATTTAAACATTTGCCAACAAATCACTGCGCGC 1200
 Db ||||| 1249 GCTGCAACCACTGTACTGTGCAAGAAATTTAAACATTTGCCAACAAATCACTGCGCGC 1308
 Qy ||||| 1201 CTGCAACCTGCGCAGTCCATCTTTGTGGAAGGGAATGTGCGCCCTTCTGCTGCTCACT 1260
 Db ||||| 1309 CTGCAACCTGCGCAGTCCATCTTTGTGGAAGGGAATGTGCGCCCTTCTGCTGCTCACT 1368
 Qy ||||| 1261 CGGTGACCGGTGAGAGAGGCTGTCTCCGTGGGCAAGTGAACCAAGTCTCTCGTGAAGCT 1320
 Db ||||| 1369 CGGTGACCGGTGAGAGAGGCTGTCTCCGTGGGCAAGTGAACCAAGTCTCTCGTGAAGCT 1428
 Qy ||||| 1321 GTGGCTCTGGGACCCAGAGAGAGGCGCGCTGTGACGTCAACCAAGCAACCTGCTTGG 1380
 Db ||||| 1429 GTGGCTCTGGGACCCAGAGAGAGGCGCGCTGTGACGTCAACCAAGCAACCTGCTTGG 1488
 Qy ||||| 1381 GGCCCTTCATCAAGACACCGGCTTGAAGTCTGAAGCAAGTGAACACCGCATTCGGCAGG 1440
 Db ||||| 1489 GGCCCTTCATCAAGACACCGGCTTGAAGTCTGAAGCAAGTGAACACCGCATTCGGCAGG 1548
 Qy ||||| 1441 AGCGCGCTGGAACCACTGTGCACTTTGTCTTCAAGCTGTGACCTTGAAGTGGCA 1500
 Db ||||| 1549 AGCGCGCTGGAACCACTGTGCACTTTGTCTTCAAGCTGTGACCTTGAAGTGGCA 1608
 Qy ||||| 1501 ATATCAACAGCATCCGTCTGTCAACTCCCAAGTGCACCAAGTGGGAGCAAGAAATGGA 1560
 Db ||||| 1609 ATATCAACAGCATCCGTCTGTCAACTCCCAAGTGCACCAAGTGGGAGCAAGAAATGGA 1668
 Qy ||||| 1561 AAGGAGTGGCCGGGAGACCAAGAGCTTCCAGGGCCCCCATGCCCCAATGATGGCGGCT 1620

Db ||||| 1669 AAGGAGTGGCCGGGAGACCAAGAGCTTGCACAGGCGCCCCCATGCCCCAATGATGGCGCT 1728
 Qy ||||| 1621 GAGCCCCCTGGTCCCGGTGGTGGGCTTGCATGTCACTGTGCGGTTGGATTCGGGAGC 1680
 Db ||||| 1729 GAGCCCCCTGGTCCCGGTGGTGGGCTTGCATGTCACTGTGCGGTTGGATTCGGGAGC 1788
 Qy ||||| 1681 GCAACCGGCTTCAAGCAAGGCTTGAAGTCAAGAGAGAGAGAGGCTGGCTGGGGAGT 1740
 Db ||||| 1789 GCAACCGGCTTCAAGCAAGGCTTGAAGTCAAGAGAGAGAGAGGCTGGCTGGGGAGT 1848
 Qy ||||| 1741 TGCAGAGCGTTCAGATGTGCAACAGAGAGAGCTGCCCGTGAATGCTGTTATCCAAAC 1800
 Db ||||| 1849 TGCAGAGCGTTCAGATGTGCAACAGAGAGAGCTGCCCGTGAATGCTGTTATCCAAAC 1908
 Qy ||||| 1801 CTTGCTTCCCGGAGAGCCAGTGAAGAGAGCTTCCCGATGGGCTGTGCTATGAGGCTCT 1860
 Db ||||| 1909 CTTGCTTCCCGGAGAGCCAGTGAAGAGAGCTTCCCGATGGGCTGTGCTATGAGGCTCT 1968
 Qy ||||| 1861 GGCCTTGGGCTTCTTGGGCAATGAGACCCACTGTGAGACCTGACAGAGTGGCTTGG 1920
 Db ||||| 1969 GGCCTTGGGCTTCTTGGGCAATGAGACCCACTGTGAGACCTGACAGAGTGGCTTGG 2028
 Qy ||||| 1921 TCCCGCAATCTGCTTCTTCCACAGCAAGGTGCTGCTGTGTCAACACTCACTGAGCT 1980
 Db ||||| 2029 TCCCGCAATCTGCTTCTTCCACAGCAAGGTGCTGCTGTGTCAACACTCACTGAGCT 2088
 Qy ||||| 1981 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
 Db ||||| 2089 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2148
 Qy ||||| 2041 AAGCAACCAAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
 Db ||||| 2149 AAGCAACCAAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2208
 Qy ||||| 2101 ACAACTGCAACAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
 Db ||||| 2209 ACAACTGCAACAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2268
 Qy ||||| 2161 AGTGAAGTGCAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
 Db ||||| 2269 AGTGAAGTGCAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2328
 Qy ||||| 2221 TGAAGGCTGCGCCCAACCTCAATCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
 Db ||||| 2329 TGAAGGCTGCGCCCAACCTCAATCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2388
 Qy ||||| 2281 AAGATTAAGTGCAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
 Db ||||| 2389 AAGATTAAGTGCAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2448
 Qy ||||| 2341 GCGATGCTGTGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
 Db ||||| 2449 GCGATGCTGTGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2508
 Qy ||||| 2401 AGCTCTCTTCAATCCCGGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
 Db ||||| 2509 AGCTCTCTTCAATCCCGGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2568
 Qy ||||| 2461 ACAATGCTGCTTACGTGCAACAACCTTCCAGATTCGACACAGACAAATGAGAGAGAGT 2520
 Db ||||| 2569 ACAATGCTGCTTACGTGCAACAACCTTCCAGATTCGACACAGACAAATGAGAGAGAGT 2628
 Qy ||||| 2521 AGGCTGCTGCTGAGACATTTGAGAGAGAGTGTCTTCAATGAACGAGACAAATTTGCTCT 2580
 Db ||||| 2629 AGGCTGCTGCTGAGACATTTGAGAGAGAGTGTCTTCAATGAACGAGACAAATTTGCTCT 2688
 Qy ||||| 2581 AGCTTCAACACCTGACACAGAGAGACACGAGTGTGACGTTGTGGGAGATCACTGTGAC 2640
 Db ||||| 2689 AGCTTCAACACCTGACACAGAGAGACACGAGTGTGACGTTGTGGGAGATCACTGTGAC 2748
 Qy ||||| 2641 ACTGCCCCCTGCTGCAACAACCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
 Db ||||| 2749 ACTGCCCCCTGCTGCAACAACCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2808

Db	361	GAATATGATGAGAGGCGCAACCAAGACCAAGCACTGCCCCCTACATCTCCAGC	420
Qy	2777	CAACCAAGGTGACCATGACAGAGACGGCCAGGGCGACGGCTGTGACCTTGATGATGACAA	2836
Db	421	CAACCAAGGTGACCATGACAGAGACGGCCAGGGCGACGGCTGTGACCTTGATGATGACAA	480
Qy	2837	CGATGGCGTCCCCGATGACAGAGGACAACTGCGGGCTGTGTTCAACCCAGACCAAGAGAG	2896
Db	481	CGATGGCGTCCCCGATGACAGAGGACAACTGCGGGCTGTGTTCAACCCAGACCAAGAGAG	540
Qy	2897	CTTGACACGTGATGACAGGGGTGATATTGTAAAGATGATTTTGACATGACAAACATCCC	2956
Db	541	CTTGACACGTGATGACAGGGGTGATATTGTAAAGATGATTTTGACATGACAAACATCCC	600
Qy	2957	AGATATTGATGATGTGTCTCTTAAACAAATGCAATCACTGAGACAGACATTCAGAACTT	3016
Db	601	AGATATTGATGATGTGTCTCTTAAACAAATGCAATCACTGAGACAGACATTCAGAACTT	660
Qy	3017	CCAGATGTGTCCTTGGATCCCAAGGAGACCAACCAATTGATCCCACTGGGTGATTCG	3076
Db	661	CCAGATGTGTCCTTGGATCCCAAGGAGACCAACCAATTGATCCCACTGGGTGATTCG	720
Qy	3077	CCATCAAGGCAAGAGAGTGTGACAGACCCCACTGGACCCCGGGATGCGCTGTAGTTC	3136
Db	721	CCATCAAGGCAAGAGAGTGTGACAGACCCCACTGGACCCCGGGATGCGCTGTAGTTC	780
Qy	3137	TGACGAGTTTGGGTCTGTGACTTCACTGGACATTCATCTAAGTAACTGACCGGAGCA	3196
Db	781	TGACGAGTTTGGGTCTGTGACTTCACTGGACATTCATCTAAGTAACTGACCGGAGCA	840
Qy	3197	CGATATGCGCGCTTCTCTTGTGTTACAGTCAAGACAGCGCTTCTAAGTGTGATGTC	3256
Db	841	CGATATGCGCGCTTCTCTTGTGTTACAGTCAAGACAGCGCTTCTAAGTGTGATGTC	900
Qy	3257	GAAGCAGGTGACGACGACTACTGGAGAGACAGCCCAACGCGGGCTATGGCTACCTCGG	3316
Db	901	GAAGCAGGTGACGACGACTACTGGAGAGACAGCCCAACGCGGGCTATGGCTACCTCGG	960
Qy	3317	CGTGTCCCTCAAGGTGTGTAATTCACCAACGCGGACCGGGACACTGAGAACCGGCT	1020
Db	961	CGTGTCCCTCAAGGTGTGTAATTCACCAACGCGGACCGGGACACTGAGAACCGGCT	1080
Qy	3377	GTGSCACACGGGGAACACGCGGGGACGTGCGAATCTTATGGACGACCCCAAGAACAT	3436
Db	1021	GTGSCACACGGGGAACACGCGGGGACGTGCGAATCTTATGGACGACCCCAAGAACAT	1080
Qy	3437	TGAGTGAAGGACTACACGCGCTATAGGTGACCTGATCTCAAGGCCCAAGACTGCTA	3496
Db	1081	TGAGTGAAGGACTACACGCGCTATAGGTGACCTGATCTCAAGGCCCAAGACTGCTA	1140
Qy	3497	CATCAGAGTCTTATGATGAGAGGAAACAGGTATGGACGACCTCAGAGACTTATGTA	3556
Db	1141	CATCAGAGTCTTATGATGAGAGGAAACAGGTATGGACGACCTCAGAGACTTATGTA	1200
Qy	3557	CCAAACCTACGCTGGCGGGCGCTGGGTCTATTGTCTTCTCAAGAAATGCTATATT	3616
Db	1201	CCAAACCTACGCTGGCGGGCGCTGGGTCTATTGTCTTCTCAAGAAATGCTATATT	1260
Qy	3617	CTCAGACTCAAGTACAGAAATGCAAGATATTAAACAAAGTTGCTGCAATTCGCGCAAT	3676
Db	1261	CTCAGACTCAAGTACAGAAATGCAAGATATTAAACAAAGTTGCTGCAATTCGCGCAAT	1320
Qy	3677	GCCCTGTGATGCAATGCTGCTTACACACTCAGTTCAATGTGTGCTTGTGCTTCTCT	3736
Db	1321	GCCCTGTGATGCAATGCTGCTTACACACTCAGTTCAATGTGTGCTTGTGCTTCTCT	1380
Qy	3737	CTCTAGCAGACCTTCTCTCTTGAACCTTAACTCTATGCTTCTTAACTCCCGCAGC	3796
Db	1381	CTCTAGCAGACCTTCTCTCTTGAACCTTAACTCTATGCTTCTTAACTCCCGCAGC	1440
Qy	3797	AACCCCAACCAAGTGCCTTCAAGATATAATATCAATGAGACGAGAGTGAACATCT	3856
Db	1441	AACCCCAACCAAGTGCCTTCAAGATATAATATCAATGAGACGAGAGTGAACATCT	1500
Qy	3857	AACCCCTAAGAGAAACCGTTGTGATATATGACCTTATGTGAGAGTGAATGGG	3916
Db	1501	AACCCCTAAGAGAAACCGTTGTGATATATGACCTTATGTGAGAGTGAATGGG	1560
Qy	3917	CATGCCATTCATGCTTTTCTGTTGTTTAAAAAGATGACGTTTACATATAAATG	3976
Db	1561	CATGCCATTCATGCTTTTCTGTTGTTTAAAAAGATGACGTTTACATATAAATG	1620
Qy	3977	TAAATCTTATGTAATATGATATAGAGTGAAGGAAATCTGTGATAGGCATT	4036
Db	1621	TAAATCTTATGTAATATGATATAGAGTGAAGGAAATCTGTGATAGGCATT	1680
Qy	4037	ATGATTAATTAAGCATGAAAAATATGCTGAACTACTTTGTGCTTAAAGTTGCTACTA	4096
Db	1681	ATGATTAATTAAGCATGAAAAATATGCTGAACTACTTTGTGCTTAAAGTTGCTACTA	1740
Qy	4097	TTCTTGAATTGAGTGTCTTACATAGACACAAATCCGCTAAATTAATTAACAA	4156
Db	1741	TTCTTGAATTGAGTGTCTTACATAGACACAAATCCGCTAAATTAATTAACAA	1800
Qy	4157	GGGTCAATTCAAATTTGAAGTAAATGTTTATGTAAGAGATTAAGAACACAGGCATA	4216
Db	1801	GGGTCAATTCAAATTTGAAGTAAATGTTTATGTAAGAGATTAAGAACACAGGCATA	1860
Qy	4217	GCAATATGATTAAGTACCTGATTAATGCGAACATGTTAAACGTTTCAAAATTAAT	4276
Db	1861	GCAATATGATTAAGTACCTGATTAATGCGAACATGTTAAACGTTTCAAAATTAAT	1920
Qy	4277	CGAATCTGCTCTGTGCTTCAATGAAGCCCTCATGTGAGTAGAGATCAGTTTCATC	4336
Db	1921	CGAATCTGCTCTGTGCTTCAATGAAGCCCTCATGTGAGTAGAGATCAGTTTCATC	1980
Qy	4337	AAAGAACAAATCTTGTGCAATGGGTGTATGGGTTCCAGATGTGATTTGGCAATC	4396
Db	1981	AAAGAACAAATCTTGTGCAATGGGTGTATGGGTTCCAGATGTGATTTGGCAATC	2040
Qy	4397	CTCATTTAAGTAAAGGTTAGCAGAGCAAGGTGCGTGTATAGCTGCTGTGTCGCGC	4456
Db	2041	CTCATTTAAGTAAAGGTTAGCAGAGCAAGGTGCGTGTATAGCTGCTGTGTCGCGC	2100
Qy	4457	TGTGTGTGCGGAGAGCTCTGCTGATGCTTCTCCCACTTGTGCTGCTGAGAGAA	4516
Db	2101	TGTGTGTGCGGAGAGCTCTGCTGATGCTTCTCCCACTTGTGCTGCTGAGAGAA	2160
Qy	4517	CCAGAGCAGACGACAGGCGGAAAGGCGCATCTAAGCGGTATCTAGGCTTTGCTAAT	4576
Db	2161	CCAGAGCAGACGACAGGCGGAAAGGCGCATCTAAGCGGTATCTAGGCTTTGCTAAT	2230
Qy	4577	GCGGCAAGTGTCTTTTACCTGATTTGATGATCATTCAATTAAGTTCCAGTTATAAT	4636
Db	2221	GCGGCAAGTGTCTTTTACCTGATTTGATGATCATTCAATTAAGTTCCAGTTATAAT	2280
Qy	4637	ATTGTGTAATTAATTAATTAAGTGAATAGAGCACTCATTTACAGTAACCTTAATT	4696
Db	2281	ATTGTGTAATTAATTAATTAAGTGAATAGAGCACTCATTTACAGTAACCTTAATT	2340
Qy	4697	TAAATATGCTAGTAAACATATGATTAATTTCTAGAAACAACTCTTAATAGAT	4756
Db	2341	TAAATATGCTAGTAAACATATGATTAATTTCTAGAAACAACTCTTAATAGAT	2400
Qy	4757	ATAATCCGTGAAATATAGGCTGATATATTAAGTTGACAGATAGACATGCTAGA	4816
Db	2401	ATAATCCGTGAAATATAGGCTGATATATTAAGTTGACAGATAGACATGCTAGA	2460
Qy	4817	AGCTGTAACAGAAATCATAGAAATATAGAGAGTTATGATGAACTTAAATATATA	4876
Db	2461	AGCTGTAACAGAAATCATAGAAATATAGAGAGTTATGATGAACTTAAATATATA	2520
Qy	4877	TGTTGCGACGATTTTATGTTAAATTTGTTATAGTTTATCTGCTGTATATGAAAT	4936
Db	2521	TGTTGCGACGATTTTATGTTAAATTTGTTATAGTTTATCTGCTGTATATGAAAT	2580

QY 4937 CTTTAAATCAACGCTGAAAGAAATCAGCAATTTAGTCTTCCAGGACACCCCAATATC 4996
Db 2581 CTTTAAATCAACGCTGAAAGAAATCAGCAATTTAGTCTTCCAGGACACCCCAATATC 2640
QY 4997 AGTCATGTGTAATGACACAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 5056
Db 2641 AGTCATGTGTAATGACACAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 2700
QY 5057 TTTTGTGTTTAAAGTTGATGATCTTCTCGAGGAAATAGTCACTCATCCACATCCACAT 5116
Db 2701 TTTTGTGTTTAAAGTTGATGATCTTCTCGAGGAAATAGTCACTCATCCACATCCACAT 2760
QY 5117 AAGGGTTTGTAGAGAGAGTCTGCTGCTGATGATGATGATGATGATGATGATGATG 5176
Db 2761 AAGGGTTTGTAGAGAGAGTCTGCTGCTGATGATGATGATGATGATGATGATGATG 2820
QY 5177 CTTTCTGTTAATAGTATCATCTTCTATGCCAAGAGGAAACATCCATTAACCTTTAGTC 5236
Db 2821 CTTTCTGTTAATAGTATCATCTTCTATGCCAAGAGGAAACATCCATTAACCTTTAGTC 2880
QY 5237 TTAATGTACATTCGATTCATTAATAATGATGATGATGATGATGATGATGATGATG 5296
Db 2881 TTAATGTACATTCGATTCATTAATAATGATGATGATGATGATGATGATGATGATG 2940
QY 5297 TGTGTTGTTGTTTCTGCTGACCTTTTCTATTTTTCGCTGCTGCTGCTGCTGCTGCTG 5356
Db 2941 TGTGTTGTTGTTTCTGCTGACCTTTTCTATTTTTCGCTGCTGCTGCTGCTGCTGCTG 3000
QY 5357 AACGAAGCGTTGGGATACCTTCAATTAATGATGATGATGATGATGATGATGATGATG 5416
Db 3001 AACGAAGCGTTGGGATACCTTCAATTAATGATGATGATGATGATGATGATGATGATG 3060
QY 5417 TTTCTGTTGTTGGGCTCAACGCTGATGATGATGATGATGATGATGATGATGATGAT 5476
Db 3061 TTTCTGTTGTTGGGCTCAACGCTGATGATGATGATGATGATGATGATGATGATGAT 3120
QY 5477 GAATGTACATATTTTGTGTAATTTATGATGATGATGATGATGATGATGATGATGAT 5536
Db 3121 GAATGTACATATTTTGTGTAATTTATGATGATGATGATGATGATGATGATGATGAT 3180
QY 5537 TGATGAACGTCATGTTTTCGCAAGACTGTAATATTTATTTATGATGATGATGATGAT 5596
Db 3181 TGATGAACGTCATGTTTTCGCAAGACTGTAATATTTATTTATGATGATGATGATGAT 3240
QY 5597 CAAAATTTCCACACTGAAACCTGCACTGATGATGATGATGATGATGATGATGATGAT 5656
Db 3241 CAAAATTTCCACACTGAAACCTGCACTGATGATGATGATGATGATGATGATGATGAT 3300
QY 5657 AGGAATAAATGTAAGAAAGGTTTCTAAAAAAGGTTTCTAAAAAAGGTTTCTAAAA 5695
Db 3301 AGGAATAAATGTAAGAAAGGTTTCTAAAAAAGGTTTCTAAAAAAGGTTTCTAAAA 3339

BTTHROM2 4697 bp mRNA linear YAM 22-JUL-2000
B.taurus mRNA for thrombospondin 2.
X96540
VERSION X96540.1 Gi:2995137
KEYWORDS thrombospondin 2.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Aguesse-Germon,S., Penhoat,A., Chen,H., Mosher,D.F., Chambaz,E.M.,
Mammalia; Bovidae; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 Danik,M., Chinn,A.M., Lafuillade,B., Keramidas,M.,
Aguesse-Germon,S., Penhoat,A., Chen,H., Mosher,D.F., Chambaz,E.M.
and Feige,J.J.
TITLE Bovine thrombospondin-2: complete complementary deoxyribonucleic
acid sequence and immunolocalization in the external zones of the
adrenal cortex

JOURNAL Endocrinology 140 (6), 2771-2780 (1999)
MEDLINE 99272286
PUBMED 10342868
REFERENCE 2
AUTHORS Feige,J.J.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-1996) J.J. Feige, Inserm U 244, DBMS/BRCE,
CEA/Grenoble, 17 rue des Martyrs, F-38054 Grenoble Cedex 9, France
REMARK revised by [3]
REFERENCE 3 (bases 1 to 4697)
AUTHORS Feige,J.J.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1998) J.J. Feige, Inserm U 244, DBMS/BRCE,
CEA/Grenoble, 17 rue des Martyrs, F-38054 Grenoble Cedex 9, France
COMMENT On Mar 28, 1998 this sequence version replaced gi:2695840.
FEATURES
source
1..4697
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cell_type="primary cultures of fasciculata-reticularis
cells"
/dev_stage="adult"
1..2066
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="D268C1"
/cell_type="primary cultures of fasciculata-reticularis
cells"
/dev_stage="adult"
2067..4697
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="PAC-6"
/cell_type="primary cultures of fasciculata-reticularis
cells"
/dev_stage="adult"
/notes="obtained by RACE-PCR"
501..4013
/codon_start=1
/product="thrombospondin 2"
/protein_id="CAA65385.1"
/db_xref="GI:2995138"
/db_xref="GCA:Q95116"
/db_xref="SWISS-PROT:Q95116"
/translation="MLWPLLLALWAPSAQGDQDDEDAFLDLSISNINRKTIGAKQ
FRGDPSPVAYRFVRFYIPVSAEHLGITAMRRKEGFFLTASMKQDRSRGTLILA
LEGPGATHRQFEIVSNGPADTLDITYVDGTQHVISLEDVGLADSQKQNTVQVGTET
YSLVVGCDLMDSPALDEPFVHLOTERRSMVYTKGAARSHFRGLQNVLYVFNESVE
DILSKGCOOSOGAETNAISENTEHLSPMVTMEHVGPSSAEKSPVCHSEBELGSM
IRELSGLHIVNQLHENLAKVSNDAQPLMELIGGPKTRNVSAQWODGRFFAENETWV
VDSCTKCKFKIVCHQISCPTACDAEFWVEGECPCPCVDGEGSGMFAEWTSCT
ATCGSTGQGRGSCDVTSTNCLGPSIQTRACSLGRCDHRIHQDGGWHSWSPSSCSVT
CGVNTVRLNCSVPVQMGSRGSKGRETACQCPGPFVDRGSPWSPWSACTVTC
AGGIRERTVCSNPEPGHGGKCVGAGQCMNRKSCPIIDGCLSNPCFPFGACSSFP
DWSGSCGSPGFLNGTTCEDLDECAVVDVCFATSKAHRCVNTNPGVHCLPCPPRY
KGNQFVGLAARTEKQVCEPENCKDTHSCHRAECTIYLGHFSDPMYKCCQGY
AGDGLICGSDSLDGFNENLVCATNATVCKDNCPLLPNSQGFDDXGIGACDD
DDNDGVSDEKNCQLFLNPRQFDYDKDSVGBRCNCPYHNPQAQIDTDNNGEGDACS
VIDDGDVNERNCBPVYNTDQRTDGGVDHCDNCPVHNPFDQTDVDNVLVGQC
DNNED:DEGHQNNQNCPIPNANQADHRRGQGDACSDDDNDGIDPDRDNCRLVA
NPQEDSDGDRGDAKDFDNDIPIIDVCFENNAISETDFRNFQVHLDYKGTQ
IDNWRVHOGKELVOTANSDPGIAVGFDFSVDFSGTFYVNTDRDDYAGVFGYQ
SSRFVYVMWQVQTVWEDQPTAYGVSGLKVVNSTTGTGCHLRNALMHTGTEG
QVRLMHPDKNIGKDYTAVRWELTHRPKTYIRVLVHSGKQVWADSGPIYDQTYAGG
RLGLFVSQBMVYFSLKYECDV"
555..4010
/product="thrombospondin 2"
2721..2723
/notes="clone PAC-1"
/replace=""/>

ORIGIN

Query Match	50.8%	Score 2845.2	DB 4	Length 4697	
Best Local Similarity	84.6%	Pred. No. 0			
Matches 3268	Conservative	0	Mismatches 578	Indels 16	Gaps 6
QY	120	GCAGGAGCAGGATGCTCTGAGAGCTGGTCTGTGTGCTCTGTGGGTGTGGCCAGCAG	179		
DB	489	GGAAGCGCAGGATGCTGTGSCACTGCTGCTGTGSCCTGTGGGCTGGCCAGCGCT	548		
QY	180	CRAGCTGGTCAACAGGCAAAAGACACACCTTCGACCTTTTCAGTATCAGACATCAAC	239		
DB	549	CAGCAGGAGACCAAGCAGGAGCACCGCTTTCGACCTTTCAGCATCAGCAACATCAAC	608		
QY	240	CGCAAGACCATTGGCGCCAAAGCAGTTCGCGGGGCCGACCCCGCGCTGTACCGC	289		
DB	609	CGCAAGACCATTGGCGGCCAAAGCAGTTCGCGGGGCCGACCCGCGCTGTACCGC	668		
QY	300	TTGCTGGCTTTGACTACATCCACCGGTGAAACGACATGACCTCAGCAGATCAACAAG	359		
DB	669	TTGCTGGCTTTGACTACATCCCGCGGTGAGCGCGGAGCCTTGGGCCCGATCACCGAG	728		
QY	360	ATCATGCGGAGAGGAGGGCTTCTTCTCTCACGGCCCCAGCTCAAGCAGGACGGCAATGC	419		
DB	729	GCCATGCGCGCAGGAGGGCTTCTTCTGACGGCCAGCATGAAGCAGGACCGCGGTCC	788		
QY	420	AGGGGACGCTGTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGCAAGTTCGAGATCGTC	479		
DB	789	CGGGGCACTTGTCTGGCAGCTGGAGGGGCCGGGCCACGACAGGCAAGTTCGAGATCGTG	848		
QY	480	TCCAAACGGCCCCGGGACACGCTGGATCTCACCTTACTGGATTTGACGGCACCCCGCATGTG	539		
DB	849	TCCAAACGGCCCCGGGACACCTTGGACCTCACTTACTGGGTGGACGGCACCCAGCACGTC	908		
QY	540	GTCTCCCTTGAGGACGCTGGCTTGGCTGACCTGCGAGTGGAGACGTCACCGTCAGGTG	599		
DB	909	ATCTCCCTTGAGGACGCTGGGCTTGGCTGACTCCAGTGGAAAGACGTCACCTGTCAGGTG	968		
QY	600	GCTGGCAGAGACTACAGCTTGACGCTGGGCTGGACCTCATAGACAGCTTCGCTCTGGAC	659		
DB	969	ACGGGAGAGACTACAGCTGTACGCTGGGCTGCGACCTGATGGACAGCTTCGCGCTGGAC	1028		
QY	660	GAGCCCTTTCAGGACACTTCGAGCGGCGAAGAGCGGATGTACGTGGCCCAAGGCTCT	719		
DB	1029	GAGCCCTTTCAGGACACTTCGACCGAGAGGAGCGGATGTACGTGACCAAGGGCGCA	1088		
QY	720	GCCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAAAGCTTCACTAGTGTGTGAAACTCT	779		
DB	1089	GCCCGCAGAGAGCTTCAGGGGTTTGCTGCGAAGCTTCTACTAGTCTTGTGAAACTCT	1148		
QY	780	GTGGAAGATATCTTAAGCAAGAGGTTGCCAGCAAGCCGAGGAGCTGAGATCAAGCC	839		
DB	1149	GTGAGGATCTTCTGAGCAAGAAAGTTGTGAGCAGAGCGGAGGAGCTGAAACCAATGCC	1208		
QY	840	ATCAGTGAGAAACAGAGACGCTGCGCTGGGTCCGATGTGCACCCAGTACGTGGC	899		
DB	1209	ATCAGTGAGAAACAGAGACGCTGCACCTGAGCCCATGCTGTCACCATGAGCAAGTGGC	1268		
QY	900	CCAGCTCAGAGAGAGGCCCGAGGTGTGCAACGCTCGTCGAGGAGCTGGGAAACATG	959		
DB	1269	CCAGTGCAGAGAGAGGCCCGAGGTGTGAGCACTCTGTGAGGAGCTGGCAGCATG	1328		
QY	960	GTCCAGGAGCTCTCGGGGCTCCAGTCTCTGTGAAACCAAGCTCAGCGAGAACCTCAAGAGA	1019		
DB	1329	ATCCAGAGCTCTCGGGGCTGCAGCTCATCTGTGAACCAAGCTCCACAGAACCTCGCAAA	1388		
QY	1020	GTGTGGAATGATAACCACTTTCTGTGGAGCTCATTTGGTGGCCCTCTCAAGCAGAGAAC	1079		
DB	1389	GTGTCAAAATGACAACCACTTTCTGTGGAGCTCATTCGGCGGGCGGCCCCAGACCAAGAAC	1448		
QY	1080	ATGTCAGCTTCTGGCAGGATGGCCGGTTCTTTGCGGAAATGAAACGTGGGTGGTGCAC	1139		
DB	1449	GTGTCCGCTCTGCAAGAGCGCCGGTTCTTTGCGGAGATGAGACTGGGTGGTGGAC	1508		

Qy	1140	AGTGTGACACGCTGTATCTTGTCGAGAAATTTAAACCATTTGCCACCAATATCACTGCGCG	1119
Db	1509	AGCTGTACCAAGTGCACGTGTCAGAAATTTAAGACTGTTTGGCACCAATTCAGCTGCGCG	1568
Qy	1200	CTGTCAACCTGCGCCAGTCCATCCTTTGTGGAGGGCAATGCTGCCCTTCCCTGCCTCCAC	1259
Db	1569	CCGCGACGTGTGCGGACCCCTGGTTCTGTGGAGGGCGAGTGTCTGCCGCTCTGCGTCCA-	1627
Qy	1260	TCGGTGAACGGTGTAGAGAGGCTTGTTCTCGTGGGCAGAGTGGACCCAGTGTCTCCGTGACG	1319
Db	1628	-----TGACGGAGAGAAAGGCTGGTCCCGTGGCGGAGTGGACGAGTGTCTCAGCCACC	1682
Qy	1320	TGTGGCTCTGGGACCCAGACAGAGAGGCGCGTCTGTGACGTCAACGACCAACCTGCTTG	1379
Db	1683	TGCGGGTGGGACCCAGCAGCGGGCGCTCTCTGTGA-TGTACCAAGCAACCTGCTGCTG	1742
Qy	1380	GGGCCCTCCATCAGACACGGGCTTCAGTCTGAGCAAGTGCACACCCGCATCCGGCAG	1439
Db	1743	GGGCCGTCCATCAGACACGGGCTCGAGCTGGGCAAGTGGCAGCACCCGCATCCGGCAG	1802
Qy	1440	GAGGGGGCTGGAGCCACTGGTCACCTTGCTCTTCATGTCTGTGACCTGTGAGATTGGC	1499
Db	1803	GACGGCGCTGGAGCCACTGGTCGCGTGTCTCTCTGTCTCAGTGAACCTGCGCGTCCGC	1862
Qy	1500	AATATCACCGCATTCGTCTTCGAACCTCCCACTGCCCAGATGCCCAGATGGGGGCAAGATTGC	1559
Db	1863	AACGTACCCGATATCCGCCCTCTGCACTGCCCACTGCCGAGTGGCGGAGATGGGGGCCGAGCTGC	1922
Qy	1560	AAAGGGAGTGGCCGGGAGACAAAGCCTGTCAGGGCGCCCCATGCCCAATCGATTGGCGCG	1619
Db	1923	AAGGGCAGCGGCGGTGAGACCAAGGCGTGCAGGGCCCGCCCTGCCCGGTGGATTGGCGCG	1982
Qy	1620	TGGAGCCCTGGTCCCGTGGTCCCACTGCCAGTGCACNTGTCGGTGGATCCCGGGAG	1679
Db	1983	TGGAGCCCCGTGGTCCCGTGGTCCCACTGCCAGTGCACAGTCACTTGCTGTGAGGGATCCGTGAG	2042
Qy	1680	CGCACCCGGTCTGCACACAGCCCTGAGCCTCAGTACGAGGGGAAGCCTGCTGGGGGAT	1739
Db	2043	CGGACACGCTCTGCACACAGCCCGAGCCCGCCAGCAGCGGGGCAAGACTGCTGGGGGGC	2102
Qy	1740	GTGCAGAGCGGTGAGATGTGCACACAGAGAGCTGCCCCGTGGATGCTGTTATTCACAC	1799
Db	2103	GCCAGGAGCAACAGATGTGTACAGGAAGAGTGTCCCATAGACGCTGCCTGTGTCCAAC	2162
Qy	1800	CCCTGTTCCTGGGAGCCAGTGCAGCAGTTTCCCGATGGGTCTCGTCTCATGCGGCTCC	1859
Db	2163	CCCTGTCTCCTCGAGCTGAGTGAGCAGCTTCCCCACGCGCTCCTGTCTCTGGGGTCC	2222
Qy	1860	TGCCCTGGGGCTTCTGGCAATGGCACCCACTGTGAGACCTTGGACGAGTGTGCCCTG	1919
Db	2223	TGCCCGGGGGCTTCTTGGGCAACGGCACCCCATGTGCGAGACCTGGACGAGTGTGCCCTG	2282
Qy	1920	GTCCCCGACATCTGCTTCTCCACAGCAAGGTGCTCGCTGTGTCAACACTCAGCCTTGGC	1979
Db	2283	GTACGAGACGTGTGTTTCGCAAACAGCAAGGCACACCGCTGTGTCAACACCAACCCCGCC	2342
Qy	1980	TTCCACTGCTGCCCTGCCCGCCCGATACAGAGGGAAACAGCCCGTGGGGTGGCGCTG	2039
Db	2343	TACCACCTGCTTCGCCCTCCCGCCGCTACAGGGGAACCAAGCCCTTGGTGTGCGGCTG	2402
Qy	2040	GAAGCAGCCAGACGGAAAAAGCAAGTGTGTGAGCCCGAAACCCCATGCAAGGACAAGACA	2099
Db	2403	GAGCGCGCCAGGACTGAGAAAGCAGGTGTGTGAGCCCGAGAACCCCTGCAAGGACAAGACC	2462
Qy	2100	CACAACTGCCACRAGCAGCGGAGTGATCTTACTTGGGCCACTTCAGCGACCCCATGTAC	2159
Db	2463	CACAGTGTCCACCGGCACGCGAGTGTATCTCTGTGGCCACTTCAGGACCCCATGTAC	2522
Qy	2160	AAGTGCAGTGTCCACAGACAGGCTACGCGGGCGAAGGGCTCATCTGTGGGGAGGATCTCGAC	2219
Db	2523	AAGTGCAGTGTCCACAGCGGGTACGCGGGTCAAGGGGTCTATCTGTGGGGAGGATCTAGAC	2582

2y 2220 CTGACGGCTGCCCCAACCTCAATCTGGTCTGCGCCACCAACGCCACCTACCACTGCATC 2279
Db 2583 CTGATGGCTGGCCCAACAAGAACTTGGTGTGGCCACCAACGCCACCTACCACTGCCTC 2642
2y 2280 AAGGATAAATGCCCCCACTCTGCCAAATCTTGGGCGAGGAAGACTTTGACAAAGGACGGGAAT 2339
Db 2643 AAGGATAAATGCCCCCTCTCTGCCCAACTCAGGGCAAGAAAGACTTCGACAAAGGATGGCATC 2702
2y 2340 GGCATGCTGTGATGATGACGATGACATGACGCTGTGACCGATGAGAAGGACAACTGC 2399
Db 2703 GGGACGCCCTGCGACGACGATGACAAACGACGGCGTCTCGACGAGAAAGGACAACTGC 2762
2y 2400 CAGCTCTCTTCAATCCCGCCGACGCTGACTATGACAAAGGATGAGGTGGGGACCGCTGT 2459
Db 2763 CAGCTTCTCTTCAACCCCGCTCAGTTCGACTACGACAAAGATGAGTTCGGGGACCGGTGC 2822
2y 2460 GACAACTGCCCTTACGTGACAAACCCCTGCGGACGATGACGACAAACAAATGAGAGGGT 2519
Db 2823 GACAACTGCCGTATGTTTCAACACCCCGCCGACGATGACGACAAACAAACCGGGGAGGT 2882
2y 2520 GACGCTGCTCCGTGGACATGATGGGGACGATGCTTCAATGAACGAGACAATGTGCC 2579
Db 2883 GACGCTGCTCCGTGGACATGACGCGGACGATGCTTCAACGAGCGAGCAACTGTGCC 2842
2y 2580 TACGCTTACAACTGACGAGGACCAACCGTGTGACGATGATGACGCTGTGGGGATCACTGTGAC 2639
Db 2943 TACGCTTACAACTGACGAGGACCAACCGTGTGACGATGATGACGCTGTGGGGATCACTGTGAC 3002
2y 2640 AACTGCCCCCTGTTGCAACCCCTGACGACGACGCTGACGATGACCTTGTGGGAC 2699
Db 3003 AACTGTCGCTGGTGGACAAACCCCGACGACGACGCTGACGACGACCTGCTGGGAGAC 3062
2y 2700 CAGTGTGACAAACGAGGACATAGATGACGACGCGCCACGACAAACACGAGGACAACTGC 2759
Db 3063 CAGTGTGACAAACGAGGACATGACGAGGACGCGCCACGACAAACACGAGGACAACTGC 3122
2y 2760 CCTTACATCTCAACGCCAACGAGCTGACCATGACGACGCGCCAGGCGGCGCTGT 2819
Db 3123 CCCACATCTCCCAACGCGCAACGAGCGGACCATGACGCGCGCCAGGCGGCGCTGT 3182
2y 2820 GACCTGATGATGACAAAGTGGGTCCCGGATGACGAGGACAACTGCGGCTGTGTTTC 2879
Db 3183 GACTCGGACGACGACATGATGGATCCCGACGACGAGGACAACTGCGGCTGTGCGCC 3242
2y 2880 AACCCGACGAGGAGCTTGGACGCTGATGACGAGGCGGTGATTTCTAAGATGATTT 2939
Db 3243 AACCCGACGAGGAGCTGATGAGGCGGACGCGGCTGGGACGCTTGTAAAGACGACTTC 3302
2y 2940 GACATGACAACTCCCAATGATGATGATGCTGCTGAAACAAATGCCATCAGTGAG 2999
Db 3303 GACAAACGACGATTTCTGATATTGACGACGCTGTGTCGAGAACACGACCATCAGCGAG 3362
2y 3000 ACAGACTTCAGGAATTCAGATGCTCCCTTGGATCCAAAGGAGCACCCCAATTTGAT 3059
Db 3363 ACAGACTTCAGGAATTCAGATGCTCCCTTGGATCCAAAGGAGCACCCCAATTTGAT 3422
2y 3060 CCCAACTGGGTCTTTCGACATCAAGGACGAGTGTTCAGACGACCAACTCGGACCCC 3119
Db 3423 CCCAACTGGGTCTTTCGACATCAAGGACGAGTGTTCAGACGACCAACTCGGACCCC 3482
2y 3120 GGCATGCTGTAGTGTTCAGAGTTGGGTCTGTGGACTTCAGTGACATTTACGTA 3179
Db 3483 GGCATGCTGTAGTGTTCAGAGTTGGGTCTGTGGACTTCAGTGACATTTACGTA 3542
2y 3180 AACACTGACGGGACGACGACTATGCGGCTCTGCTTGGTTACCACTCAAGCAGCCGC 3239
Db 3543 AACACTGACGGGACGACGACTATGCGGCTCTGCTTGGTTACCACTCAAGCAGCCGC 3602
2y 3240 TTCTATGTTGATGTGAAGCAGGTGACGACGACCTACTGGGAGGACCAAGCCACGCG 3299
Db 3603 TTCTATGTTGATGTGAAGCAGGTGACGACGACCTACTGGGAGGACCAAGCCACGCG 3662
2y 3300 GCCTATGCTACTCGGCGTGTCCCTCAAGTGGTGAACCTCCACCGGGACGCGGCGAG 3359

Db 3663 GCCTACGGCTACTCGGGGTGTCCCTCAAGGTGGTGAATCTCACACCGGCGACGGGTAG 3722
2y 3360 CACCTGAGGAACGCGCTGTGGCACACCGGGAAACACGCGGGGAGGTCCGAACCTTATGG 3419
Db 3723 CACCTGAGGAACGCGCTGTGGCACACCGGGAAACACAGAGGGACAGGTTTCGCACTATGG 3782
2y 3420 CACGACCCCAAGGAACATTTGGTGGAGGACTACACGGCCTATAGTGGACCTGACTCAC 3479
Db 3783 CACGACCCCAAGGAATATCGGCTGGAGGACTACATCGCTACCGGTGCATCTGACCCAC 3842
2y 3480 AGSCCAAGACTGGCTACATCAGAGTCTTAGTGATGAAGGAAACAGGTTCATGSCAGAC 3539
Db 3843 AGSCCTAAGACAGGCTACATAAGAGTCTTAGTACATGAAGGAAACAGGTTCATGSCAGAC 3902
2y 3540 TCAGACCTATCTATGACAAACCTTACCTGGCGGGCGCTGGGTCTATTTGCTCTCTCT 3599
Db 3903 TCAGACCCATCTATGACAAACCTTACCTGGCGGGCGCTGGGTCTATTTGCTCTCTCT 3962
2y 3600 CAAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATCAGAGATATTTAAACAAGATTT 3659
Db 3963 CAAAGATGGTCTACTTCTCGACCTCAATATGAATGACAGATGTCTAAGCAAGATTT 4022
2y 3660 GTGCAATTCGGGAATCGCTGTGATGCGATGCTGCTCCTAGACACCTCAGTTCATTTGTG 3719
Db 4023 GCTGTGTTTTCAGCAAGTACTGTAAATGC--TGTACCCAAACACCTCAGTTCATTTCCA 4080
2y 3720 GTCTTGTGGTCTCTCTCTAGCAGACCTCTCTGCTTGAACCTTAACTCTGATGTT 3779
Db 4081 GTGCTTCAGTACTCTCTTAGCA--AACCTCTATCCCTGACCCCTAACCTGAGTGT 4138
2y 3780 CTTACCTCTCTGCGAGCAACCCCAACCCCAAGTGTGCTTCAGAGGATAAATATCAATGGAA 3839
Db 4139 CTTACCTCTCTCTCTCAA--CCCAAGCCCAATTTGCTTCAGAGGATAAATATCAATGGAA 4197
2y 3840 CGCAGAGATGAACATCAACCCACCTAGAGG--AAACAGTGTGGTGTATATGAGACTTTA 3898
Db 4198 CTGAAGATGAACGCTCAACCCATCAGGAAAGCAGTTTGAACCCACGAGACTTCA 4257
2y 3899 TGTGAGTGAATTTGGCATGCCATTCATTTGCT--TTTCTTGTGTTTAAAAAG 3954
Db 4258 TGTGAGTGAATTTGGCATGATATTCATTTGTTTCTTTCTCTGTTAAAAAG 4317
2y 3955 AATGAGTTTACATATAAATG 3976
Db 4318 AATGAGTTTACATATAAATG 4339
RESULT 9
BC053702
LOCUS
DEFINITION
Mus musculus thrombospondin 2, mRNA (cDNA clone MGC:60568
IMAGE:30062369), complete cds.
ACCESSION
BC053702
VERSION
MGC.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 4125)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, I., Wang, J., Hsieh, P.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonald, M.P., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Udell, T.B., Toshiki, S.,
Carrin, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

599	CCAACTTCCTGGAGGATGTGGGCTGGCTGACTCCAGTGGAAAGATGTGACTGTGCAGG	658
598	TGGTGGCGAGACCTACAGCTTGACAGTGGGCTGGGACCTCATAGACAGCTTCGCTCTGG	657
659	TGGCCAGTGACACTATAGCTGTATGTGGGCTGGATCTTATCGACAGTGTCACTCTGG	718
658	ACGAGCCCTTCTAGGACCACTCGAGCGGGAAGACAGCCGATGTACGTGGCCAAAGGCT	717
719	AAGAACCATTTCTATGAGCAGCTAAGATGAGACAGAGCAGATGTATCTGGCCAAAGTG	778
718	CTGCCAGAGAGTCACTTCAGGGGTTTCCTTTCAAGACGTCCACTAGTGTGTGAAAAC	777
779	CATCTCAGAGAGTCACTTCAGGGGCTTCTCAGCAATGTCCATCTCGTGTTCAGATT	838
778	CTGTGGAGAGATTTCTTAAGCAAGAGGTTGCCAGCAAGGCCAGGAGCTCAGATCAACG	837
839	CTGTGGAGATATCTTAGCAGAAAGGCTGTCAACACAGCCAGGAGCTGAGTCAACA	898
838	CCATCAGTGAACACACAGAGACCTCGGCTCGGTCGCGATGTCAACACGAGTACGTGG	897
899	CCATCAGTGAACATACAGAGACTCTCCATCTGAGCCCTCATCACCAACAGATCTCGTGG	958
898	GCCCCAGCTCAGAGAGAGGCCCGAGGTGTGCGAACGCTCGTGCGAGGAGCTGGGAAACA	957
959	TCCAGGTTGTGAGAGGACACAGAGAGTGTATCGCATCTCTCGAGGAGTTGAGCAACA	1018
958	TGGTCCAGGAGCTCTCGGGCTCCACGTCTCTGTGAAACACAGCTCAGCGAGAACCTCAAGA	1017
1019	TGATGAATGAGCTCTCTGAGACTCCACGTATGGTGAACCGAGCTGAGCAAGAACCTGGAGA	1078
1018	GAGTGTGGAATGATAACCACTTCTCTGGGAGCTCATTTGGTGGCCCTCCTAAGACAAGGA	1077
1079	GAGTGTCTAGTGATAACCACTTCTTTTGGAGCTCATTTGGGGGCCCTCTGAGACAGAA	1138
1078	ACATGTCACTTGTGCGAGATGGCCGGTTCCTTTGCGGAAATGAAACGTGGGTGGTGG	1137
1139	ACATGTCACTGTGTGCGAGGGCCGAATCTTTGCGAGAAATGAAACCTGGGTGGTGG	1198
1138	ACAGTGCACACAGTGTACCTGCAAGAAATTTAAACACATTTGCCACCAATCACCTGCC	1197
1199	ATAGTTGTACCATGCACCTGCAAGAAATTTAAACAGTCTGCGCATCAGATCACCTGCT	1258
1198	CGCTGCAACCTGGCCAGTCCATCTTTGTGGAAGGGAATGCTGCCCTTCCTGCCCTCC	1257
1259	CACCTGCAACTGTGCCAACCCCATCTTTTGTGGAAGGCGAGTGTGTCATCTCTGTTTCC	1318
1258	ACTCGTGGACGCTGAGGAGGCTGTGCTCCGTGGGCAGAGTGGAACCCAGTGTCCGTGA	1317
1319	ACTCTGCAGACAGTATGAGGCTGTCTCCGTGGGCAGAGTGGACCGAGTGTCTGTCA	1378
1318	CGTGTGCTCTGGACCCACAGAGAGGCGGTCTCTGTGAAGTCAACAGCAACACCTGCT	1377
1379	CCTGTGCTCTGGACCCACAGAGAGGCGGTCTTGTGTATGTACACAGCAACACCTGCC	1438
1378	TGGGGCCCTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCAATCCGGC	1437
1439	TGGGCCCTCCATTCACAGACATGCAGCTGGGCAAAATGTATACGAGAATCCGTC	1498
1438	AGGACGGGCTGAGGACCATGTGTACCTTGTCTTCATCTCTGTGACCTGTGGAGTTG	1497
1499	AGAATGAGGCTGGAGTCACTGTGTACCTGTGTCTTCATGTCTCGTGTACTTGTGGAGTTG	1558
1498	GCAATATCACACGATCCGCTCTCTGCAACTCCCACTGCCAGTGCCTCCAGATGGGGGCAAGATT	1557
1559	GCAATGTCAACCGCATACGTCTCTGCAACTCACCACTGCGCTGCCAGATGGGTGGCAAGAACT	1618
1558	GCMAAGGAGTGGCCGGGAGCAAGCTGCCAGGGGCCCCCATGCCCAATCGATGCC	1617
1619	GCMAAGGAGGCGGGCCGGGAAACCAACCTCTGTACGGTGTCTCGTGGCCCAATGATGCC	1678
1618	GCTGAGGCCCTTGCTCCCTGTGTGGCCTGTGCTACCTGTGCGCGGTGGATCCGGG	1677

1679	GCTGGAGCCCTGGTCCCTTGGTCTAGCGCTGCACAGTTACCTGTCTGGAGGATCCGTG	1737
1678	AGCGCACCCGGGTCTGSAACAGCCCTAGAGCCTCAGTACGGAGGAAAGCCTCGTGGGGG	1737
1739	AGGCTCACGTGTTTGCACAGCCCTGAGCCCCAGTATGGAGGAAAGCACTGTGTGGGG	1798
1738	ATGTGAGGAGCGTCAGATGTGCAACAAGAGGAGCTGCCCGCTGGATGGCTGTTTATCCA	1797
1799	ATGTGACAGAACACCAATGTGTGCAACAGAGAACTGCCCTATTGATGGGTGCTTATCCA	1858
1798	ACCCCTGCTTCCCGGAGACCCAGTGCAGCAGCTTCCCAGTGGGTCTGTGTCATGGCGCT	1857
1859	ACCCTGTGTTTCTGAGGACCAAGTGAACAGCTTCCCTGATGGGTCTGTGCTGTGGCT	1918
1858	CTTGCCTGTGGGCTCTTCTTGGGCAATGGCAACCACTGTGAGGACCTGCGAGAGTGTGCC	1917
1919	CCTGCCAGTGGCTTCTTGGGCAATGGTACCCACTGTGAGGACCTGGATGAGTGTGCTG	1978
1918	TGGTCCCCAGATCTGCTTCTCCACAGCAAGGTGCTCGCTGTGTCAACACTCAGCGCTG	1977
1979	TGGTCAAGATATTTGCTTCTCAACTAACAAGCTCCCCGCTGTGTCAACCAACACCCGG	2038
1978	GCTTCCACTGCCCTGCCCTGCCGCCCCCGCATACAGAGGGAACCAAGCCCGTGGGGTCGGCC	2037
2039	GCTTCCACTGCCCTGTGTCACCAACGCTACAAAGGGGAACCAACCTTCGTGTGCGCC	2098
2038	TGGAAGCAGCAAGACGGAAGAAGCAAGTGTGTAGAGCCCGAACCAGATGCAAGGACAGA	2097
2099	TGAGGATGTAGGACAGAAAAACAAGTGTGTAGCCAGAGATTCATGTAAAGACAGA	2158
2098	CACAACTGCCACAAGACCGGAGTGCAATCTACTTGGGCCCACTTCAGCGACCCCAATGT	2157
2159	CTCACAGCTGCCACAAGATGCAAGTGTCACTTACCTGGGCCCACTTTAGTGAACCCATGT	2218
2158	ACAAGTGCAGTCCGACACAGGTAGCGGGCAGCGGCTCATCTCGGGGAGACACTCGG	2217
2219	ACAAGTGTAGTCCAGATTGGCTACGAGGTGATGGGCTCATCTCGGGGAGAGACTCAG	2278
2218	ACCTGAGCGCTGGCCCCAACCTCAATCTGGTCTGGCCACCAACCGCACCTACCACTGCA	2277
2279	ACCTGGATGGCTGGCCCCAACCAACACTGGTGTGTGCTACTAATGCCACCTACCAACGCA	2338
2278	TCAGGATACTGCCCCCATCTGCCAAATCTCGGCGAGGAAGACTTTGACAAAGACGGGA	2337
2339	TCAGGACAACTGCCCCAAACTGCCAAATTCGGGCAGAGAGATTTTGATAGGATGGAA	2398
2338	TTGGCGATGCTGTGATGATGACGATGACAATGACCGGTGTGACCGATGAGAAAGACAAT	2397
2399	TCGGAGATGCTTGTGACGAGGACGATGACAATGACCGTGTGAGCGATGACAGGACAAAT	2458
2398	GCCAGCTCTCTTCAATCCCGCCAGCGCTGACTATGACAAGGATGAGTTGGGACCGCT	2457
2459	GCCAGCTCTCTTCAATCCCGCTCAATTAGACTATGACAAGGATGAGTTGGAGACCGCT	2518
2458	GTGACAACTGCCCTTACGTGCAAAACCTGCCAGATTCGACACAGACAACATGGAGAGG	2517
2519	GTGACAACTGCCCTATGTGCAAAACCCAGACAGATTCGACACAGACAACATGGCGAGG	2578
2518	GTGACGCTCTCCGTGGACATTTGATGGGACCATGTCTTCAATGAACAGAGACAATGTCT	2577
2579	GGATGCCCTCTGTGTGCATTTGAACGAGACGATGTTTTCAATGAGCGGAGACAATTGTC	2638
2578	CCTACGTCTTACAACTGACACGAGGACACCGGATGGTGAACGGTGTGGGGGATCATCTGTG	2637
2639	CATATGCTTACAACTGACAGAGACATGATGATGACGCGCACCAAGACAACCAAGACAAC	2698
2638	ACAACTGCCCTTGGTGCAAAACCTGACCAAGACCGAGTCGATGCAATGATCTGTTGGGG	2697
2699	ACAAATGCTCTGTGTGCAAAACCCAGATCAGATCGATCAGGACAATGATCTCGTTGGAG	2758
2698	ACAGTGTGCAAAACACGAGGACATATGATGACGAGCGCCACCAAGACAACCAAGACAAC	2757
2759	ACAGTGTGCAAAACATGAGGACATGATGATGACGCGCACCAAGACAACCAAGACAAC	2818

2758 GCCCTACATCTCCAAAGCCAAACAGGCTGACCATGACAGAGCGGCGGCGAGCCCT 2817
2819 GCCCATACATCTCCAAAGCCAAACAGGCTGACCATGACAGAGCGGCGGCGAGCCCT 2878
2818 GTGACCTGATGATGACAAAGATGGCGTCCCGATGACAGGCAAACTGCGGCTTGTGT 2877
2879 GCGACTCTGATGATGACAAAGATGGCGTCCCGATGACAGGCAAACTGCGGCTTGTGT 2938
2978 TCACCCAGACCCAGGAGGACTTGACCGGTGATGAGCGGGTGATTTTGTAAAGATGATT 2937
2939 TCACCCAGACCCAGGAGGACTTGACCGGTGATGAGCGGGTGATTTTGTAAAGATGACT 2998
2938 TTGCAATGACAAACATCCAGATATTGATGATGTGTCTCGAAACAAATGCCATCAGTG 2997
2999 TTGCAATGATTAATGTCCAGATATTGATGATGTGTGCCCTGAGAACAAATGCCATCAGTG 3058
2998 AGACAGACTTCAGGAATCTTCAGATGTGTCCCTTGGATCCCAAGGAGCACCCCAATTTG 3057
3059 AGACAGACTTCAGGAATCTTCAGATGTGTCCCTTGGATCCCAAGGAGCACCAAAATTTG 3118
3058 ATCCCAACTGGGTCAATTCGCCATCAAGGCAAGGAGCTGTTCAGACAGCCAACTCGGACC 3117
3119 ATCCCAACTGGGTAAATTCGTCAACAGGCAAGGAGCTGTTCAGACAGCAAACTCAGACC 3178
3118 CCGCATCGCTGTAGCTTTGACAGATTTGGCTGTGGACTTCAGTGCGACATTTACG 3177
3179 CTGGCATCGCTGTAGCTTTGACAGATTTGGCTGTGGACTTCAGTGCGACATTTCTATG 3238
3178 TAAACACTGACCGGAGCAGACACTATCCCGGCTTCGTCTTTGGTTACAGTCAAGCAGCC 3237
3239 TCAACACTGACCGGAGCAGACTATCCCGGCTTCGTCTTTGGTTACAGTCAAGCAGCC 3298
3238 GCTTCTATGTGGTATGTGAAGCAGTGTGACGAGCTACTCTGGGAGGACCAACCCACGC 3297
3299 GCTTCTATGTGGTATGTGAAGCAGTGTGACGAGCTACTCTGGGAGGACCAACCCACGC 3358
3298 GGGCTATGGTACTCCGGCGTGTCCCTCAAGGTGTGAACTCCACACGGGAGCAGGCG 3357
3359 GGGCTTACGGCTACTCTGGTGTGTCACTCAAGTGTGTAATCTCCAGACTGTGTCTGGG 3418
3358 AGACCTGAGGAAACGGCTGTGGGACACAGGGGAAACAGCCGGGCGAGTGTGCAACTTAT 3417
3419 AGACCTGAGGAAATCGCTGTGGGCGACGGGAAACACAGAAAGCCAGTGTCCGACTCTAT 3478
3418 GGCACGACCCAGGAAATCTGGCTGGAGGACTACAGGCTTATAGTGTGCACCTGACTC 3477
3479 GGCATGACCCCAAAACATTTGGCTGGAAAGACTACATGCTACAGTGTGCACCTGATTC 3538
3478 ACAGGCCAAGACTGGCTACATCAGAGTCTTAGTCATGAAAGGAAACAGGTCATGGCAG 3537
3539 ACAGGCCAAGACTGGCTACATCAGAGTCTTAGTCATGAAAGGAAACAGGTCATGGCTG 3598
3538 ACTCAGGACCTATCTATGACCAACCTACGCTGTGGGCGGCTGGGTCTATTTGTCTTCT 3597
3599 ACTCAGGACCAATTTATGACCAACCTACGCTGTGGGCGGCTGGGTCTATTTGTCTTCT 3658
3598 CTCAGAAATGGTCTATTTCTCAGACCTCAAGTACGAAATCAGAGATATTTAAACAGAT 3657
3659 CCCAAGAGATGGTCTATTTCTCGACCTCAAGTATGAGTATGAGTGCAGAGATGCCCTAG- GAGCA 3717
3658 TTGCTGCAATTTCCGGATGCGCTGTGATGATGATGATGATGATGATGATGATGATGATG 3717
3718 GGGCTCCAGCTCCAGCAATGTC--TGCAACACCCCTTTTACAGACATCAGTCAATCT 3775
3718 TGGTCTTTGTGGCTCTCTCTCTAGCAGACCTCTCTGTCCCTTTGACCTTAACCTGATGG 3777
3776 TGGCACTTGTGGCTTTCTGTCTTCTGCAATTTGGCAATTTCTGTCTTCTTCTTCTTCTG 3834
3778 TTCTTCACTCTCTGCGACCAACCCCAAGTGTCTTTCAGAGGATTAATATCATG 3837
3835 ATCTACACCTCT-TCATGACCAACCAAGTCCAGTGTCTTCAAGGAGAAACATCAATG 3893

QY 3838 AACGAGAGATGAACATCTAACCCACTAGAGAAACAGATTTGGTGATATATGAGACTTT 3897
Db 3894 CACTC--CAGAGCTTCCAGCTGCTCTGGAACCATTTGGATGATATGAGCTCA 3950
QY 3898 ATGCGAGTGAATTTGGGATGCGCATTACATTCCTTTTCTTTTCTTTTAAAGAAAT 3957
Db 3951 CCGTGAGCGAAGACCGGAGCATTCGCTGTGTCTTCTTTTCTTTTAAAGAAAT 4010
QY 3958 GAGCTTTACATATAAATGTAATTTACTTATTGTATTGTATGATATGAGTGTGAAGGA 4017
Db 4011 GACGTTTACATGT-AAATGTAATTTACTTTCAGTATTATGTATATGAGTTCGAAGGA 4069
QY 4018 ATACTGTCAATAACCATATGATAAATTAAGCATGAAATA 4060
Db 4070 GTATTGTGTTTAAAGTCATCTCATAAATTAAGCATGAAATA 4112

RESULT 10
HUMTHRSPD HUMTHRSPD 2780 bp mRNA linear PRI 03-AUG-1993
LOCUS Human thrombospondin mRNA.
DEFINITION M81339
ACCESSION M81339.1 GI:339678
VERSION thrombospondin.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2780)
AUTHORS Labell,T.L., Milewicz,D.J., Distche,C.M. and Byers,P.H.
TITLE Thrombospondin II: partial cDNA sequence, chromosome location, and
expression of a second member of the thrombospondin gene family in
humans
JOURNAL Genomics 12 (3), 421-429 (1992)
MEDLINE 92217961
PUBMED 1559694
COMMENT Original
FEATURES
Location/Qualifiers
1..2780
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="fibroblast"
/tissue_type="connective"
/dev_stage="adult"

ORIGIN
Query Match 48.5%; Score 2763.6; DB 9; Length 2780;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2769; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1808 CCGGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTTGGTCTATGCGGCTCTGCCCTGT 1867
Db 1 CCGGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTTGGTCTATGCGGCTCTGCCCTGT 60
QY 1868 GGGCTTCTGGCATGACCGCATGTGAGGACTGAGGAGTGGCTGGTGGTGGTGGTGGTGGT 1927
Db 61 GGGCTTCTGGCATGACCGCATGTGAGGACTGAGGAGTGGCTGGTGGTGGTGGTGGTGGT 120
QY 1928 CATCTGCTTCTCCACAGCAAGGTGCTCTGCTGTGTGTCAACACTCAGCTGGCTTCCACTG 1987
Db 121 CATCTGCTTCTCCACAGCAAGGTGCTCTGCTGTGTGTCAACACTCAGCTGGCTTCCACTG 180
QY 1988 CTTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2047
Db 181 CTTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 2048 CAAGACGGAAGCAAGTGTGTGAGCCCGGAAACCCATGCAAGGACAGACACAACTG 2107
Db 241 CAAGACGGAAGCAAGTGTGTGAGCCCGGAAACCCATGCAAGGACAGACACAACTG 300
QY 2108 CCACAGACCGGAGTGCATCTACCTGGGCACTTACGACACCCCATGTACACAGTGGCA 2167

301 CCACAGCAGCGGAGTGCACTCTACCTGGGTCACTTACGGGACCCCATGTACAAAGTGCGA 360
2168 GTGCCAGACAGGCTACGCGGCGACGCGCTCATCTCGGGGAGGACTCGGACCTGACCG 2227
361 GTGCCAGACAGGCTACGCGGCGACGCGCTCATCTCGGGGAGGACTCGGACCTGACCG 420
2228 CTGGCCCAACCTCAATCTGGTCTCGGCCACCAACGCCACTTACCTGATGATCAAGATAA 2287
421 CTGGCCCAACCTCAATCTGGTCTCGGCCACCAACGCCACTTACCTGATGATCAAGATAA 480
2288 CTGGCCCAACCTCAATCTGGTCTCGGCCACCAACGCCACTTACCTGATGATCAAGATAA 2347
481 CTGGCCCAACCTCAATCTGGTCTCGGCCACCAACGCCACTTACCTGATGATCAAGATAA 540
2348 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2407
541 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
2408 CTTCAATCCCGCCAGGCTGACTATGACAAAGGATGAGTTGGGACCGCTGTGACAACTG 2467
601 CTTCAATCCCGCCAGGCTGACTATGACAAAGGATGAGTTGGGACCGCTGTGACAACTG 660
2468 CCCTTAGTGTGACAAACCTCCGAGATCGACACAGACAAATGGAGAGGATGACCGCTG 2527
661 CCCTTAGTGTGACAAACCTCCGAGATCGACACAGACAAATGGAGAGGATGACCGCTG 720
2528 CTCGGTGGACATGATGGGACGATGCTTCAATGAACGAGACAAATGTCCTTACGTCCTA 2587
721 CTCGGTGGACATGATGGGACGATGCTTCAATGAACGAGACAAATGTCCTTACGTCCTA 780
2588 CAACACTGACAGAGGACACGATGATGATGATGATGATGATGATGATGATGATGATGAT 2647
781 CAACACTGACAGAGGACACGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
2648 CTTGGTGGACAAACCTGACAGACCGGACGATGATGATGATGATGATGATGATGATGATG 2707
841 CTTGGTGGACAAACCTGACAGACCGGACGATGATGATGATGATGATGATGATGATGATG 900
2708 CAACAAAGAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2767
901 CAACAAAGAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
2768 CTTCAACGCGCAACCTGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 2827
961 CTTCAACGCGCAACCTGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
2828 TGATGACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2887
1021 TGATGACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
2888 CCGAGGACCTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2947
1081 CCGAGGACCTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
2948 CAACATCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3007
1141 CAACATCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
3008 CAGGAACTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3067
1201 CAGGAACTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
3068 GGTCAATCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3127
1261 GGTCAATCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
3128 TGTAGGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3187
1321 TGTAGGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
3188 CCGGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3247
1391 CCGGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

3248 GGTGATGTGGAAGCAGGTGACGACGACCTACTTGGAGGACCGACCCACGCGGGCTATGG 3307
1441 GGTGATGTGGAAGCAGGTGACGACGACCTACTTGGAGGACCGACCCACGCGGGCTATGG 1500
3308 CTACTCCCGCTGTCCCTCAAGTGTGGTGAACCTCCACACCGGGGACGGGCGAGCCTTGAG 3367
1501 CTACTCCCGCTGTCCCTCAAGTGTGGTGAACCTCCACACCGGGGACGGGCGAGCCTTGAG 1560
3368 GAAACGCGCTGTGGGACACCGGGGAAACACCGCGGGGACGGTGGGAACTTATGGACGACCC 3427
1561 GAAACGCGCTGTGGGACACCGGGGAAACACCGCGGGGACGGTGGGAACTTATGGACGACCC 1620
3428 CAGGAACTTGGCTGGAGGACTACACGGGCTATAGTGGGACCTGACTCACAGGCCCAA 3487
1621 CAGGAACTTGGCTGGAGGACTACACGGGCTATAGTGGGACCTGACTCACAGGCCCAA 1680
3488 GACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAACACAGTCACTGGCAGACTCAGGACC 3547
1681 GACCGGCTACATCAGAGTCTTAGTGCATGAAGGAAACACAGTCACTGGCAGACTCAGGACC 1740
3548 TATCTATCACAACCTACGCTGGCGGCGCTGGTCTATTTGCTTCTCTCAAGAAAT 3607
1741 TATCTATCACAACCTACGCTGGCGGCGCTGGTCTATTTGCTTCTCTCAAGAAAT 1800
3608 GGTCTATTCTCAGACCTCAAGTACGAATGACAGATATTTTAAACAGATTTGCTGCAAT 3667
1801 GGTCTATTCTCAGACCTCAAGTACGAATGACAGATATTTTAAACAGATTTGCTGCAAT 1860
3668 TCCGCAATGCCCTGTGCATGCCATGTCCTCAGACCTCAGTTCATTTGGTGGCTTGT 3727
1861 TCCGCAATGCCCTGTGCATGCCATGTCCTCAGACCTCAGTTCATTTGGTGGCTTGT 1920
3728 GGTCTCTCTCTAGCAGACCTCCTGTCCTTGAACCTTAACTCTGATGGTCTTCACT 3787
1921 GGTCTCTCTCTAGCAGACCTCCTGTCCTTGAACCTTAACTCTGATGGTCTTCACT 1980
3788 CTTGCGACAGCCCAACCCAGTGCCTTCAGAGGATAAATATCAATGGAACCGCAGAGA 3847
1981 CTTGCGACAGCCCAACCCAGTGCCTTCAGAGGATAAATATCAATGGAACCGCAGAGA 2040
3848 TGAAACATCTAACCCACTAGAGGAAACCAAGTTTGGTATATAGACATTTATGGAGTG 3907
2041 TGAAACATCTAACCCACTAGAGGAAACCAAGTTTGGTATATAGACATTTATGGAGTG 2100
3908 AAAATTTGGCATGCCATTCATTTGCTTTTCTTTTAAAGAAATGACGTTTACA 3967
2101 AAAATTTGGCATGCCATTCATTTGCTTTTCTTTTAAAGAAATGACGTTTACA 2160
3968 TATAAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4027
2161 TATAAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2220
4028 TAAGCATTTATGAATAATTAAGATGAATAATTAATTAATTAATTAATTAATTAATTAAG 4087
2221 TAAGCATTTATGAATAATTAAGATGAATAATTAATTAATTAATTAATTAATTAATTAAG 2280
4088 TTGTCACTATTCTTGAATTAAGTTGCTCTACAATGACACAAATCCCGCTTAAATAAT 4147
2281 TTGTCACTATTCTTGAATTAAGTTGCTCTACAATGACACAAATCCCGCTTAAATAAT 2340
4148 TATAAACAGGGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4207
2341 TATAAACAGGGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2400
4208 ACAGCATATGACAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4267
2401 ACAGCATATGACAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
4268 AAAATAAAGCACT 4327
2461 AAAATAAAGCACT 2520

2Y	4328	AGTTTCATCAAGAGCAAAACATCCTTCGCAATGGGTGTGTGATCGGTTCCAGATGTGGATT	4388
2b	2521	AGTTTCATCAAGAGCAAAACATCCTTCGCAATGGGTGTGTGATCGGTTCCAGATGTGGATT	2580
2Y	4388	TGGCAAAACCTCATTTAAAGTAAAAAGGTTAGCAGAGCAAAAGTGCGGTGCTTTAGCTGCTGC	4447
2b	2581	TGGCAAAACCTCATTTAAAGTAAAAAGGTTAGCAGAGCAAAAGTGCGGTGCTTTAGCTGCTGC	2640
2Y	4448	TTGTGCGGCTGTGGTGTGGGGAGGCTCTGCTGCTGAGCTTCCTTCCGACAGCTTGTGCTGC	4507
2b	2641	TTGTGCGGCTGTGGTGTGGGGAGGCTCTGCTGCTGAGCTTCCTTCCGACAGCTTGTGCTGC	2700
2Y	4508	TGAGAGAAACACAGACAGACGACAGCCGCGGAAAAAGCGCATCTAAACGGCTATCTAGGCT	4567
2b	2701	TGAGAGAAACACAGACAGACGACAGCCGCGGAAAAAGCGCATCTAAACGGCTATCTAGGCT	2760
2Y	4568	TTGGTAACTCGGACAAAG 4585	
2b	2761	TTGGTAACTCGGACAAAG 2778	
RESULT 11			
BD129562 4108 bp DNA linear PAT 18-SEP-2002			
LOCUS Polynucleotides and polypeptides of METH1 and METH2.			
DEFINITION BD129562			
ACCESSION BD129562.1 GI:23224507			
VERSION JP 2002501077-A/17.			
KEYWORDS unidentified			
SOURCE unidentified			
ORGANISM unclassified.			
REFERENCE 1 (bases 1 to 4108)			
AUTHORS Arispe,L.I., Hastings,G.A. and Ruben,S.M.			
TITLE Polynucleotides and polypeptides of METH1 and METH2			
JOURNAL Patent: JP 2002501077-A/17 15-JAN-2002.			
COMMENT BETH ISRAEL DEACONESS MEDICAL CENTER,HUMAN GENOME SCIENCES INC			
OS Unknown			
PN JP 2002501077-A/17			
PD 15-JAN-2002			
PR 22-JAN-1998 JP 2000528581			
PF 23-JAN-1998 US 60/072928,28-AUG-1998 US 60/098539 PI			
PI LUISA IRUELA ARISPE,GREGG A HASTINGS,STEVEN M RUBEN PC			
C07K14/47,A61K38/00,A61K48/00,A61P35/00,A61P43/00,CL2N1/21, PC			
CL2N5/10.			
PC CL2N15/09,CL12P21/02,A61K37/02,CL12N5/00,CL2N15/00 CC			
Description of Unknown Organisation:Unknown			
FH Key Location/Qualifiers			
FT source 1..4108			
FT Location/Qualifiers			
1..4108			
/organism="unidentified"			
/mol_type="genomic DNA"			
/db_xref="taxon:32644"			
FEATURES			
source			
ORIGIN			
Query Match 48.3%; Score 2753.2; DB 6; Length 4108;			
Best Local Similarity 82.6%; Pred. No. 0;			
Matches 3223; Conservative 0; Mismatches 668; Indels 9; Gaps 6;			
Qy	118	CTGACAGAGCAGATGGTCTGGAGGCTGTCTCTGGCTCTGTGGGTGTGGCCACGCA	177
Db	205	CAGGTGGAGCAAGATCTCTGGGCATCGGCCCTGCTGGCTCTGGGCATAGGGCCAAAG	264
Qy	178	CGCAAGCTGGTCCACAGCAAAAGACACAGCTTCGACCTTTTCAGTATCAGCAACATCA	237
Db	265	CTTCTGCTGGTGACCAACGCTCAAGGACACTTCAATTGACCTTTTCAGCATCAGCAACATTA	324
Qy	238	ACCGCAGACCATTTGGGCCCHAGCAGTTCGCGGGCCGACCCCGGCGTCCGGCTTACC	297
Db	325	ACCGGAAGACCATCGGTGCCAAGCAGTTCGAGGGCTGACCCCGGGGTGCCCGCTTACC	384
Qy	298	GCTTCGTGCGCTTTGACTATCATCCACCGGTGAACGAGATGACCTCAGCAAGATCACCA	357

1465	TGGGCCCCCTCCATTTCAGACAAAGCANTGACGCTGGGCAAAATGTGATACGAGAATCCGCTC	1524
1497	AGAACCGCGCTGGAGCCCATCGTGCACCTTTGGTCTTTCACTGCTCTGTGACCTGTGGAGTTTG	1497
1525	AGAAATGGAGGCTGGAGTCACTGCTGCACCCTGGTCTTCACTGCTCCGCTGACTGTGTGGAGTTG	1584
1498	GCAATATCACACGANTCCGCTCTCGAACTCCGCCAGTGCCCAGTACCCAGATGGGGGCAAGAAAT	1557
1585	GCAATGTACCCCAGATACGTCTCTGCAATCTCACAGTGCCTCCAGATGGGTGGGCAAGACT	1644
1558	GCAAAGGAGTGCCTCGGGAGACCAAGACCTTCGACGGCGCCCCATCCCAATCGATGGCC	1617
1645	GCAAAGGACAGCGCCGGGAACCAAAACCTGTGAGCGTGATCCGTCGCCAATTAATGATGGCC	1704
1618	GCTGGAGCCCTCGTCCCCTGGTTCGGCTGCACTGTCACTCTGCGCGTGGGATCCGGG	1677
1705	GCTGGAGCCCTCGTCCCCTTGTGAGCTTGACAGTTACTGTGCTGGAGGATCCGTG	1764
1678	AGCGCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTAGGAGGAAAGGCTGCGTGGGG	1737
1765	AGCGCTCAGCTGTTTGCAACAGCCCTGAGCCCCCAGTATGGAGGGAAAGGACTGTGTCCGGG	1824
1738	ATGTGCAGGAGCGTCAGATGTGCAACAAGAGGAGCTGCCCGCTGGAGTGGCTGTTTATCCA	1797
1825	ATGTGCAGAGAACACCAATGTGCAACAGAGAGCTGCCCTATTGATGGGTGCTTATCCA	1884
1798	ACCCCTGTTCCCGGAGCCCACTGCMGAGCTTCCCGATGGGTCTGTGTCATGCGGCT	1857
1885	ACCCGTGTTTCTGTGAGCCCAAGTGCAACAGCTTCCCTGATGGGTCTGTGCTGTGGCT	1944
1858	CNTGCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTCGGACGAGTGCACC	1917
1945	CCTGCCAGTGGCTTCTCGGCAATGGTATCCACTGTGAGGACCTGGATGAGTGTGCTG	2004
1918	TGCTCCCCGACATCTGCTTCTCCACMGCAAGTGCCTCGCTGTGTCAACACTCAGCCTG	1977
2005	TGCTCAGAGATATTTGCTTCTCAACTAACAAAGCTCCCGCTGTGTCAACACCAACCCGG	2064
1978	GC'TTCACTGCCTGCCTGCCCCCGATACAGAGGGAACCAAGCCGTCGGGGTCCGGC	2037
2065	GC'TTCACTGCCTGCCTTGTCCACCAAGTGTACAGGGGAACCAACCTTCGTGTGTGGCC	2124
2038	TGGAAGCAGCCAGACGGAAAGCAAGTGTGTGAGCCCGAAACCCATGCAAGGACAAGA	2097
2125	TGAGGATGTATGACAGAAAAACAAGTGTGTGAGCCAGAGATTCATGTATAGGACAAGA	2184
2098	CACACAATGCCACAAGCAGCGAGTGCATCTACTTGGGCCCACTTCAGCGACCCCATGT	2157
2185	CTCACAGCTGCCACAAGAAATGCAGAGTGCATCTACTTGGGCCCACTTTAGTGTACCCCATGT	2244
2158	ACAAGTGCAGTGCACAGAGTGTACGGCGCAGCGGCTCATCTCGGGGAGGACTCGG	2217
2245	ACAAGTGTAGTGCCAGATTTGGCTTACCGAGTGTATGGGCTCATCTCGGGGAGGACTCAG	2304
2218	ACCTGGACGCTGGCCCCAACCTCAATCTGGTCTGCGCCACCAACGCCACCTACCACTGCA	2277
2305	ACCTGGATGCTGGCCCCAAACAAACCTGGTGTGCTACTAATGCCACCTACCACTGCA	2364
2278	TCGAAGNTACTGCCCCCATCTGCCAATTTCTGGGCAAGGAGACTTTGACAAAGCGGGA	2337
2365	TCGAAGGCAACTGCCCCCAACTGCCAATTTCCGGGCAAGGAGATTTTGTATAGAGTGGAA	2424
2338	TTGGCGATGCTGTGATGTACGATGACAATGACCGTGTGACCGATGAGAAGGACAACCT	2397
2425	TCGGAGATGTTGTGACGAGGACGATGACAATGACCGTGTGAGCGATGAGAAGGACAAT	2484
2398	GCACGCTCTTCAATCCCGCCAGCTGCATATGACAAGGATGAGTTGGGACCGCT	2457
2485	GCCAGCTTCTTCAATCCCGCTCAATTAGACTATGACAAGATGAGTTGGAGACCGCT	2544
2458	GTGACAATCCCTTACGTGCACAACCTGCCAGATTCGACACAGACAACAATGGGAGAGG	2517
2545	GTGACAATCCCTTATGTGCACAACCCAGCACAGATTCGACACAGACAACAATGGGAGG	2604

Qy	2518	GTGACGCGCTGCTCCGTGGGACATTGATGGGGA	CGATGTCCTTCAATGAACGAGACAAATTGTC	2577
Db	2605	GGGATGCGCTGCTCTGTGGACATTGACGGAGAC	ATGTTTCAATGAGCGGAGACAAATTGTC	2664
Qy	2578	CCTACGCTCTACAAACACTGACACGAGGGGAC	CACGGATGGTGACCGGTGTGGGGGATCACTGTG	2637
Db	2665	CATATGCTTACAAACACTGACACGAGAGATAC	CGGATGGTGATGCGGTGGGTGACCACTGTG	2724
Qy	2638	ACAACTGCCCGCTGGTGGACAAACCTTGACCA	GACCGACGCTGGGACATGACCTTTGTTGGGG	2697
Db	2725	ACAAATTGCTCTGTGATGACCAACCCAGATCA	GATCGATCAGGACCAATGATCTCGTTGGAG	2784
Qy	2698	ACCAAGTGTGACAAACACGAGGACATAGATGA	CACACGCGCCACCAAGAACAAACCAAGACAACT	2757
Db	2785	ACCAGTGTGACAAACATAGAGGACATAGATGA	TGATGACGCGCCACCAAGAACAAACCAAGACAACT	2844
Qy	2758	GCGCTACATCTCCAAAGCCAAACGAGCTGACC	ATGACAGAGAGCGCCAGGCGGACGCCT	2817
Db	2845	GCCCATACATCTCCAACTCCAAACGAGCTGACC	ATGACAAACGACGGCAAGGGCGATGCCT	2904
Qy	2818	GTGACCCCTGATGATGACAAACGATGGCGGTCC	CGGATGACAGGGGACAACTGCGCGCTTGTGT	2877
Db	2905	GCGACTCTGATGATGACAAATGATGGTGTTC	CCAGATGACAGGGGACAACTGCGCGCTTGTGT	2964
Qy	2878	TCAAACCGACACGAGGAGACTTGGACGGTGA	TGCGGAGGGGTGATATTGTTAAAGATGATT	2937
Db	2965	TCAAACCGACACGAGGAGACTTCGGA	CGGTGACCGCGAGGTGACATTGTTAAAGATGACT	3024
Qy	2938	TTGCAATGACAAACATCCACAGATATTGATGA	TGTGTCTCTGAAAACAATGCCATCAGTG	2997
Db	3025	TTGCAATGATAATGTCCACAGATATTGATGA	TGTGTGCTCTGAGAACAAATGCCATCACTG	3084
Qy	2998	AGACAGACTTCAGGAACCTCCAGATGGTCCCTT	TGGATCCCAAGGGACCAACCCCAATTG	3057
Db	3085	AGACAGACTTCAGAACTCCAGATGGTCCCTCT	GTGATCCCAAGGGGACCAACAATAATG	3144
Qy	3058	ATCCCACTGGGTCATTTCGCCATCAAGGCAAG	GAGTGGTTCAGACAGCGCAACTCGGACC	3117
Db	3145	ATCCCACTGGGTAATTTCGTACCAAGGCAAG	AGAGTGGTTCAGACAGCAAAACTCAGACC	3204
Qy	3118	CCGGCATCGGCTGAGTTTTGACGATTTGGGTCT	GAGACTTCAGTGGGCACATCTCAAG	3177
Db	3205	CTGGCATCGGCTGAGTTTTCGACGATTTGGGTCT	GTGGACTTCAGTGGGCACATCTCTATG	3264
Qy	3178	TAAACACTGACCGGACGACGACTATCGCGGCTT	CGTCTTTGGTTACCAGTCAAGCAGCC	3237
Db	3265	TCAACACTGACCGGATGATGACTA	CGCTTTGTCTTTGGCTATCAGTCAAGCAGCC	3324
Qy	3238	GCCTCTATGTTGGTGTGGAACGAGTGACGACG	ACCTTACTCGGAGGACCAAGCCCAAGC	3297
Db	3325	GCCTCTATGTTGGTGTGGAACGAGTGACCA	GACCTTACTCGGAGGACCAAGCCCAAGC	3384
Qy	3298	GGGCGTATGCGCTACTCGGCGTGTCCCTCAAG	STGTGAACTCCACACCGGGACCGGCG	3357
Db	3385	GGGCTTACGCGTACTCTGTGTGTCTCACTCAA	AGTGGTAAAACCTCCAGCTGTGACTCGCG	3444
Qy	3358	AGCACCTGGGAAACGCGCTCTGGCACACGGG	GAACACGCGGGGACGACCGCGGGGACGTGG	3417
Db	3445	AGCACCTGGAGGAATGCCCTGTGGCACACGG	GAACACGAAGGCCAGGTCCGGACTCTAT	3504
Qy	3418	GGCACGACCCAGGAACATTGGCTGGGAAGCA	CTACACGGCGCTATAGGTGGCACTTGACTC	3477
Db	3505	GGCATGACCCCAAAAACATTGGGCTGGAAGA	CACTACATGCGCTCAGGTGGCACTTGATT	3564
Qy	3478	ACAGGCCCPAGACTGGCTTACATCAGAGTCTT	AGTGTAGTGAAGAAACACGTCATGGCAG	3537
Db	3565	ACAGGCCCTAAGACAGGCTTACATGAGAGTCTT	AGTGTAGTGAAGAAACACGTCATGGCTG	3624
Qy	3538	ACTCAGGACCTATCTATGACAAACCTPACGCT	GGCGGGCGGCTGGGTCATTGTTCTTCT	3597
Db	3625	ACTCAGGACCAATTTATGACAAACCTPACGCT	GGTGGACGGCTGGGCTGTGTTGTTCTTCT	3684

2y 3598 CTCAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATCAGAGATATTAAACAAGAT 3657
 2b 3685 CCCAAGAGATGGTCTATTCTCGGACCTCAAGTATGATGTCAGAGATGCTAGA-CAGCA 3743
 2y 3658 TTGCTGATTTCCGGCAATGCCCTGTGCATGCGCATGTCCTAGACACCTCAGTTCATTG 3717
 2b 3744 GGGCTCCAGCTCCAGCAATGTC--TGCAACAACACCCCTTCTTAGACACATCAGTCCATCT 3801
 2y 3718 TGGTCCCTTGGCTTCTCTCTAGCAGCACCTCTCTGCTCCCTTGACCTTAACCTCTCATGG 3777
 2b 3802 TGGCACTTGGCTTCTCTCTAGCAGCACCTCTCTGCTCCCTTGACCTTAACCTCTCATGG 3860
 2y 3778 TTCTTCACTCTCCGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 3837
 2b 3861 ATCTACACCTCTCTCTCTAGCAGCACCTCTCTGCTCCCTTGACCTTAACCTCTCATGG 3919
 2y 3838 AACCAAGAGATGACATCTACCTACCACTAGAGGAAACCACTTGGTGTATATATAGACTT 3897
 2b 3920 CACTC---CAAGACTTCCAGCTCTGCTGCTGGAACAATTTGGATGAGATATAGAGCTCA 3976
 2y 3898 ATGTGAGTGAATTTGGCATGCCATTACATTCCTTTTCTTTTGTGTTTAAAGAAAT 3957
 2b 3977 CCGTGGAGCGAAGACCGAGCATTCGGCTGTGTGCTTTTCTTTTGTGTTTAAAGAAAT 4036
 2y 3958 GACCTTTACATATAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4017
 2b 4037 GACCTTTACATGT-AAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4095

RESULT 12
 MUSTSP2B 4108 bp mRNA linear ROD 11-FEB-2002
 LOCUS Mus musculus thrombospondin 2 (THBS2) mRNA, complete cds.
 DEFINITION
 ACCESSION L07803 M87275
 VERSION L07803.1 GI:340421
 KEYWORDS thrombospondin 2.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Loherty, C.D., O'Rourke, K., Wolf, F.W., Katz, R., Seldin, M.F. and
 Dixit, V.M.
 TITLE Characterization of mouse thrombospondin 2 sequence and expression
 during cell growth and development
 J. Biol. Chem. 267 (5), 3274-3281 (1992)
 J2147583
 MEDLINE
 PUBMED 1371115

COMMENT On Feb 8, 2002 this sequence version replaced gi:202198.

FEATURES Location/Qualifiers

1..4108
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /tissue_type="kidney"
 /dev_stage="embryo"
 1..4108
 /gene="THBS2"
 219..3737
 /gene="THBS2"
 /codon_start=1
 /product="thrombospondin 2"
 /protein_id="AA53064.1"
 /db_xref="GI:567241"
 /translation="MLWALLLALIGIPRASGHVVDTSFDLFSININRKTIGAKQ
 FRGDPGPVAFYRFDYIPVPTDNLNRIVKLARRKEGFLTAOLQDKRKSTGLLV
 LEGPGRORPEIIVNSGPGPTLDLNVVNGNHTNFLEDVGLADSKWNKTVQVADT
 YSLVVGDLIDSVLEBPFEQLVYDRSMYVAKGASRESHFGLQLQNVLPVADSV
 DILSKKQCHSQGAENVFISHTETLHLSPHITDVLVQGVKRAQVCTHSCSELNN
 MNELSGHVMVNOJLKNLRSVNDQFLLELIGPLKRNMSACVGEGRIFAEENTW
 VDSCTCTCKFKVTHQITCSPATCANPFSVEGSCPSHSDDEGWSWPAWETE
 CSVTGSGTQGRGRSCDVTSNTCLGPSIQTRTCSLKGKCDTRIRQNGWSHSPWSSCS

gene

CDS

VTGCVNVRIRLNCNSVPQWQGNKCKSGRETKPCQORDPCPIDGRMSPWSPSACTV
 TCAGIIRERSVCNSPEPOYGKCDVTEHOMCKRSCPIDGCLSNPFCPPGAKCNS
 FPDGMSGCGPGLNGTHCEDLCAVVTIDICFSTNKAPRCVNTNPFCHLPCPP
 RYKNGPQFVGLEDAETEKQVCEPNCKDKTHSCHKNABCIYLGHFSDPMWKECOI
 GYAGGLICGSDSLDGLFNPNLLVCATNATYHICIKNCPKLPNSGQDDPKDNGGDA
 DEDDNDGVSDEKNDQLLDYKDEVEGRDNCNCFYVHNPAQIDIDNNGELG
 CSVIDDGVDFNERDNCFYVNTDQRTDGDGVGDHCDNCLMHNPOQIDDDNDLVD
 CQDNEDIDDDHQNQDNCFYISNQADHNDKGDACDSDDDNDGVDFDNDNCL
 VFNPEQSDSDGGRGDIKDDFNDNVPDIDVCPENNAITEITDFYFQVFPVDPDKGT
 TQIDPNVIRHOGKELVQTANSDPGIAVGDFEFGVDFSGTFYVNRDRTDDYAGFVG
 YQSSRPVVMKQVOTVYHEDKESRAYGSYSLKVNSTTGTGHELRNALHTGNT
 EGQRTLWHDPKNGKWDYATYRWHLHREPKTGMRVLVHREGKQVMAWSDSPIDQTTA
 GRLGLFVFSQEMVIFSDLKTECRDA"

ORIGIN

Query Match 48.3%; Score 2753.2; DB 10; Length 4108;
 Best Local Similarity 82.6%; Pred. No. 0;
 Matches 3223; Conservative 0; Mismatches 668; Indels 9; Gaps 6;
 QY 118 CTGAGGAGGAGGATGGTCTGGAGGCTGGTCTGCTGGCTCTGGTGGTGGTGGCCAGCA 177
 Db 205 CAGGTGGAGACAAGATGCTCTGGGCACTGGCCCTGCTGGCTCTGGGCATAGGGCAAG 264
 QY 178 CGCAAGCTGGTCACCAGGACAAAGACACAGACCTTCGACCTTTTCAGTATCAGCAACATCA 237
 Db 265 CTTCTGCTGGTGACCACTCAAGGACACTTCATTTGACCTTTTTCAGCATCAGCAACATTA 324
 QY 238 ACCGCAAGCAATTTGGCCCAAGCAGTTCCCGGGCCGCGACCCCGGGCTGGCCGCTTACC 297
 Db 325 ACCGGAAGACCATCGGTGCCAAGCAGTTCCGAGGCGCTGACCCCGGGGTGCCCGCTACC 384
 QY 298 GCTTCGTCGCTTTGACTACATCCACCGGTGAACGCGATGACCTCAGCAAGATCACCA 357
 Db 385 GTTTGTGAGTTTGACTACATCCCCCGCTGGAACACAGATGATCTCAACAGGATGTCA 444
 QY 358 AGATCATCGCGACAAGAGGGCTTTTCCTCAGCGCCAGCTCAAGCAGACGGCAAGT 417
 Db 445 AGCTTGAAGAGAGAAAGAGGGCTTTTCCTCAGAGCCCAACTGAAGCAGGACCGCAAGT 504
 QY 418 CCAGGGGACGCTGTGGCTCTGGAGGCGCCGCTCTCCAGAGGCGAGTTCCAGATCG 477
 Db 505 CTCGGGGAACGCTCTGTGTGTGAGGCGCCCGGCACTCCAGAGGCGAGTTGAGATTG 564
 QY 478 TCTCAACGGCCCGCGGACACGCTGGATCTCAGTCTAGTGGATTGACGGCACCGCGCATG 537
 Db 565 TGTCCAAATGGCCAGGGACACTTTGGACCTCAACTACTGGGTAGAAGGCAATCAGCATA 624
 QY 538 TGGTCTCCCTGGAGGACGTCGGCTGGTGTGACTCGCAGTGAAGAACTCAGCTGCGAGG 597
 Db 625 CCAACTTCTGGAGGATGTGGGCTGGCTGACTCCAGTGAAGAAATGTGACTGTGCGAGG 684
 QY 598 TGGCTGGCGAGACCTACAGCTTGACGCTGGGCTGGACCTCATAGACAGTTCGCTCTGG 657
 Db 685 TGGCCAGTGACACCTATAGCTGTATGTGGCTGCGATCTTATCGACAGTGTCACTCTGG 744
 QY 658 ACAGCCCTTCTAGAGCACCTGAGGCGGAAAGAGCGGATGTACGTGCGCCAAAGGCT 717
 Db 745 AAGAAACCACTTATAGCAGCTAGAAAGTAGACAGGAGGAGGATGTACGTGCGCCAAAGTG 804
 QY 718 CTGCCAGAGAGAGTCACTTTCAGGGGTTTGGCTTTCAGAACTCCACCTAGTGTGAAACT 777
 Db 805 CATCTCGAGAGAGTCACTTCAGGGCTTGTGCGAGAATGTCCATCTGCTGTGTTCAGATT 864
 QY 778 CTGTGGAAGATATCTTAAGCAAGAGGGTGTCCAGCAAGGCGGAGGCTAGATCAAG 837
 Db 865 CTGTGGAAGATATCTTAAGCAAGAAAGCTGTCAACACAGCCAGGAGCTGAAGTCAACA 924
 QY 838 CCATCAGTGAAGAACACAGAGACGCTGCGCCTGGGTGCCCATGTCAACACCGAGTACCTGG 897
 Db 925 CCATCAGTGAACATACAGAGACTCTCCATCTGAGCCCTTCAATCACCACAGATCTCGTGG 984
 QY 898 GCCCAGCTCAGAGAGGAGGCGCGAGGTGTGCGAACCGTCTGTGAGAGGCTGGGAACA 957

985 TCAGGGTGTGGAGAGGACAGAGGTTGTACGCACTCTCGCGAGGAGTTGAGCAACA 1044
 986 TGGTCCAGGAGCTCTCGGAGCTCCAGTCTCTGTAACAGCTCAGCGAGAACTCAAGA 1017
 1045 TGATGAATGAGCTCTCTGAGCTGCACTCATGGTGAACAGCTGAGCAAGAACTGGAGA 1104
 1018 GAGTGTGGAATGATTAACAGATTTCTCTGGAGGCTCATTTGGTGGCCCTCTCTAAGACAAGA 1077
 1105 GAGTGTCTAGTGATAACCACTTCTTTGGAGCTCATTTGGGGCCCTCTGAAAGACAAGAA 1164
 1078 ACATGTGAGCTTCTGCGAGGATGGCGGTTCTTTGCGGAATAAGAACTGGGTGGTG 1137
 1165 ACATGTGAGCTTGTGCGAGAGGGCGAATCTTTGCGAAGAAATGAACCTGGGTGGTG 1224
 1138 ACAGCTGCACCACTGACCTGACCAAGAAATTTAAACCAATTTGCGCAACCAATCACTGGCC 1197
 1225 ATAGTTGTACCATGACCTGCAAGAAATTTAAACAGCTCTGCCATCAGATCAGCTGCT 1284
 1198 CGCTGCAACCTCGCGAGTCCATCTTTGTGAAGCGAATCTGCCCTTCTCGCTGCC 1257
 1285 CACTGCAACTTGTGCCAACCACTTTTGTGAGAGCGAGTGTCTCCATCTGTCTAC 1344
 1258 ACTCGGTGAGCGGTGAGGAGGCTGTCTCCGTGGGACAGTGGACCCAGTGTCCGTGA 1317
 1345 ACTCTGACAGAGTATGAGGCTGTCTCCGTGGGACAGTGGACCGAGTGTCTGTGCA 1404
 1318 CGTGTGCTCTGGAGCCAGCAGAGAGGCGGTCCTGTGACGTCAACAGCAACACCTGCT 1377
 1405 CTTGTGCTCTGGAGCCAGCAGAGAGGCGGTCCTGTGATGTCAACAGCAACACCTGCC 1464
 1378 TGGGGCCCTCCATCCAGACAGGCTTTGAGTGTGAGCAAGTGTGACACCGGATCCGGC 1437
 1465 TGGGCCCTCCATTCAGCAAGACATGACAGCTGGGCAATGTGATAGCAAGAACTCCGTC 1524
 1438 AGNAGCGGCTGGAGCACTGTGTCCTTCTCATGCTCTGTGACCTGTGGAGTTG 1497
 1525 AGAATGAGGCTGGAGTCACTGTGTCACTCCCTGGTCTTCTATGCTCCGTCATTTGGAGTTG 1584
 1498 GCAATATCACAGCATCCGCTCTGTGAACTCCAGTGTCCCGCCAGATGGGGGGCAAGAAAT 1557
 1585 GCAATGTCAACCGCATACGCTCTGTCACTCACAGTGTCCCGCCAGATGGGTGGCAAGAACT 1644
 1558 GCAAGGAGTGGCGGAGACCAAGCTTCCAGAGGCGCCCATCCCAATCGATGGCC 1617
 1645 GCAAGGCGAGCGCGGAGAACCAACCTGTAGCGTGTATCCGTGCGCCAAATGTATGGCC 1704
 1618 GCTGAGCCCTGTGCTCCGCTGTGCGGCTGCACTGTCACTGTGCGGTGGGATCCGGG 1677
 1705 GCTGAGCCCTGTGCTCCCTTGTGTAGCTGTCAAGTTACCTGTGTGGAGGATCCGTG 1764
 1678 AGCGACCCGGGCTGTGCAACAGCCCTGAGCTTGTAGCGAGGAGGCGCTGTGGGGG 1737
 1765 AGCGCTCACTGTGTAACAGCCCTGAGCCCGCAGTATGAGGAGGAGGACTGTGTGGGG 1824
 1738 ATGTGAGAGGAGCTGAGTGTGCAACAGAGGAGCTGCCCGGTGGATGGCTGTTTATCCA 1797
 1825 ATGTGACAGAACACCAATGTGTGACAGAGAGCTGCCCTATTATGAGGTGCTTATCCA 1884
 1798 ACCCTGTCTCCGGAGGCGCACTGTGAGAGCTTCCCGATGGGTCTGTGTCTGTGGCT 1857
 1885 ACCCGTGTCTTCTGGAGCAAGTGTCAACAGCTTCCCTGTATGGGTCTGTGTGTGGCT 1944
 1858 CTTGCGCTGTGGGCTTCTTGGGCAATGSCACCTGTGAGGAGCTGTGAGGAGTGTGGCC 1917
 1945 CTTGCGCAAGTGGCTTCTTGGGCAATGTTACCTGTGAGGAGCTGTGAGTGTGTGCTG 2004
 1918 TGGTCCCGACATCTGCTTCTTCCAGCAAGGAGTGTGCTGTGTGTCAACACTGAGCTG 1977
 2005 TGGTCAACAGATATGCTTCTCACTAACAAAGTCTCCCGCTGTGTCAACCAACCCCGG 2064
 1978 GCTTCCATGCTGCTGCGCGCCCGATACAGAGGAGCCAGCCGCTGCGGCTGGCC 2037
 2065 GCTTCCATGCTGCTGCTTGTCAACAGCTTCAAGGGAGAACCAACCTTGTGTGTGGCC 2124

2038 TGGAGCAGCAAGACGGAAGAACAGTGTGTGAGCCCGAAACCCATGCAAGGACAAGA 2097
 2125 TGGAGGATGTGTAGACAGAAAAAACAGTGTGTGAGCCAGAGAAATCCATGTAAAGACAAGA 2184
 2098 CACAACACTGCCAAGCAGCGGAGTGCATCTACCTGGGCCACTTTCAGGAGACCCCATGT 2157
 2185 CTACAGCTGCCAAGAAATGACAGTGCATCTACCTGGGCCACTTTCAGGAGACCCCATGT 2244
 2158 ACAAGTCCGAGTCCACACAGGCTACGCGGCGACGGCTCATCTGCGGGAGACTCGG 2217
 2245 ACAAGTGTGAGTGCAGATTTGGCTACGAGGTGATGGGCTCATCTGCGGGAGACTCAG 2304
 2218 ACCTGGAGCGGTGCCCAACTCAATCTGTCTGCGCCACCAACGCGCACCTACCACTGCA 2277
 2305 ACCTGGATGGGTGCCCAACAACTCTGTGTGTGTACTAATGCGCACCTACCACTGCA 2364
 2278 TCAAGGATAACTGCTGCCCTCATCTGCCAAATTTCTGGGACGAGAGCTTTTGAAGAGATGAA 2424
 2338 TGGCGATGCTGTGATGATGACGATGACATGACGATGACGATGACGATGACGATGACGAT 2397
 2425 TCGAGATGCTGTGACGAGGACGATGACATGACGATGACGATGACGATGACGATGACGAT 2484
 2398 GCCAGCTCTCTTCAATCCCGCCAGGCTGACTATGACAAAGGATGAGGTTGGGACCGCT 2457
 2485 GCCAGCTCTCTTCAATCCCGCTCAATTTAGACTATGACAAAGGATGAGGTTGGAGACCGCT 2544
 2458 GTGACAACTGCGCTTACGTGCACAACTCCCGCCAGATCGACAGACAAACAAATGGAGG 2517
 2545 GTGACAACTGCGCTTACGTGCACAACTCCCGCCAGATCGACAGACAAACAAATGGAGG 2604
 2518 GTGACCGCTGCTCGGTGACAACTTGTGGGACGATGTCTTCAATGAACGAGACAATTTGTC 2577
 2605 GGGATGCTGCTCTGTGACATTTGACGAGACGATGTTTTCAATGAGCGAGACAATTTGTC 2664
 2578 CCTAGCTTCAACACTGACAGGAGACGAGTGTGAGCGTGTGGGGATCACTGTG 2637
 2665 CATATGTCTCAACACTGACAGAGATACGAGTGTGATGGGCTGGGTGACCACTGTG 2724
 2638 ACACTGCGCCCTGTGTGACAACTGACAGACCGAGTGTGACAAATGACCTTGTGGGG 2697
 2725 ACAATTTGCTCTGTGACAACTGACAGATCAGATCAGATCAGATCAGATCAGATCAGAT 2784
 2698 ACCAGTGTGACAACTGACAGGACATGATGACAGGCGCCACAGAACTCAGGACAACT 2757
 2785 ACCAGTGTGACAACTGACAGGACATGATGATGACGCGCCACAGAACTCAGGACAACT 2844
 2758 GCCCTTACATCTTCCAACTGACAGGCTGACATGACAGAGCGCCAGGCGGACGCT 2817
 2845 GCCCATACATCTTCCAACTTCCAACTGACAGGCTGACATGACAGAGCGGCGATGCT 2904
 2818 GTGACCTGTGATGACAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2877
 2905 GCGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2964
 2878 TCAACCCAGACCCAGAGGACTTGGACGCTGATGACGCGGTGATGATGATGATGATGATGAT 2937
 2965 TCAACCCAGACCCAGAGGACTTGGACGCTGATGACGCGGTGATGATGATGATGATGATGAT 3024
 2938 TTGCAACTGACAACTTCCAGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 2997
 3025 TTGCAACTGATTAATTCCTGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 3084
 2998 AGACAGACTTCCAGAACTTCCAGATGCTCCCTTGGATCCCAAGGGAGACCCCAATTTG 3057
 3085 AGACAGACTTCCAGAACTTCCAGATGCTCCCTTGGATCCCAAGGGAGACCCCAATTTG 3144
 3058 ATCCCAACTGGGTCTATTCGCCATCAAGGCAAGGAGCTGGTTTCAGACAGCCCACTCGGACC 3117
 3145 ATCCCAACTGGGTCTATTCGCCATCAAGGCAAGGAGCTGGTTTCAGACAGCCCACTCGGACC 3204

[illegible]

D	b	28511	GTTTGTGTTAAAAAGAAATGACGGTTTACATATAAAATTGAATTACTTATTGTATTATGTGTT	28452
Y	y	4001	ATATGGAGTTGAAGGGAATACTGTGCATAAGCCATTATGATAAATTAAGCATGAAAATA	4060
D	b	28451	ATATGGAGTTGAAGGGAATACTGTGCATAAGCCAATATGATAAATTAAGCATGAAAATA	28392
Y	y	4061	TTCCTGAACTACTTTTTTGTTGGTCTTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACA	4120
D	b	28391	TTCCTGAACACTACTTTTTTGTTGGTCTTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACA	28332
Y	y	4121	ATGACACACAAATCCCGCTAAATAAATATAAACAAAGGTCAAATCAAATTTGAAGTAAT	4180
D	b	28331	ATGACACACAAATCCCATTAAATTAATATAAACAAAGGTCAAATCAAATTTGAAGTAAT	28272
Y	y	4181	GTTTITAGTAAGGAGAGATTAGAAGACAACAGGCAATAGCAATGACATTAAGCTACCGATT	4240
D	b	28271	GTTTITAGTAAGGAGAGATTAGAAGACAACAGGCAATAGCAATGACATTAAGCTACCGATT	28212
Y	y	4241	ACTAANTCGGAACATGTAAACACAGTTACAAAAATAAACGAACCTCCTCTGTCTCTACAAT	4300
D	b	28211	ACTAANTCGGAACATGTAAACACAGTTACAAAAATAAACGAACCTCCTCTGTCTCTACAAT	28152
Y	y	4301	GAAGGCCCTCATGTGCGTAGAGATGACGTTTTTCATCAAAGAACAAACATCTTGC AAAATG	4360
D	b	28151	GAAGGCCCTCATGTGCGTAGAGATGACGTTTTTCATCAAAGAACAAACATCTTGC AAAATG	28092
Y	y	4361	GGTGTGATCGGTTCCAGATGTGGATTTGGCAAAACCCTCATTTAAGTAAAGGTTACGAG	4420
D	b	28091	GGTGTGATCGGTTCCAGATGTGGATTTGGCAAAACCCTCATTTAAGTAAAGGTTACGAG	28032
Y	y	4421	AGCAAAAGTCGGTGTCTTTAGCTGCTGCTTTGTGCGCGTGTGTGTGCGGAGGCTCTCGCC	4480
D	b	28031	AGCAAAAGTCGGTGTCTTTAGCTGCTGCTTTGTGCGCGTGTGTGTGCGGAGGCTCTCGCC	27972
Y	y	4481	TGAGCTTCTTCCCCAGCTTTTGCTGCTGAGAGAAACAGAGCAGACGCAAGGCGCGGAA	4540
D	b	27971	TGAGCTTCTTCCCCAGCTTTTGCTGCTGAGAGAAACAGAGCAGACGCAAGGCGCGGAA	27912
Y	y	4541	AAGCGCATCTAACGGGTATCAGGCTTTGGTAACTGCGGACAACTGCTCTTTTACCTGAT	4600
D	b	27911	AAGCGCATCTAACGGGTATCAGGCTTTGGTAACTGCGGACAACTGCTCTTTTACCTGAT	27852
Y	y	4601	TTCATGATACATTTCAATTAAGGTTCCAGTTAPAAATATTTTGTTAATATTTTAAAGTGA	4660
D	b	27851	TTCATGATACATTTCAATTAAGGTTCCAGTTAPAAATATTTTGTTAATATTTTAAAGTGA	27792
Y	y	4661	CTATAGAATGCAACTCCATTTACCAGTAACCTTTTAAATATGCTGTAAGTAAACATATG	4720
D	b	27791	CTATAGAATGCAACTCCATTTACCAGTAACCTTTTAAATATGCTGTAAGTAAACATATG	27732
Y	y	4721	TAGTATAAATTTCTAGAAAACAAACATCTATAAGTATATAATCCTGTGAAAATATGAGCT	4780
D	b	27731	TAGTATAAATTTCTAGAAAACAAACATCTATAAGTATATAATCCTGTGAAAATATGAGCT	27672
Y	y	4781	TGATAATATTAAGTTGTCAGATGAAGCATGCTAGAGCTGTAAACAGAAATACATAGAGAA	4840
D	b	27671	TGATAATATTAAGTTGTCAGATGAAGCATGCTAGAGCTGTAAACAGAAATACATAGAGAA	27612
Y	y	4841	TAATGAGGAGTTTATGATGGAACTTTAAATATAATAATGTGCGACGGAATTTTGTCTCAAT	4900
D	b	27611	TAATGAGGAGTTTATGATGGAACTTTAAATATAATAATGTGCGACGGAATTTTGTCTCAAT	27552
Y	y	4901	ATTTGTTACTGTTATCTATCTGCTGTATAGGAATCTTTTAAATTC AAACCGCTGAAAAGA	4960
D	b	27551	ATTTGTTACTGTTATCTATCTGCTGTATAGGAATCTTTTAAATTC AAACCGCTGAAAAGA	27492
Y	y	4961	ATCAGATTTAGTCTTTGCCAGGCACACCCAAATAATCAGTCATGTGTAATATGCAACAAGTT	5020
D	b	27491	ATCAGATTTAGTCTTTGCCAGGCACACCCAAATAATCAGTCATGTGTAATATGCAACAAGTT	27432
Y	y	5021	TGTTTTGTGTTTTGTTTTTTTTTGTGGTTGGTTGTTTTTTTTTGTGCTTTAAGTTGCATGATC	5080

[illegible]

CDS	1. .3537	Query Match	35.7%; Score 2036; DB 5; Length 3537;
	/gene="THBS1"	Best Local Similarity	73.6%; Pred. No. 0;
	/codon_start=1	Matches 2594; Conservative	0; Mismatches 930; Indels 0; Gaps 0;
	/product="thrombospondin"		
	/protein_id="AA051437.1"		
	/db_xref="GI:212764"		
	translation="MLQSRLLMLAVFTLLWSSDAODAKEBENTFDLLQISNIRK TIGAKLFRGPAPAPAYEFIFDHI PPKPEKPKIKVILRONEGFIISATLRQPOQS QVTLALRPGISERQFEIISNGRANTLLIYWDGFQNVISLEDVLDLADSQWNLTV QVIGENLNYVGCDDLSFILBEPFYQLKAENSRMTVAQNSIRENHFRLQNLNHLI FDTSLEDVRLKGGQORSOSTENTINSETEILLHSPAVTEYVGEKTEKKAFCDRSC EELGTFMLRGLRIVNNLADNLQKSEENIMWELIGNPNTLKNQSCVQWQDGRVFA DSEWIKVSTCTKQDSKIQHGTICFPVSCADPSEIEGCPVCSHSDSDSEGWSP WSDMTVCSTQSGTQMRGSCDVTRGACTGPHIQTRMCRFKKDKIRIQDGGWSHS PWSGTCVGVGNITRILKNSPIPOMGKNVCNGRETEKCBKAPCVNGOWGWPSP WSACTVTCGGIRSRRLCNSRPEPOYGKNCVGDTEKHOHDMKDCPILDGCLSNPCFP GAEONSYPDGSWSGCPAGPLNGTWCELDDECIADVCFKYNQVHRCVNTNPGFH KLCEPRYKGSQPGVGLGVATKQVCEPENCPCOKTHSCHSKASCIYLGHFSDPMY CPCERTFAGRGICGEDSDJGPMNNNLVCAANATYVDMNCPILPNSGQDFDKO KGKGDDEDDNVEDDKDCPLLFNRPQFDYDKDEVGRCDNCPYVFNHPAQIDTN NKGESCAVDIDGDIENERUNCYVNTQSDTGDGVQDCDNCPLMHNPDQTDAD NLVDGQNNPQEDIDEDHQNKQDNCYFIENANQADHDKDGKDACPDDNDNGIPDD RNDCLRKYNEQSDSDGGRGDI CKDDFDNDVPDI FDCVPENNAISETDFRKFQVNP LDPKGTAOIPDNWIVRHQGLVOTANSDPGIAVGYDERVDFSGTFYVNTGHRLLNAD AGFVFGQSSSRFVYLMWKOVTQYWEDEKPTRAVGYSEVSLKVNVTGTGHELRNAL WHTGNTPOQVRLMHPDKLQWKOZYAYRWELLHRPKTGLLKLVLVEGKQVWVDSGPI YDTTFAGRLGLVFSQBMVIFSLLKYECRDA"		
QY	127	GCAGGATGCTGGAGGCTGGCTCTGCTGGCTCTGCTGGGTGGCCGAGCAGCAGCTG	186
DB	14	GCAGGCTGTGTGGCTTGTCTGTCATAAACCTGTGGGTTCCTCAGATGCTCAGGATG	73
QY	187	GTCCACGAGCAAAAGACACGACTTTCGACCTTTTCAGTATCAGCAACATCAACCGCAAGA	246
DB	74	ATGCCAAAGAGAGAGAGAATACCTTTGATTACTTCAAATCAGTAAACATAAAGCAAGA	133
QY	247	CCATTGGGCGCAGCAGTTCGGGGCGCCGACCGCGGCTTACCGCTTCGGTGC	306
DB	134	CAATTGGAGCAAAATGTGTTGGGGTCAGATCCGCTATCCCGCAATTCGTTTCAATTC	193
QY	307	GCTTTGACTATCCACCGGTGAACGAGATGACCTCAGCAAGATCACAAGATCATGC	366
DB	194	GGTTTGACCATATACCTCCATTTAAACAGAGAAAGTTTAAAAAGATTGTTAAACTCATAC	253
QY	367	GCAGAGAGAGCGCTTCTCTCACGGCCGACGCTCAGCAGCGCGCAAGTCCAGGGGCA	426
DB	254	GGCAAAATGAGGCGCTTATCTCTTCAGCCACCTTGAGACAGACAGCAATCTAGAGGCA	313
QY	427	CGCTGTGTGCTCTGAGGCGCCCGGTCTCTCCAGAGGACAGTTCAGATCGTCTCCAAAG	486
DB	314	CTATCTCTGCTTTAGAGGCTCTCGGCATCAGTGAGAGGACAGTTTGAATAAATTTCCAAATG	373
QY	487	GCCCGCGACACGCTGGATCTCACTACTGATGTGAGCGCACCGCGCATGTGGTCTCCC	546
DB	374	GCGAGCAACACCTTGHACCTCATTTATGGGTGGATGGCTTCAGAAAGTAAATTTCCC	433
QY	547	TGAGAGACTCGGCTGGCTGACTCGCAGTGGAGAACGTCACCGTCAAGTGGCTGGCG	606
DB	434	TGGAAGACCTGGACCTTGTGTACTCGCAGTGGAGAACCTCACCGTCAAGTAAACGAG	493
QY	607	AGACCTTACAGCTTGCAGCTGGGCTCGACCTCATAGACAGCTTCGCTCTGACGAGCGCT	666
DB	494	AGAACTTAAACCTCTATGTGTGGCTGTGACCTTATTGACAGCTTCATCTCTGGAGAGCTT	553
QY	667	TCTACGAGCACTTCGAGGCGGAAAAAGACCGGATGTATCGTGGCCAAAGGCTCTGCCAGAG	726
DB	554	TCTATGAGCAACTGAAGACAGAGAAACAGCAGAAATGTATGTGGCCAAAAGGCTTCCATTCGGG	613

1694 TTCTGAGCAGAGTCAACAGTTACCCGATGGATCGTGTCTATCTGGGCCATGCCAG 1753
 1867 TGGGCTTTCTGGCAATGGCACCACCTGTGAGACCTGGACAGTGTGCCCTGGTCCCG 1926
 1754 CAGTTTCTTGGCAATGGTACAGTCTGTGAGGATCTTGTAGTGTATAGTGTGTGAG 1813
 1927 ACATCTGCTTCTCCACAGCAAGGTGCTCGTGTGTCAACACTCAGCCTGGCTTCCACT 1986
 1814 ATGTTTCTTAAAGTGAATCAGTCCATCGTGTGTGAACACAAATCCGGGTTCCTATT 1873
 1987 GCCTGCCCTCCCGCCCGATACAGAGGGAACAGCCCGTCCGGGTCCGCTGGAGCAG 2046
 1874 GCTTGCATGCTCTCCCGTTTAAAGGAAGTCAAGCCTTACCGAGTAGGCTGGAGTTG 1933
 2047 CCAAGCGGAAAGCAAGTGTGTGAGCCGAAACCCATGCAAGGCAAGACACAACT 2106
 1934 CCAAGCAGAGAGCAAGTCTGTGAACCTGAGAATCCATGCAAGGCAAGACACAGCT 1993
 2107 GCCACAGCAGCGGAGTGTCTTACCTGGGCACTTACGCGCCCACTTACGCGCCCACTCAAGTGG 2166
 1994 GCCATAAATCTGCAGAGTGCATTTATCTGGGTCACTTTCAGTGATCTCTATGTCAAAATGG 2053
 2167 AGTGCCACAGAGGTACGCGGGGACCGGGCTCATCTCGGGGAGGACTCGGACCTGGACG 2226
 2054 AATGTAGCAGAGTTATGCTGTGTGATGAGCGCATCTGTGTGAGGATTCAGATTTGGATG 2113
 2227 GCTGGCCCAACCTCAATCTGCTGTGCGCCACCAAGCCACTACCACTGATCAAGGATA 2286
 2114 GATGGCCAAATAAATCTGGTTGTCTGCTAATGCTACGTATCACTGTGTGAAGGATA 2173
 2287 ACTGCCCCCACTGCCCCAAATCTGGGAGGAAAGACTTTGAAGGAGCGGATTTGGCGATG 2346
 2174 ACTGCCCCCTCTGCTAACTCTGGCCCAAGAGACTTTGATAAAGATGGCAAGGAGATG 2233
 2347 CTTGTGATGATGACGATGCAATGACCGTGTGACGATGAGAGGACAACTGCCACTCC 2406
 2234 CTTGTGATGAGGATGATGACAAATGATGCTGTGAAGATGACAAAGACAAATTTGCCCTCTTC 2293
 2407 TCTTCAATCCCGCCAGGCTGACTATCAAGATGAGTGTGGGACCGGTGTGACAACT 2466
 2294 TGTTCATCTCTGTCAGTTGATTTATGACAAAGTGAAGTTGTGACCGCTGTGATTAAT 2353
 2467 GCCCTTACGTGCAACACCTGCCAGATGACACAGACAAACATGAGAGGGGTGACGCT 2526
 2354 GCCCTTATGTGCAACACCCGACAGATTCACACAGATAATAATGGGGGGGTGATTCAAT 2413
 2527 GCTCCGTGACATTTGATGGGACGATGCTTCAATGAACGAGACAAATGTCCTACGTCT 2586
 2414 GTGCTGTGATTTGATGGAGATGACAAATTTTATGAAACGAGATAATGTCCTACGTTT 2473
 2587 ACAACACTGACAGAGGACACCGATGGTGAACCGTGTGGGGATCACTGTGACAACTGCC 2646
 2474 ATAATACAGATCAGAGTGATACAGATGGTGTGATGGATGGTGTGATGATAAAGTGTG 2533
 2647 CCCTGGTGCACACCTGACACAGACCGAGTGGACATGACCTTGTGGGGACAGGTGTG 2706
 2534 CGCTAATGCAATATCCAGACCGAGCTGATGAGATAACGATCTGTGTGGTGAACAGTGTG 2593
 2707 ACAACACAGGACATAGATGACACCGCCACCAAGAACCAACAGGACAACTGCCCTTACA 2766
 2594 ACAACATGAGGACATAGATGAAGATGGCCACCAAGAACCAAGATAAAGTGCCTTACA 2653
 2767 TCTCAAGCCCAACAGGCTGACCATGACAGAGACGCGGAGGAGCGCTGTGACCTG 2826
 2654 TCCCAATGCTAAACAGGCTGACCATGATAAAGATGTTAAAGGGGATGCTGTGATCTCTG 2713
 2827 ATGATGACAGATGGGTGCTCCCGATGACAGGGAACACTCGCGGCTTGTGTTCAACCCAG 2886
 2714 ATGATGACAAATGATGTTATCCAGATGACAGGGAACATTTGCGCTCAGATACAACTCTG 2773
 2887 ACCAGGAGACTTGCAGCGTGTGATGGAGCGGGTGTATTTTGAAGATGATTTTGACATG 2946

2774 AGCAGGAGGACTCTGATGGTGTATGCGCAGAGGTGATATTTGCAAGATGACTTTGACGATG 2833
 2947 ACAACATCCAGATATTTGATGATGTGTCTCTGAAAAAATGCCATCAGTGAGACAGACT 3006
 2834 ACAATGTTCCAGATATTTTGTATGTATGTCTGAAAAAATGCCATCAGTGAAACTGATT 2893
 3007 TCAGGAACTTCCAGATGGTCCCTTGGATCCCAAGGAGCAACCCCAATGATGCCAACT 3066
 2894 TCAGAAAGTTCAGATGGTCCCTCTGGAACCAAGGAAACAGCTCAGATTTGATCCCACT 2953
 3067 GGGTCATTTCGCCATCAAGGCAAGGAGTGTTCAGACAGCAACCTCGACCCCGGCACTG 3126
 2954 GGGTATTTCCGCCCAAGGCAAGGAACTGTGTGAGACTGCCAACTCTGATCTCTGGAATAG 3013
 3127 CTGTAGTGTGACAGTGTGGTCTGTGACTTTCAGTGGACATTTCTACGTAACACTG 3186
 3014 CTGTAGTGTATGAGTTCAGTCTGTGTGACTTTCAGTGGACATTTCTATTTAACACAG 3073
 3187 ACCGGGACGACGACTATGCCGGCTTCGTCTTTGTTTACAGTCAAGCAGCGCTTCTATG 3246
 3074 ACCGTGATGATGACTATGCTGGCTTTGTTTGGCTACCACTCCAGCAGCGCTTTTATG 3133
 3247 TGGTATGTGAAAGAGTGAACGACACTTACTGGGAGGACCAACCCCGGGGCTTATG 3306
 3134 TTCTGATGTGAAAGCAGGTCTACTCAGACCTACTGGGAGGACAAACCCCAAGGCTTATG 3193
 3307 GCTACTCCGGCGTGTCCCTCAAGGTGTGAACTCCACACGGGACGGGCGAGCACCTGA 3366
 3194 GCTATCTGGTGTGCTCACTCAAGGTAGTGAATTCACAACTGGTACTTGGGAAACACTTGC 3253
 3367 GGAACGCTGTGGCACACGGGGAAACCGCGGGCAGGTGCGAACCTTATGGCACAGACC 3426
 3254 GAAATGCTCTTTGGCAATACAGGAAACACCCCTGACAGGTGCGCACTTTATGGCATGATC 3313
 3427 CCAGGAACTATGGCTTGAAGGACTACAGCGCTTATAGTGGCACTGACTCACAGGCCCCA 3486
 3314 CTAGAACTTTGGCTTGAAGATTTATCTGATACAGGTGGCATTTGATTCAGAGCCTA 3373
 3487 AGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAACAGGTGATGCGACACTCAGAAC 3546
 3374 AAACAGGACTAATAAAGTTCTAGTGTATGAAGGAAAGCAAGTCAATGCTGATCTGGAC 3433
 3547 CTATCTATGACCAACCTACCTGCGGGCGCTGGGTCTATTTGCTCTCTCAAGAAA 3606
 3434 CAATCTATGATACAACTTTGCTGTGGACGATTAGGTCTATTTGCTCTCTCAAGAAA 3493
 3607 TGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAA 3650
 3494 TGGTCTATTTCTGACCTCAATATGATGACAGATGCTTGA 3537

RESULT 15

G06722
 LOCUS human STS WI-7830, 2026 bp DNA linear STS 19-OCT-1995
 DEFINITION G06722
 ACCESSION G06722.1 GI:859967
 VERSION STS; STS sequence; primer; sequence tagged site.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2026)
 AUTHORS Hudson, T.
 TITLE Whitehead Institute/MIT Center for Genome Research; Physically Mapped ESTs
 JOURNAL Unpublished (1995)
 COMMENT Contact: Thomas Hudson
 Whitehead Institute/MIT Center for Genome Research
 Whitehead Institute for Biomedical Research
 9 Cambridge Center, Cambridge MA 02142 USA
 Tel: 617 252 1900

Query Match	33.6%	Score 1912.8	DB 11	Length 2026	
Best Local Similarity	97.1%	Pred. No. 0			
Matches 1977	Conservative	0	Mismatches 48	Indels 10	Gaps 5
QY	3651	ACAAGATTTCTGCTGCAATTCGGCAATTCGCCCTGTGCATGCCATGGTCCCTAGACACCTCAG	3710		
Db	1	ACAAGATTTCTGCTGCAATTCGGCAATTCGCCCTGTGCATGCCATGGTCCCTAGACACCTCAG	60		
QY	3711	TTCAATGTGTGCTTCTGTGGCTTCTCTCTCTAGACAGACCTCTGTGCTTGCCTTAACT	3770		
Db	61	TTCAATGTGTGCTTCTGTGGCTTCTCTCTCTAGACAGACCTCTGTGCTTGCCTTAACT	120		
QY	3771	CTGATGTTCTTTCACCTCTCCGACGCAACCCCAACCCCAAGTGCCTTCAGAGGATAAATA	3830		
Db	121	CTGATGTTCTTTCACCTCTCCGACGCAACCCCAACCCCAAGTGCCTTCAGAGGATAAATA	180		
QY	3831	TCAATGGAACGCGAGAGTGAACATCTTAACCCCTCTAGAGGAACACGTTGGTGATATATG	3890		
Db	181	TCAATGGAACGCGAGAGTGAACATCTTAACCCCTCTAGAGGAACACGTTGGTGATATATG	240		
QY	3891	AGACTTTATGTGGAGTGAATAATTTGGGCATGCCATTACATTCGTTTTCTTGTTGTTAA	3950		
Db	241	AGACTTTATGTGGAGTGAATAATTTGGGCATGCCATTACATTCGTTTTCTTGTTGTTAA	300		
QY	3951	AAAGAATGACGTTTACATATATAAATGTAATTTACTTTGTATTATTGTGTATATGAGTT	4010		
Db	301	AAAGAATGACGTTTACATATATAAATGTAATTTACTTTGTATTATTGTGTATATGAGTT	360		
QY	4011	GAAGGGAAATCTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATTTCTCTGAACT	4070		
Db	361	GAAGGGAAATCTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATTTCTCTGAACT	420		
QY	4071	ACTTTTGGTGGTTAAAGTTGTCACTATTCCTGTAATAGAGTTGCTCTACAATGACACACA	4130		

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

M nucleic - nucleic search, using sw model

Run on: March 10, 2004, 08:01:57 ; Search time 1386.29 Seconds
(without alignments)
17454.974 Million cell updates/sec

Title: US-10-084-817-25
Perfect score: 5696
Sequence: 1 gactacgcgcactgcagg.....ggtttctataaaaaaaaaa 5696

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseqn_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	5696	100.0	5696	8	ACH03798 Human cDN
2	5576.6	97.9	5784	6	ABL62660 Colon ade
3	5576.6	97.9	5784	6	ABZ35081 Human gen
4	5576.6	97.9	5784	6	ABK10277 Human cDN
5	5576.6	97.9	5784	6	ABN95662 Gene #216
6	5576.6	97.9	5784	6	AD40611 Human thr
7	5576.6	97.9	5784	6	ABV94768 Human pan
8	5576.6	97.9	5784	7	ABQ77406 Human THB
9	5576.6	97.9	5784	8	AAD55115 Human THB
10	5576.6	97.9	5784	9	ADD31094 Human cDN
11	5576.6	97.9	5784	9	ADE85079 Farnesyl
12	3718.4	65.3	3787	3	AAC77795 Human can
13	3591.2	63.0	3596	3	AA88669 Human thr
14	3591.2	63.0	3596	7	ABX14061 cDNA enco
15	3429.4	60.2	3522	4	AAH4535 Human col
16	2753.2	48.3	4108	2	AAZ32016 Human MET
17	2753.2	48.3	4108	5	AAC90073 L07803 cD
18	2741.4	48.1	4170	6	ABL35019 Rat cDNA
19	1881.6	33.0	2837	5	AAC77795 Human can
20	1881.6	33.0	2837	5	AAC90072 M64866 cD
21	1612.2	28.3	5289	2	AAZ32052 Human MET
22	1612.2	28.3	5289	5	AAC90309 AB005287
23	1552	27.2	5721	4	AAH02923 Human she

24	1552	27.2	5722	2	AAZ32012	Aaz32012 Human MET
25	1552	27.2	5722	4	AAF95238	Aaf95238 Human var
26	1552	27.2	5722	5	AAC90069	Aac90069 X14787 cD
27	1552	27.2	5722	6	ABZ34907	Abz34907 Human gen
28	1552	27.2	5722	6	ABV94226	Abv94226 Breast ca
29	1552	27.2	5722	6	ABN97206	Abn97206 Gene #370
30	1552	27.2	5722	7	ACC46751	Acc46751 Human COP
31	1552	27.2	5722	7	ABX08757	Abx08757 Angiogene
32	1552	27.2	5722	8	ACC84978	Acc84978 Human thr
33	1552	27.2	5724	6	AAD40610	Aad40610 Human thr
34	1550.4	27.2	4433	2	AAZ32014	Aaz32014 Human MET
35	1550.4	27.2	4434	5	AAC90071	Aac90071 X04665 cD
36	1550.4	27.2	4434	9	ADD18445	Add18445 Human pro
37	1550.4	27.2	6132	5	ABV24661	Abv24661 Human pro
38	1550.4	27.2	7231	6	ABE62773	Abe62773 Prostate
39	1550.4	27.2	7231	9	ADE25694	Ade25694 Human cDN
40	1550.4	27.2	7232	6	AAS94912	Aas94912 Human can
41	1531.4	26.9	5830	3	AAC77811	Aac77811 Human can
42	1523.8	26.8	4339	2	AAZ32054	Aaz32054 Human MET
43	1523.8	26.8	4339	5	AAC90311	Aac90311 M87276 cD
44	703.8	12.5	713	4	AAH34534	Aah34534 Human col
45	687.8	12.1	2468	5	AA506013	Aas06013 Angiotens

ALIGNMENTS

RESULT 1

ACH03798	ID	ACH03798 standard; cDNA; 5696 BP.
XX	AC	ACH03798;
XX	AC	ACH03798;
DT	26-SEP-2003	(first entry)
XX	DE	Human cDNA differentially expressed in lung cancer #3.
XX	KW	Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;
XX	KW	respiratory disorder; lung cancer; asthma; human.
OS	Homo sapiens.	
XX	PN	US2003065157-A1.
XX	PD	03-APR-2003.
XX	PF	04-APR-2002; 2002US-00116802.
XX	PR	04-APR-2001; 2001US-0281593P.
XX	PA	(LASE/) LASEK A W.
XX	PI	Lasek AW;
XX	DR	WPI; 2003-540803/51.
PT	New combination comprising cDNAs that are differentially expressed in	
PT	respiratory disorders, useful for diagnosing or treating respiratory	
PT	disorders e.g., lung cancer, chronic obstructive pulmonary disease,	
PT	emphysema or asthma.	
PS	Claim 1; Page; 39pp; English.	
CC	The invention relates to a combination comprising cDNAs or their	
CC	complements that are differentially expressed in respiratory disorder.	
CC	The combination is useful for preparing a composition for diagnosing or	
CC	treating respiratory disorders e.g. lung cancer, chronic obstructive	
CC	pulmonary disease, emphysema or asthma. The present sequence represents	
CC	human cDNA differentially expressed during lung cancer	
SQ	Sequence 5696 BP; 1438 A; 1424 C; 1483 G; 1351 T; 0 U; 0 Other;	
XX	Query Match	100.0%; Score 5696; DB 8; Length 5696;

2161 AGTGCAGTGCACAGACAGGCTACCGCGGCGACCGGGCTCATCTCGGGGAGGACTCGGACC 2220
2161 AGTGCAGTGCACAGACAGGCTACCGCGGCGACCGGGCTCATCTCGGGGAGGACTCGGACC 2220
2221 TGGAGCGCTGCGCCCAACCTCAATCTGCTGCGCCACCAACGCGCACTACCACTGCAATCA 2280
2221 TGGAGCGCTGCGCCCAACCTCAATCTGCTGCGCCACCAACGCGCACTACCACTGCAATCA 2280
2281 AGGATAACTGCCCCCATCTGCCAAATCTCGGCGAGGAAGACTTTGACAAAGGACGGGATTG 2340
2281 AGGATAACTGCCCCCATCTGCCAAATCTCGGCGAGGAAGACTTTGACAAAGGACGGGATTG 2340
2341 GCGATGCTGTGATGATGACGATGACATGACATGACATGACATGACATGACATGACATGAC 2400
2341 GCGATGCTGTGATGATGACGATGACATGACATGACATGACATGACATGACATGACATGAC 2400
2401 AGTCTCTCTTCAATCCCGCCGACGCTGATGATGACAAAGGATGAGTTGGGACCGCTGTG 2460
2401 AGTCTCTCTTCAATCCCGCCGACGCTGATGATGACAAAGGATGAGTTGGGACCGCTGTG 2460
2461 ACAACTGCCCTTAGGTGACAACTCCGCCAGATCGACACAGCAACAAATGAGAGGGTG 2520
2461 ACAACTGCCCTTAGGTGACAACTCCGCCAGATCGACACAGCAACAAATGAGAGGGTG 2520
2521 ACGCTGCTCCGTGGACATTTGATGGGACGATGTCTTCAATGAACGAGACAAATTTGTCCT 2580
2521 ACGCTGCTCCGTGGACATTTGATGGGACGATGTCTTCAATGAACGAGACAAATTTGTCCT 2580
2581 ACGTCTACACACTGACAGAGGACACGATGGTGACCGTGTGGGGATCACTGTGACA 2640
2581 ACGTCTACACACTGACAGAGGACACGATGGTGACCGTGTGGGGATCACTGTGACA 2640
2641 ACTGCCCTCTGCTGACAACTGACAGACCGCTGACCAATGACCTTTGTTGGGGACC 2700
2641 ACTGCCCTCTGCTGACAACTGACAGACCGCTGACCAATGACCTTTGTTGGGGACC 2700
2701 AGTGTGACAAACAGGAGCATGATGACAGCGGACACAGGACCAACAGGACCACTGCC 2760
2701 AGTGTGACAAACAGGAGCATGATGACAGCGGACACAGGACCAACAGGACCACTGCC 2760
2761 CTTACATCTCCACGCGCAACAGGCTGACCATGACAGAGCGCGGCGAGCGCGCTGTG 2820
2761 CTTACATCTCCACGCGCAACAGGCTGACCATGACAGAGCGCGGCGAGCGCGCTGTG 2820
2821 ACCCTGATGATGACACAGTGGGCTCCCGATGACAGGACCAACTGCCGCTTGTGTTCA 2880
2821 ACCCTGATGATGACACAGTGGGCTCCCGATGACAGGACCAACTGCCGCTTGTGTTCA 2880
2881 ACCCAGACAGGAGGACTTGGACGCTGATGACGCGGCTGATATTTGTAAGATGATTTG 2940
2881 ACCCAGACAGGAGGACTTGGACGCTGATGACGCGGCTGATATTTGTAAGATGATTTG 2940
2941 ACAATGACACATCCCAAGATTTGATGATGTGTCTCTGAAAAAATGCCATCAGTGAGA 3000
2941 ACAATGACACATCCCAAGATTTGATGATGTGTCTCTGAAAAAATGCCATCAGTGAGA 3000
3001 CAGACTTCAGGAATTCAGATGGTCCCTTGATGACGCGGCTGATATTTGTAAGATGATTTG 3060
3001 CAGACTTCAGGAATTCAGATGGTCCCTTGATGACGCGGCTGATATTTGTAAGATGATTTG 3060
3061 CCAACTGGGTCATTCGCAATCAAGCAAGAGCTGTGTTGACAGCGCAACTCGGACCCCG 3120
3061 CCAACTGGGTCATTCGCAATCAAGCAAGAGCTGTGTTGACAGCGCAACTCGGACCCCG 3120
3121 GCATCGCTAGGTTTGGACGATTTGGTCTGTGGACTTCACTGACGACATTTAGCTAA 3180
3121 GCATCGCTAGGTTTGGACGATTTGGTCTGTGGACTTCACTGACGACATTTAGCTAA 3180
3181 ACATGACCGGACGACGATATGCCGGCTTCTGTTGGTTACCACTCAAGCAGCGCT 3240
3181 ACATGACCGGACGACGATATGCCGGCTTCTGTTGGTTACCACTCAAGCAGCGCT 3240

3241 TCTATGTGGTGTATGTGGAAAGCAGGTGACGAGACCTACTGGGAGGACCGCCACGCGGG 3300
3241 TCTATGTGGTGTATGTGGAAAGCAGGTGACGAGACCTACTGGGAGGACCGCCACGCGGG 3300
3301 CCTATGGCTACTCGGGGTGTCCCTCAAGGTGTGTAACTCCACACCGGGACGCGCGAGC 3360
3301 CCTATGGCTACTCGGGGTGTCCCTCAAGGTGTGTAACTCCACACCGGGACGCGCGAGC 3360
3361 ACCTGAGGAAACGCGCTGTGGCACACGCGGACACGCGCGGCGAGGTGGACCTTATGGC 3420
3361 ACCTGAGGAAACGCGCTGTGGCACACGCGGACACGCGCGGCGAGGTGGACCTTATGGC 3420
3421 ACGACCCACAGAAACATTTGGCTTGGAGGACTACACGGCTTATAGTGGCACCTGACTCACA 3480
3421 ACGACCCACAGAAACATTTGGCTTGGAGGACTACACGGCTTATAGTGGCACCTGACTCACA 3480
3481 GCGCCAGACATGGCTTACATCAGAGTCTTAGTGATGAAGAAACAGGTCTATGCGAGCT 3540
3481 GCGCCAGACATGGCTTACATCAGAGTCTTAGTGATGAAGAAACAGGTCTATGCGAGCT 3540
3541 CAGGACCTATCTATGACCAACCTACGCTGGCGGCGCTGGGTCTATTTGCTCTCTC 3600
3541 CAGGACCTATCTATGACCAACCTACGCTGGCGGCGCTGGGTCTATTTGCTCTCTC 3600
3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTG 3660
3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTG 3660
3661 CTGCATTTCCGGCAATGCCCTGTGCATGCTCCTAGACACCTCAGTTCAATTGTGG 3720
3661 CTGCATTTCCGGCAATGCCCTGTGCATGCTCCTAGACACCTCAGTTCAATTGTGG 3720
3721 TCCCTGTGGCTTCTCTCTAGCAGACCTCCTGTCTCCTTGAACCTTAACCTGATGTTTC 3780
3721 TCCCTGTGGCTTCTCTCTAGCAGACCTCCTGTCTCCTTGAACCTTAACCTGATGTTTC 3780
3781 TTCACCTCTCCAGCAACCCCAACCCAGTGCCTTTCAGAGGATAAATCAATGAAC 3840
3781 TTCACCTCTCCAGCAACCCCAACCCAGTGCCTTTCAGAGGATAAATCAATGAAC 3840
3841 GCAGAGATGAAACATCTAACCCACTAGAGGAAACAGTTTGGTGATATATGAGACTTTATG 3900
3841 GCAGAGATGAAACATCTAACCCACTAGAGGAAACAGTTTGGTGATATATGAGACTTTATG 3900
3901 TGGAGTGAAATTTGGGATGCGCATTAATTGCTTTTCTGTTTGTGTTTAAAGAAATGAC 3960
3901 TGGAGTGAAATTTGGGATGCGCATTAATTGCTTTTCTGTTTGTGTTTAAAGAAATGAC 3960
3961 GTTTACATATAAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4020
3961 GTTTACATATAAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4020
4021 CTGTGCATTAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4080
4021 CTGTGCATTAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4080
4081 CTTAAAGTTGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4140
4081 CTTAAAGTTGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4140
4141 AATAAATTTATAAACAAGGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4200
4141 AATAAATTTATAAACAAGGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4200
4201 GAAGACACAGGATAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4260
4201 GAAGACACAGGATAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4260
4261 CAGTTACAAAAATTAACGAACTCTCTCTTGTCTCAATGAAGAAACCTCATGTGACGTA 4320
4261 CAGTTACAAAAATTAACGAACTCTCTCTTGTCTCAATGAAGAAACCTCATGTGACGTA 4320
4321 GAGTGCAGTTTTCATCAAGAGACAAACATCCTTGCBAATGGGTGTGATGCGGTTCCAGAT 4380

02-OCT-2000; 2000US-0237278P.
02-OCT-2000; 2000US-0237294P.
02-OCT-2000; 2000US-0237295P.
02-OCT-2000; 2000US-0237316P.
03-OCT-2000; 2000US-0237425P.
03-OCT-2000; 2000US-0237598P.
03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237606P.
03-OCT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-0244867P.
01-NOV-2000; 2000US-0245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
Soppet DR, Weaver Z;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 997; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour

Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;

Query Match 97.9%; Score 5576.6; DB 6; Length 5784;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

1 GACTACGCTGCACGAGGCGCGTCTCTCGCTCCAGCAGAGCTGCGCTTCTGACTC 60

109 GAGCATCTGCACTGCAGGCGCGTCTCTCGCTCCAGCAGAGCTGCGCTTCTGACTC 168

61 GGTCCGAGACCTAAACCACTATCACTGATCTTTTGGCAACCCAGAGCTCAGCTG 120

169 GGTCCGAGACCTAAACCACTATCACTGATCTTTTGGCAACCCAGAGCTCAGCTG 228

121 CAGGAGCAGGATGCTTGGAGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

229 CAGGAGCAGGATGCTTGGAGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288

181 AAGCTGTCACAGGACCAAGACAGACCTTTCAGTATCAGCAATCAAC 240

289 AAGCTGTCACAGGACCAAGACAGACCTTTCAGTATCAGCAATCAAC 348

241 GCAAGACCATTTGGCGCCAAAGCAGTTCCGCGGCGCCGACCCCGGCTGCGGCTTACCGCT 300

349 GCAAGACCATTTGGCGCCAAAGCAGTTCCGCGGCGCCGACCCCGGCTGCGGCTTACCGCT 408

301 TCGTGGCTTTGACTATCCACCGGTGAACGAGATGACCTCAGCAAGATCAACCAAGA 360

409 TCGTGGCTTTGACTATCCACCGGTGAACGAGATGACCTCAGCAAGATCAACCAAGA 468

361 TCATGCGGCAAGAGGAGGCGCTTCTTCTCAGGCGCCAGCTCAAGCAGGACGGCAAGTCCA 420
469 TCATGCGGCAAGAGGAGGCGCTTCTTCTCAGGCGCCAGCTCAAGCAGGACGGCAAGTCCA 528
421 GGGCAGCGCTGTTGGCTCTGGAGGCGCCCGGTCTCTCCAGAGGAGCTTCCAGATCGTCT 480
529 GGGCAGCGCTGTTGGCTCTGGAGGCGCCCGGTCTCTCCAGAGGAGCTTCCAGATCGTCT 588
481 CCAACGGCCCCGCGGACACGCTGGATCTCACTACTGGATTGACGGACCGCGGATGTGG 540
589 CCAACGGCCCCGCGGACACGCTGGATCTCACTACTGGATTGACGGACCGCGGATGTGG 648
541 TCTCCCTGGAGAGCTGGGCTGCTGACTCGAGTGGAGAGAGCTCACCGTCAGAGTGG 600
649 TCTCCCTGGAGAGCTGGGCTGCTGACTCGAGTGGAGAGAGCTCACCGTCAGAGTGG 708
601 CTGCGAGACCTACAGCTTTCACGCTGGGCTGCGACCTCATAGACAGCTTCCCTCTGAGC 660
709 CTGCGAGACCTACAGCTTTCACGCTGGGCTGCGACCTCATAGAGCCAGTGTCTCTGAGC 768
661 AGCCCTTTCAGAGCAGCTGACGGGGAAGAGCCGATGTAGTGGCCAAAGGCTCTG 720
769 AGCCCTTTCAGAGCAGCTGACGGGGAAGAGCCGATGTAGTGGCCAAAGGCTCTG 828
721 CCAGAGAGCTCACTTCAGGGGTTTGTCTTCAAGAACGTCACCTAGTGTGTTGAAACCTG 780
829 CCAGAGAGCTCACTTCAGGGGTTTGTCTTCAAGAACGTCACCTAGTGTGTTGAAACCTG 888
781 TGGAGATATTCTAAGCAAGAGGTTTCCAGAGAGGCGCAGGAGCTGAGATCAACGCCA 840
889 TGGAGATATTCTAAGCAAGAGGTTTCCAGAGAGGCGCAGGAGCTGAGATCAACGCCA 948
841 TCAGTGAGAACACACAGAGAGCTGCGGCTGCGCATGTCCACACCGAGTACCTGGGCCC 900
949 TCAGTGAGAACACACAGAGAGCTGCGGCTGCGCATGTCCACACCGAGTACCTGGGCCC 1008
901 CCAGCTCAGAGAGAGGCGCAGGCTGTCGAAACGCTCTGTCGAGAGCTGGGAAACATGG 960
1009 CCAGCTCAGAGAGAGGCGCAGGCTGTCGAAACGCTCTGTCGAGAGCTGGGAAACATGG 1068
961 TCCAGAGCTCTCGGGGCTCCAGCTCTGTCGTAACACAGCTCAGCGAGAACCTCAAGAGAG 1020
1069 TCAGAGCTCTCGGGGCTCCAGCTCTGTCGTAACACAGCTCAGCGAGAACCTCAAGAGAG 1128
1021 TGTGAAATGATAACCAAGTTCCTCTGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGAACA 1080
1129 TGTGAAATGATAACCAAGTTCCTCTGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGAACA 1188
1081 TGTGAGCTTGTGGCAGAGTGGCGGTTCTTTGGGAAATGAAACGTCGGTGGTGACA 1140
1189 TGTGAGCTTGTGGCAGAGTGGCGGTTCTTTGGGAAATGAAACGTCGGTGGTGACA 1248
1141 GCTGCACCAACGCTGACCTGCAAGAAATTTAAACCATTTGGCCACCAATCACTGCCCCG 1200
1249 GCTGCACCAACGCTGACCTGCAAGAAATTTAAACCATTTGGCCACCAATCACTGCCCCG 1308
1201 CTGCAACCTGGCAGTGCATCTTTTGGAGAGGGAATGTGCTGCTTCTTCTGCTCCACT 1260
1309 CTGCAACCTGGCAGTGCATCTTTTGGAGAGGGAATGTGCTGCTTCTTCTGCTCCACT 1368
1261 CGCTGGAGCTGAGAGAGGCTGCTCTCGTGGGAGAGTGGACCCAGTGTCTCCGTCAGCT 1320
1369 CGCTGGAGCTGAGAGAGGCTGCTCTCGTGGGAGAGTGGACCCAGTGTCTCCGTCAGCT 1428
1321 GTGGCTTGGGAGCCAGCAGAGAGGCGGCTCTGTGACGTCAACAGCAACACCTGCTTGG 1380
1429 GTGGCTTGGGAGCCAGCAGAGAGGCGGCTCTGTGACGTCAACAGCAACACCTGCTTGG 1488
1381 GSCCTTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCACTCCGCGAGG 1440
1489 GSCCTTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCACTCCGCGAGG 1548
1441 ACGGCGGCTGGAGGCCACTTGGTCACTTGTGCTTGTGACCTGTGGAGTGGCA 1500

Db	1549	ACGGGAGTGGAGCCACTGGTCACTTGGTCTTCACTGCTGTAACCTGAGATTGGCA	1608
Qy	1501	ATATCAACGATCCGTCTGCACTCCCAAGTCCCAAGATGGGGGCAAGATTGCA	1560
Db	1609	ATATCAACGATCCGTCTGCACTCCCAAGTCCCAAGATGGGGGCAAGATTGCA	1668
Qy	1561	AAGGAGTGGCCGGAGACCAAGCTGCGAGGGGCGCCCAATGGCAATGATGGCCCT	1620
Db	1669	AAGGAGTGGCCGGAGACCAAGCTGCGAGGGGCGCCCAATGGCAATGATGGCCCT	1728
Qy	1621	GAGGCCCTGGTCCCGTGGTGGCTGGCTGCACTGTCACCTGGCCGGTGGATCCGGAGC	1680
Db	1729	GAGGCCCTGGTCCCGTGGTGGCTGGCTGCACTGTCACCTGGCCGGTGGATCCGGAGC	1788
Qy	1681	GACCCCGGTCTGCAACAGCCCTGAGCCTCACTAGAGAGAGAGCCCTGGTGGGGATG	1740
Db	1789	GACCCCGGTCTGCAACAGCCCTGAGCCTCACTAGAGAGAGAGCCCTGGTGGGGATG	1848
Qy	1741	TGAGAGAGCTCAGATGTGCAACAAGAGAGCTGCCCTGGATGGCTGTATCAACC	1800
Db	1849	TGAGAGAGCTCAGATGTGCAACAAGAGAGCTGCCCTGGATGGCTGTATCAACC	1908
Qy	1801	CCTGTTCCCGGAGACCAAGTGCAGACCTTCCCGATGGGTCTGTCATGCGGCTCT	1860
Db	1909	CCTGTTCCCGGAGACCAAGTGCAGACCTTCCCGATGGGTCTGTCATGCGGCTCT	1968
Qy	1861	GCCCTGGAGCTTCTTGGGCAATGGCAACCCTGTGAGAGACTGGAGAGCTGGCCCTG	1920
Db	1969	GCCCTGGAGCTTCTTGGGCAATGGCAACCCTGTGAGAGACTGGAGAGCTGGCCCTG	2028
Qy	1921	TCCCGACATCTGCTTCTTCCACAGCAAGTGGCTGGTGTGTCAACTAGCTGGCT	1980
Db	2029	TCCCGACATCTGCTTCTTCCACAGCAAGTGGCTGGTGTGTCAACTAGCTGGCT	2088
Qy	1981	TCCACTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2040
Db	2089	TCCACTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2148
Qy	2041	AAGCAGCCCAAGCAAGAAAGCAAGTGTGTAGCCCGCAAACTGACAGCAACAAC	2100
Db	2149	AAGCAGCCCAAGCAAGAAAGCAAGTGTGTAGCCCGCAAACTGACAGCAACAAC	2208
Qy	2101	ACAACTGCCAAGACAGCGGAGTGCATCTAGGCGCACTTACGACACCCCACTGACA	2160
Db	2209	ACAACTGCCAAGACAGCGGAGTGCATCTAGGCGCACTTACGACACCCCACTGACA	2268
Qy	2161	AGTGGAGTGCAGACAGGCTTACGCGGAGCAAGGCTCATCTGCGGGAGAGACTGGACC	2220
Db	2269	AGTGGAGTGCAGACAGGCTTACGCGGAGCAAGGCTCATCTGCGGGAGAGACTGGACC	2328
Qy	2221	TGAGAGGCTGGGCGCAACCTCAATGTGTGCGGCAACAAGCGCACTTACGACAGCA	2280
Db	2329	TGAGAGGCTGGGCGCAACCTCAATGTGTGCGGCAACAAGCGCACTTACGACAGCA	2388
Qy	2281	AGGATTAAGTCCCGCACTTGGCAATCTGGGCAAGAGAGCTTTGACAAGAGCGGATGG	2340
Db	2389	AGGATTAAGTCCCGCACTTGGCAATCTGGGCAAGAGAGCTTTGACAAGAGCGGATGG	2448
Qy	2341	GGGATGCTGTATGTATGACATGACATGACAGGTGTGCGATGAGAGAGCAACTGCC	2400
Db	2449	GGGATGCTGTATGTATGACATGACATGACAGGTGTGCGATGAGAGAGCAACTGCC	2508
Qy	2401	AGTCTCTTCAATCCCGCAAGCTGACTATGACAAGATGAGGTTGGGAGCGCTGTG	2460
Db	2509	AGTCTCTTCAATCCCGCAAGCTGACTATGACAAGATGAGGTTGGGAGCGCTGTG	2568
Qy	2461	ACAACTGCCAAGCAAGCAAGCTGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	2520
Db	2569	ACAACTGCCAAGCAAGCAAGCTGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	2628
Qy	2521	ACGCTGCTCCGTGACATTTATGGGAGAGATGTCTTCAATGACAGCAATGTCTCT	2580
Db	2629	ACGCTGCTCCGTGACATTTATGGGAGAGATGTCTTCAATGACAGCAATGTCTCT	2688
Qy	2581	AGCTTCAACAACCTGACAGAGAGCAAGGATGGGATGGGATGGGATGGGATGGGAT	2640
Db	2689	AGCTTCAACAACCTGACAGAGAGCAAGGATGGGATGGGATGGGATGGGATGGGAT	2748
Qy	2641	ACTGCCCCCTGGTGCACAACCTTGCACAGCCGAGCTGAGCAATGACCTTGTGGAGC	2700
Db	2749	ACTGCCCCCTGGTGCACAACCTTGCACAGCCGAGCTGAGCAATGACCTTGTGGAGC	2808
Qy	2701	AGTGTGACAAACAGAGACATAGATGACAGCCGACCAAGAAACAACAGAGCAACTGCC	2760
Db	2809	AGTGTGACAAACAGAGACATAGATGACAGCCGACCAAGAAACAACAGAGCAACTGCC	2868
Qy	2761	CCTACATCTCCAAACCCCAACAGGCTGACATGACAGAGACGCGCCAGGCGACGCTGTG	2820
Db	2869	CCTACATCTCCAAACCCCAACAGGCTGACATGACAGAGACGCGCCAGGCGACGCTGTG	2928
Qy	2821	ACCTGATGATGACAAAGATGGCTGCTCCGATGACAGAGCAACTGCGGCTGTGTCA	2880
Db	2929	ACCTGATGATGACAAAGATGGCTGCTCCGATGACAGAGCAACTGCGGCTGTGTCA	2988
Qy	2881	ACCCAGACAGAGAGACTTGCAGGATGATGACAGGAGTATTTGTAAGATGATTTTG	2940
Db	2989	ACCCAGACAGAGAGACTTGCAGGATGATGACAGGAGTATTTGTAAGATGATTTTG	3048
Qy	2941	ACATGACAACTCCAGATATTGATGATGTGTCTGAAACAATGCGATCACTGAGCA	3000
Db	3049	ACATGACAACTCCAGATATTGATGATGTGTCTGAAACAATGCGATCACTGAGCA	3108
Qy	3001	CAGACTTGCAGAACTTGCAGATGTGCTCCCTGGATCCCAAGAGCAACCCAAATTGATC	3060
Db	3109	CAGACTTGCAGAACTTGCAGATGTGCTCCCTGGATCCCAAGAGCAACCCAAATTGATC	3168
Qy	3061	CCAATGGGTATTTGGCATTCGCAATCAAGCAAGAGACTGGTTCAGACAGCAACTGGAC	3120
Db	3169	CCAATGGGTATTTGGCATTTCCCATCAAGCAAGAGACTGGTTCAGACAGCAACTGGAC	3228
Qy	3121	GCATGGCTGATGATTTGAGAGGATTTGGGCTGTGAGACTTCACTGAGGACATCTAGTAA	3180
Db	3229	GCATGGCTGATGATTTGAGAGGATTTGGGCTGTGAGACTTCACTGAGGACATCTAGTAA	3288
Qy	3181	ACACTGACCGGAGCGAGCTATGCGGCTTGTCTTGGTTACAGTAAAGACGCGCT	3240
Db	3289	ACACTGACCGGAGCGAGCTATGCGGCTTGTCTTGGTTACAGTAAAGACGCGCT	3348
Qy	3241	TCTATGATGATGATGAGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3300
Db	3349	TCTATGATGATGATGAG	3408
Qy	3301	CCTATGCTACTCCCGGCTGTGCTCCCTCAAGTGTGAACTTCAACAAGGAGAGAGAG	3360
Db	3409	CCTATGCTACTCCCGGCTGTGCTCCCTCAAGTGTGAACTTCAACAAGGAGAGAGAG	3468
Qy	3361	ACCTGAG	3420
Db	3469	ACCTGAG	3528
Qy	3421	ACGACCCAGAGAACTTGGCTGAGAGAGACTACAAGGCTTATAGTGGCACTTGACTACA	3480
Db	3529	ACGACCCAGAGAACTTGGCTGAGAGAGACTACAAGGCTTATAGTGGCACTTGACTACA	3588
Qy	3481	GGCCCAAGAGTGGCTCACTCAGAGCTTATGATGATGAGAGAGAGAGAGAGAGAGAG	3540
Db	3589	GGCCCAAGAGTGGCTCACTCAGAGCTTATGATGATGAGAGAGAGAGAGAGAGAGAG	3648
Qy	3541	CAGAGCTTATCTATGACAAACCTACGCTGGCGGAGCGCTGGCTTATTTGCTTCTTC	3600
Db	3649	CAGAGCTTATCTATGACAAACCTACGCTGGCGGAGCGCTGGCTTATTTGCTTCTTC	3708
Qy	3601	AAAGAAATGGCTTATTTCTGAGACTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAG	3660
Db	3709	AAAGAAATGGCTTATTTCTGAGACTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAG	3768

DE Human gene expression profile polynucleotide SEQ ID NO 193.
 XX
 XX Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
 KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
 KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
 KW gene expression; gene; ss.
 XX
 OS Homo sapiens.
 PN WO200274979-A2.
 XX
 XX 26-SEP-2002.
 PD
 XX 20-MAR-2002; 2002MO-US008456.
 PF
 XX 20-MAR-2001; 2001US-0276947P.
 FR
 XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 PA
 XX
 XX Wan J, Wang Y;
 PI
 XX WPI; 2002-740862/80.
 DR
 XX
 XX New gene expression profile generated from primary, endothelial,
 PT epithelial, and muscle cell types, useful for identifying disease
 PT pathologies involving alterations of gene expression, e.g. cancer.
 XX
 PS Claim 5; Page 401-403; 850pp; English.
 XX
 XX The invention relates to a gene expression profile comprising one or more
 CC genes (ABZ24889-ABZ35632) and generated from a cell type. The cell type
 CC is a coronary artery endothelium, umbilical artery or vein endothelium,
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
 CC endothelium, myometrium microvascular endothelium, keratinocyte
 CC epithelium, bronchial epithelium, mammary epithelium, prostate
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
 CC small airway epithelium, renal epithelium, umbilical artery smooth
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
 CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
 CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
 CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast.
 CC osteoblasts or prostate stromal cell. The gene expression profile is used
 CC for determining the level of RNA expression for a sample, determining the
 CC phenotype of a cell and distinguishing cell types. The gene or a protein
 CC expression profile is useful in identifying disease pathologies involving
 CC alterations of gene expression. The assessment of expression profiles may
 CC provide meaningful information with respect to tumour type and stage,
 CC treatment methods, and prognosis. The gene or protein expression profile
 CC may also be used for creating microarrays. The microarray is useful for
 CC genetic and physical mapping of genomes, DNA sequencing, genetic or
 CC medical diagnosis, genotyping of organisms, confirming cell or tissue
 CC identifications and in identifying promising antibiotics, antiviral or
 CC antifungal agents
 CC
 SQ Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;
 Query Match 97.9%; Score 5576.6; DB 6; Length 5784;
 Best Local Similarity 99.4%; Pred. No. 0; Mismatches 24; Indels 10; Gaps 5;
 Matches 5651; Conservative 0;

DB 289 AAGCTGGTACACAGGACAAAGACAGACCTTGACCTTTGATGACCAATCAACC 348
 QY 241 GCAAGACATTTGGCGCCCAAGACATTTCCGGGGCCCGACCCCGCGCTGCGCTTACCGT 300
 DB 349 GCAGACATTTGGCGCCCAAGACATTTCCGGGGCCCGACCCCGCGCTTACCGT 408
 QY 301 TCGTGGCTTTGATCTACATCCACCGGTGAAGACAGATGACTCAGCAAGATCACCMAA 360
 DB 409 TCGTGGCTTTGATCTACATCCACCGGTGAAGACAGATGACTCAGCAAGATCACCMAA 468
 QY 361 TCATGGCGAGAAAGAGAGGCTTCTTCTCAGCGCCACAGCTCAAGCAGAGCGCAAGTCCA 420
 DB 469 TCATGGCGAGAAAGAGAGGCTTCTTCTCAGCGCCACAGCTCAAGCAGAGCGCAAGTCCA 528
 QY 421 GGGGACGCTGTTGGCTCTGAGAGGGCCCGGCTCTCCAGAGGCGAGTTCCAGATCTCT 480
 DB 529 GGGGACGCTGTTGGCTCTGAGAGGGCCCGGCTCTCCAGAGGCGAGTTCCAGATCTCT 588
 QY 481 CCAACGCGCCCGCGGACACGCTGATCTCAGCTCAGATGAGGACCCGGCATGTGG 540
 DB 589 CCAACGCGCCCGCGGACACGCTGATCTCAGCTCAGATGAGGACCCGGCATGTGG 648
 QY 541 TCTCCCTGAGAGACGTGGGCTGCTGACTGCACTGAGAGAAACCTCACCTGCAAGTGG 600
 DB 649 TCTCCCTGAGAGACGTGGGCTGCTGACTGCACTGAGAGAAACCTCACCTGCAAGTGG 708
 QY 601 CTGGGAGACCTTACAGCTTGCACGTGGGGCTGGAGCCTCATAGACGCTTGGCTGGAGC 660
 DB 709 CTGGGAGACCTTACAGCTTGCACGTGGGGCTGGAGCCTCATAGACGCTTGGCTGGAGC 768
 QY 661 AGCCCTTCTACAGACCTGACAGCGCGAAAGACCGGATGATGCTGGCCAAAGCTCTG 720
 DB 769 AGCCCTTCTACAGACCTGACAGCGCGAAAGACCGGATGATGCTGGCCAAAGCTCTG 828
 QY 721 CCGAGAGAGTCACTTCAAGGGTTGGCTTCAAGAGTCCACCTAGCTTGAAGAACTCTG 780
 DB 829 CCGAGAGAGTCACTTCAAGGGTTGGCTTCAAGAGTCCACCTAGCTTGAAGAACTCTG 888
 QY 781 TGGAGATATTCTTAACCAAGAGGTTGGCAGCAAGCGGAGGCTGAGATCAAGCCCA 840
 DB 889 TGGAGATATTCTTAACCAAGAGGTTGGCAGCAAGCGGAGGCTGAGATCAAGCCCA 948
 QY 841 TCGTGAAGAACACAGAGAGCTGCGCTGGTCCGATTCACACCGAGTACGTGGGCG 900
 DB 949 TCGTGAAGAACACAGAGAGCTGCGCTGGTCCGATTCACACCGAGTACGTGGGCG 1008
 QY 901 CCAAGCTCAGAGAGAGGCGCCGAGGTTGCGAAGCTCTGCGAGAGAGCTGGGAAACATGG 960
 DB 1009 CCAAGCTCAGAGAGAGGCGCCGAGGTTGCGAAGCTCTGCGAGAGAGCTGGGAAACATGG 1068
 QY 961 TCCAGAGAGCTCTGGGGGCTTCCAGCTCTGTGAACCAAGTCAAGCGAAGCTCAAGAGG 1020
 DB 1069 TCCAGAGAGCTCTGGGGGCTTCCAGCTCTGTGAACCAAGTCAAGCGAAGCTCAAGAGG 1128
 QY 1021 TGTGAGATGATAACAGATTTCTCTGGAGACTATGTGGCCCTCTTAAGACAGAGACA 1080
 DB 1129 TGTGAGATGATAACAGATTTCTCTGGAGACTATGTGGCCCTCTTAAGACAGAGACA 1188
 QY 1081 TGTGAGCTTGTGGCAGAGATGGCGGCTTTCTTGGCGAAATGAACAGTGGGTGGAGACA 1140
 DB 1189 TGTGAGCTTGTGGCAGAGATGGCGGCTTTCTTGGCGAAATGAACAGTGGGTGGAGACA 1248
 QY 1141 GCTGACACAGGTGATCTGCAAGAAATTTAAACATTTGCCACCAATCACTGCGCGC 1200
 DB 1249 GCTGACACAGGTGATCTGCAAGAAATTTAAACATTTGCCACCAATCACTGCGCGC 1308
 QY 1201 CTGCAACCTGCGCAAGTCCATCTTTGTGGAAGGCGAATGCTGCTTCTGCTTCACAT 1260
 DB 1309 CTGCAACCTGCGCAAGTCCATCTTTGTGGAAGGCGAATGCTGCTTCTGCTTCACAT 1368
 QY 1261 CGGTGAGCGGTGAGAGGCGTGGTCTCCGTGGGCAAGTGAACCAAGTCTCCGTGACGT 1320

Db 1369 CGGTGGACGGTGGAGGGCTGCTCCGTGGGACAGAGTGAGCCAGCTGCTCCGTGACGT 1428
 Qy 1321 GTGGCTCTGGACCCAGAGAGAGCGCGTCTCTGTGAGCTCACAGCAACAACCTGCTTGG 1380
 Db 1429 GTGGCTCTGGACCCAGAGAGAGCGCGTCTCTGTGAGCTCACAGCAACAACCTGCTTGG 1488
 Qy 1381 GGCCCTCCATCCAGACACGGGCTTGGAGTCTGAGCAAGTGTGACACCGCATCCGGCAGG 1440
 Db 1489 GGCCCTCGATCCAGACACGGGCTTGGAGTCTGAGCAAGTGTGACACCGCATCCGGCAGG 1548
 Qy 1441 ACGGGGCTGGAGGCACTGGTCAACCTTGGTCTTATGCTCTGTGACCTGTGGAGTTGGCA 1500
 Db 1549 ACGGGGCTGGAGGCACTGGTCAACCTTGGTCTTATGCTCTGTGACCTGTGGAGTTGGCA 1508
 Qy 1501 ATATCACACGATCCGTCTCTGCAAACTCCCAAGTCCCAAGATGGGGGGCAAGATTGCA 1560
 Db 1609 ATATCACACGATCCGTCTCTGCAAACTCCCAAGTCCCAAGATGGGGGGCAAGATTGCA 1668
 Qy 1561 AAGGAGTGGCGGGAGACCAAAAGCTGCCAGGCGGCCCATCGATGGCGCGCT 1620
 Db 1669 AAGGAGTGGCGGGAGACCAAAAGCTGCCAGGCGGCCCATCGATGGCGCGCT 1728
 Qy 1621 GGAGCCCTGTCCCGTGTGGCTGCACTGTGCACTGTGCGGCTGGGATCCGGGAGC 1680
 Db 1729 GGAGCCCTGTCCCGTGTGGCTGCACTGTGCACTGTGCGGCTGGGATCCGGGAGC 1788
 Qy 1681 GCACCCGGGTCTGCAACACGCGCTGAGCCTCAGTACGGAGGGAAGGCTGCGTGGGGGATG 1740
 Db 1789 GCACCCGGGTCTGCAACACGCGCTGAGCCTCAGTACGGAGGGAAGGCTGCGTGGGGGATG 1848
 Qy 1741 TGCAGGAGCTGAGATGCAACAGAGGAGCTCCCGTGGATGGCTGTTATCCAAAC 1800
 Db 1849 TGCAGGAGCTGAGATGCAACAGAGGAGCTCCCGTGGATGGCTGTTATCCAAAC 1908
 Qy 1801 CCTGCTTCCCGGAGCCAGTGTGACAGAGCTTCCCGGATGGGCTGCTGATGGGGCTCCT 1860
 Db 1909 CCTGCTTCCCGGAGCCAGTGTGACAGAGCTTCCCGGATGGGCTGCTGATGGGGCTCCT 1968
 Qy 1861 GCCCTGGGGCTCTTGGGGAATGGCAACCACTGTGAGGAGCTCCCGTGGATGGCTGCTGG 1920
 Db 1969 GCCCTGGGGCTCTTGGGGAATGGCAACCACTGTGAGGAGCTCCCGTGGATGGCTGCTGG 2028
 Qy 1921 TCCCGGACATCTGCTTCTCCACAGCAAGTGTGCTGCTGCTCAACACTCAGCTGGCT 1980
 Db 2029 TCCCGGACATCTGCTTCTCCACAGCAAGTGTGCTGCTGCTCAACACTCAGCTGGCT 2088
 Qy 1981 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
 Db 2089 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2148
 Qy 2041 AAGCAGCCAGACGGAAGCAAGTGTGAGCCGCAAAACCCATGCAAGGCAAGACAC 2100
 Db 2149 AAGCAGCCAGACGGAAGCAAGTGTGAGCCGCAAAACCCATGCAAGGCAAGACAC 2208
 Qy 2101 ACAACTGCCAACGACGCGAGTGCATCTACCTGGGCCACTTCAGCGACCCCATGTACA 2160
 Db 2209 ACAACTGCCAACGACGCGAGTGCATCTACCTGGGGTCACTTCAGCGACCCCATGTACA 2268
 Qy 2161 AGTGGAGTGCACAGAGCTTACCGGGGACGCGGCTCATCTGGGGAGGACTCCGAGC 2220
 Db 2269 AGTGGAGTGCACAGAGCTTACCGGGGACGCGGCTCATCTGGGGAGGACTCCGAGC 2328
 Qy 2221 TGGAGGCTGGGCCCAACCTCAATCTGTCTGCGCCACCAACCGCCACTACCTGCTATCA 2280
 Db 2329 TGGAGGCTGGGCCCAACCTCAATCTGTCTGCGCCACCAACCGCCACTACCTGCTATCA 2388
 Qy 2281 AGGATACTGCCCATCTGCCAAATCTGGGAGGAGACTTGTGACAGGAGGGATTG 2340
 Db 2389 AGGATACTGCCCATCTGCCAAATCTGGGAGGAGACTTGTGACAGGAGGGATTG 2448
 Qy 2341 CGGATGCTGTGATGATGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 2400
 Db 2449 CGGATGCTGTGATGATGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 2508

Qy 2401 AGTCTCTTCTCAATCCCGCCAGGCTGACTATGACAAGATGAGTTGGGACCCCTGTG 2460
 Db 2509 AGTCTCTTCTCAATCCCGCCAGGCTGACTATGACAAGATGAGTTGGGACCCCTGTG 2568
 Qy 2461 ACAACTGCCCTTACGTGCAACAACCTGCCAGATCGACACAGCAACAATGAGAGGGTG 2520
 Db 2569 ACAACTGCCCTTACGTGCAACAACCTGCCAGATCGACACAGCAACAATGAGAGGGTG 2628
 Qy 2521 AGCTGCTCTCCGTGGACATGATGGGACGATGCTTCAATGAACGAGACAATTTGCTCT 2580
 Db 2629 AGCTGCTCTCCGTGGACATGATGGGACGATGCTTCAATGAACGAGACAATTTGCTCT 2688
 Qy 2581 AGCTTACAACTACACAGAGGACACGAGTGTGACGCTGGGGATCACTGTGACA 2640
 Db 2689 AGCTTACAACTACACAGAGGACACGAGTGTGACGCTGGGGATCACTGTGACA 2748
 Qy 2641 ACTGCCCTCTGTGCAACAACCTGACCAAGACGAGTGTGACCAATGACCTTGTGGGACC 2700
 Db 2749 ACTGCCCTCTGTGCAACAACCTGACCAAGACGAGTGTGACCAATGACCTTGTGGGACC 2808
 Qy 2701 AGTGTGACAAACAGAGGACATAGATGACGAGGACCAAGCAACAACAGGACAACCTGCC 2760
 Db 2809 AGTGTGACAAACAGAGGACATAGATGACGAGGACCAAGCAACAACAGGACAACCTGCC 2868
 Qy 2761 CCTACATCTCCAACCCAAACAGGCTGACCAATGACAGAGAGCGGCGAGCGCTGTG 2820
 Db 2869 CCTACATCTCCAACCCAAACAGGCTGACCAATGACAGAGAGCGGCGAGCGCTGTG 2928
 Qy 2821 ACCCTGATGATGACACAGTGCCTGCCGATGACAGGACCACTGCCGCTGTGTTCA 2880
 Db 2929 ACCCTGATGATGACACAGTGCCTGCCGATGACAGGACCACTGCCGCTGTGTTCA 2988
 Qy 2881 ACCCAGACAGGAGGACTTGGACGCTGATGACGCGGTGATATTTGTAAGATGATTTG 2940
 Db 2989 ACCCAGACAGGAGGACTTGGACGCTGATGACGCGGTGATATTTGTAAGATGATTTG 3048
 Qy 2941 ACATGACAACTCCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
 Db 3049 ACATGACAACTCCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3108
 Qy 3001 CAGACTTCAGAACTTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
 Db 3109 CAGACTTCAGAACTTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3168
 Qy 3061 CCAACTGGGTCTATTCGCAATCAGGCAAGGAGTGGTTTCAGACAGCAACTCGGACCCCG 3120
 Db 3169 CCAACTGGGTCTATTCGCAATCAGGCAAGGAGTGGTTTCAGACAGCAACTCGGACCCCG 3228
 Qy 3121 GCATGCTGTAGTTTTCAGAGTTTGGTCTGTGAGCTTCAGTGGCACATTTACGTAA 3180
 Db 3229 GCATGCTGTAGTTTTCAGAGTTTGGTCTGTGAGCTTCAGTGGCACATTTACGTAA 3288
 Qy 3181 ACATGACCGGAGCAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
 Db 3289 ACATGACCGGAGCAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3348
 Qy 3241 TCTATGCTGATGATGAGAGCAGGATGACGAGACTTCTGGGAGGACCCAGCCACGCGGG 3300
 Db 3349 TCTATGCTGATGATGAGAGCAGGATGACGAGACTTCTGGGAGGACCCAGCCACGCGGG 3408
 Qy 3301 CCTATGGCTACTCCGGCTGTCCCTCAAGTGTGAACTCCACACAGGAGGAGCGGCGGAGC 3360
 Db 3409 CCTATGGCTACTCCGGCTGTCCCTCAAGTGTGAACTCCACACAGGAGGAGCGGCGGAGC 3468
 Qy 3361 ACCTGAGGAGCGGCTGTGGCAGCAGGAGACCGCGGGGAGGCTGCAACCTTATGGC 3420
 Db 3469 ACCTGAGGAGCGGCTGTGGCAGCAGGAGACCGCGGGGAGGCTGCAACCTTATGGC 3528
 Qy 3421 AGCAGCCAGGAACTTGGCTGGAGGACTACAGGCGCTATAGGTGGCACCTGACTCACA 3480
 Db 3529 AGCAGCCAGGAACTTGGCTGGAGGACTACAGGCGCTATAGGTGGCACCTGACTCACA 3588

QY 3481 GGCCCAAGCTGCTACATCAGAGCTTATGTCATGAAGAAAACAGCTCATGGCAACT 3540
DB 3589 GGCCCAAGCTGCTACATCAGAGCTTATGTCATGAAGAAAACAGCTCATGGCAACT 3648
QY 3541 CAGACCTATCTATGACCAAAACCTACGCTGGCGGGCGGCTGATATTTGCTCTCTC 3600
DB 3649 CAGACCTATCTATGACCAAAACCTACGCTGGCGGGCGGCTGATATTTGCTCTCTC 3708
QY 3601 AAGAAATGCTATTTCTGACACTGCAAGTACGAATGCAAGATTTTAAACAAGATTG 3660
DB 3709 AAGAAATGCTATTTCTGACACTGCAAGTACGAATGCAAGATTTTAAACAAGATTG 3768
QY 3661 CTGCATTTCCGGCAATGGCCTGTGCAATGCAATGCTTACAGACCTCAGTTCAATG 3720
DB 3769 CTGCATTTCCGGCAATGGCCTGTGCAATGCAATGCTTACAGACCTCAGTTCAATG 3828
QY 3721 TCTTTGAGCTTCTCTCTCTGACAGCACTCTCTGCTCTTACCTTAACTCTGATG 3780
DB 3829 TCTTTGAGCTTCTCTCTCTGACAGCACTCTCTGCTCTTACCTTAACTCTGATG 3888
QY 3781 TTCACTCTCTGACAGCACTCTCTGACAGCACTCTCTGCTCTTACCTTAACTCTGATG 3840
DB 3889 TTCACTCTCTGACAGCACTCTCTGACAGCACTCTCTGCTCTTACCTTAACTCTGATG 3948
QY 3841 GCAGAGATGAACATCTAAACCACTAGAGAAAACAATTGCTGATATATGAGACTTATG 3900
DB 3949 TCAGAGATGAACATCTAAACCACTAGAGAAAACAATTGCTGATATATGAGACTTATG 4008
QY 3901 TGGAGTGAATTTGGGCAATGGCCTATACATGCTTTTCTGTTGTTTAAACAAGATGAC 3960
DB 4009 TGGAGTGAATTTGGGCAATGGCCTATACATGCTTTTCTGTTGTTTAAACAAGATGAC 4068
QY 3961 GTTTACATATAAATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4020
DB 4069 GTTTACATATAAATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4128
QY 4021 CTGTGATTAAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4080
DB 4129 CTGTGATTAAGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4188
QY 4081 CTTAAGTTGCTACTATTTCTGAAATTAAGTTGCTCTCAATGACACAAATCCGCTA 4140
DB 4189 CTTAAGTTGCTACTATTTCTGAAATTAAGTTGCTCTCAATGACACAAATCCGCTA 4248
QY 4141 AATAAATTAACAAGGCTCAATCAATTTGAAGTATGTTTAAAGAAAGATTA 4200
DB 4249 AATAAATTAACAAGGCTCAATCAATTTGAAGTATGTTTAAAGAAAGATTA 4308
QY 4201 GAAGCAACAGGCTAGCAATGATAGCTACCGATTAACTAATCGGAACATGTAAA 4260
DB 4309 GAAGCAACAGGCTAGCAATGATAGCTACCGATTAACTAATCGGAACATGTAAA 4368
QY 4261 CAGTTACAAAATTAACGAACTCTCTCTGCTCTCAATGAAGACCTCTCATGTGAGTA 4320
DB 4369 CAGTTACAAAATTAACGAACTCTCTCTGCTCTCAATGAAGACCTCTCATGTGAGTA 4428
QY 4321 GAGATGAGTTTCATCAAAAGAACAAATCCTTGCAAAATGGGTGATGCGGTTCCAGAT 4380
DB 4429 GAGATGAGTTTCATCAAAAGAACAAATCCTTGCAAAATGGGTGATGCGGTTCCAGAT 4488
QY 4381 GTGATTTGGCAAAACCTCATTTAATTAAGTAAAGTTAGCAAGCAAAAGTGGCTGTTAG 4440
DB 4489 GTGATTTGGCAAAACCTCATTTAATTAAGTAAAGTTAGCAAGCAAAAGTGGCTGTTAG 4548
QY 4441 CTGTGCTGTTGCGCGGTGATGCTGCGGGAAGGCTCTGCTGAGCTTCTTCCCAAGTT 4500
DB 4549 CTGTGCTGTTGCGCGGTGATGCTGCGGGAAGGCTCTGCTGAGCTTCTTCCCAAGTT 4608
QY 4501 TGTGCTGAGAGAAACCAAGACAGCAAGGCTGGAAGGCGCATCTAAGCGTAT 4560
DB 4609 TGTGCTGAGAGAAACCAAGACAGCAAGGCTGGAAGGCGCATCTAAGCGTAT 4668
QY 4561 CTAGGCTTTGGTAACAGGAGCAAGTGGTTTACCTGATTTGATGATACATTTCAATA 4620

DB 4669 CTAGGCTTTGGTAACAGGAGCAAGTGGTTTACCTGATTTGATGATACATTTCAATA 4728
QY 4621 GGTTCCAGTTAATAATTTGTTAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 4680
DB 4729 GGTTCCAGTTAATAATTTGTTAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 4788
QY 4681 TACAGTAACTAATTTAATAATTTGCTAGTAAACATATATGATATTAATTTCTAATAACA 4740
DB 4789 TACAGTAACTAATTTAATAATTTGCTAGTAAACATATATGATATTAATTTCTAATAACA 4848
QY 4741 AACATTAATTAATTAATTAATTTGCTAGTAAACATATGATATTAATTTGATGTTGAC 4800
DB 4849 AACATTAATTAATTAATTAATTTGCTAGTAAACATATGATATTAATTTGATGTTGAC 4908
QY 4801 GATGAAGCATGCTAGAGCTGTAAACGAATATATGAGATTAATGAGATTTATGATAG 4860
DB 4909 GATGAAGCATGCTAGAGCTGTAAACGAATATATGAGATTAATGAGATTTATGATAG 4968
QY 4861 AACCTTAATTAATTAATTTGCTAGTAAACATATGATATTAATTTGATGTTGAC 4920
DB 4969 AACCTTAAATTAATTAATTTGCTAGTAAACATATGATATTAATTTGATGTTGAC 5027
QY 4921 TGTGTTATATGGAATTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4979
DB 5028 TGTGTTATATGGAATTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5087
QY 4980 AGGCAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5039
DB 5088 AGGCAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5147
QY 5040 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5099
DB 5148 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5203
QY 5100 CTGATCCGCTCAACATTAAGGCTTAAAGAAAGTGTCTGCTGATGATGATGATG 5159
DB 5204 CTGATCCGCTCAACATTAAGGCTTAAAGAAAGTGTCTGCTGATGATGATGATG 5263
QY 5160 GGGGCAATCTTTTCCCTTTCTGTAATGATCAATCAATTCATGCGCAACAGAAC 5219
DB 5264 GGGGCAATCTTTTCCCTTTCTGTAATGATCAATCAATTCATGCGCAACAGAAC 5323
QY 5220 AATCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5279
DB 5324 GATCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5383
QY 5280 CTTTGAAGTTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5339
DB 5384 CTTTGAAGTTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5440
QY 5340 GCTGTATCCGAGAACCAAGGCTGGGATCTTCAATTAATTAATTAATTAATTAATTA 5399
DB 5441 GCTGTATCCGAGAACCAAGGCTGGGATCTTCAATTAATTAATTAATTAATTAATTA 5499
QY 5400 AGCGTCAGATTTCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5459
DB 5500 AGCGTCAGATTTCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5559
QY 5460 GATGATGTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5519
DB 5560 GATGATGTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5619
QY 5520 AATTTATGTAATGTTGATGAAGAGTATGTTTGCAGAAAGCTGTAAATTAAT 5579
DB 5620 AATTTATGTAATGTTGATGAAGAGTATGTTTGCAGAAAGCTGTAAATTAAT 5679
QY 5580 TTAATGTTCAATGTTCAAAATTTGACCAATGAAACCTGCACTTAAGTAAACCTCAT 5639
DB 5680 TTAATGTTCAATGTTCAAAATTTGACCAATGAAACCTGCACTTAAGTAAACCTCAT 5739
QY 5640 TTTTAAAGATTAACAAGAAATTAATTTGTAATAAAGTTTCT 5694

QY 1201 CTGCAACCTGCGCAGTCCATCTTTGTGGAAGGCGAATGCTGCCCTTCTGCTCCACT 1260
DB 1309 CTGCAACCTGCGCAGTCCATCTTTGTGGAAGGCGAATGCTGCCCTTCTGCTCCACT 1368
QY 1261 CGGTGGAAGGTGAGGAGGCTGTCCTCGTGGGAGAGTGAAGCCAGTGCCTCGTGAAGT 1320
DB 1369 CGGTGGAAGGTGAGGAGGCTGTCCTCGTGGGAGAGTGAAGCCAGTGCCTCGTGAAGT 1428
QY 1321 GTGCTCTGGAGCCAGAGAGAGGCGGCTCTGTGAAGTCAAGCAGAGCAACTGCTTGG 1380
DB 1429 GTGCTCTGGAGCCAGAGAGAGGCGGCTCTGTGAAGTCAAGCAGAGCAACTGCTTGG 1488
QY 1381 GGCCTCATCCAGACAGGGCTTGCATCTGACCAAGTGAAGACCCGATCCGGAGG 1440
DB 1489 GGCCTCATCCAGACAGGGCTTGCATCTGACCAAGTGAAGACCCGATCCGGAGG 1548
QY 1441 ACGGCGCTGAGCCACTGTCACCTTGTCTTCACTGTCTGTGACCTGTGAGATTGGA 1500
DB 1549 ACGGCGCTGAGCCACTGTCACCTTGTCTTCACTGTCTGTGACCTGTGAGATTGGA 1608
QY 1501 ATATCAACGCATCCGCTCTGTGCAACTCCCAAGTCCCAAGTGGGGGCAAGATTGA 1560
DB 1609 ATATCAACGCATCCGCTCTGTGCAACTCCCAAGTCCCAAGTGGGGGCAAGATTGA 1668
QY 1561 AAGGAGTGGCCGGAGACCAAGGCTGCAAGGCGGCCCAATGCCAATCGATGGCCGT 1620
DB 1669 AAGGAGTGGCCGGAGACCAAGGCTGCAAGGCGGCCCAATGCCAATCGATGGCCGT 1728
QY 1621 GAGGCCCTGTCCTCCGTCGTGTCGCTGTCATCTGTGCGGTGGATCCGGGAGC 1680
DB 1729 GAGGCCCTGTCCTCCGTCGTGTCGCTGTCATCTGTGCGGTGGATCCGGGAGC 1788
QY 1681 GCACCCGGGATCTGCAACAGCCCTGAGCTCAGTACGAGAGGAGGCGCTCGTGGGAGT 1740
DB 1789 GCACCCGGGATCTGCAACAGCCCTGAGCTCAGTACGAGAGGAGGCGCTCGTGGGAGT 1848
QY 1741 TGCAGAGCGTCAGATGTGCAACAGAGAGCTGCCCGTGAATGGCTGTTATCCAAAC 1800
DB 1849 TGCAGAGCGTCAGATGTGCAACAGAGAGCTGCCCGTGAATGGCTGTTATCCAAAC 1908
QY 1801 CCGTCTCCGGGAGCCAGTGCAGACGCTCCCGGATGGGTCCTGCTGATGGGCGCT 1860
DB 1909 CCGTCTCCGGGAGCCAGTGCAGACGCTCCCGGATGGGTCCTGCTGATGGGCGCT 1968
QY 1861 GCCCTGTGGGCTTCTTGGCAATGSCACCACTGTGAGACCTTGACGAGTGTGCTG 1920
DB 1969 GCCCTGTGGGCTTCTTGGCAATGSCACCACTGTGAGACCTTGACGAGTGTGCTG 2028
QY 1921 TCCCGAGCATCTGCTTTCACAGAGTGCCTGCTGTGTAACCTGAGGCTGAGCT 1980
DB 2029 TCCCGAGCATCTGCTTTCACAGAGTGCCTGCTGTGTAACCTGAGGCTGAGCT 2088
QY 1981 TCCAGTGCCTGCTGCTCCGCGCCGATACAGAGGAGCCAGCCGCTCGGGTTCGCTG 2040
DB 2089 TCCAGTGCCTGCTGCTCCGCGCCGATACAGAGGAGCCAGCCGCTCGGGTTCGCTG 2148
QY 2041 AAGCAGCCCAAGACGAGAAAGCAAGTGTGAGCCCGGAAACCCATGACAGAGAC 2100
DB 2149 AAGCAGCCCAAGACGAGAAAGCAAGTGTGAGCCCGGAAACCCATGACAGAGAC 2208
QY 2101 ACAACTGACCAAGACGCGAGTGCATCTGAGGCACTTTCAGCAGCCCACTGTGA 2160
DB 2209 ACAACTGACCAAGACGCGAGTGCATCTGAGGCACTTTCAGCAGCCCACTGTGA 2268
QY 2161 AGTGGAGTGCAGACAGGCTACGGGGGAGACGGGCTCATCTGCGGGAGAGACTTCGAC 2220
DB 2269 AGTGGAGTGCAGACAGGCTACGGGGGAGACGGGCTCATCTGCGGGAGAGACTTCGAC 2328
QY 2221 TGGAGGCTGCGCCAACTCAATCTGTCTGCGCCACCAAGCAGCACTACCACTGATCA 2280
DB 2329 TGGAGGCTGCGCCAACTCAATCTGTCTGCGCCACCAAGCAGCACTACCACTGATCA 2388
QY 2281 AGGATTAAGTCCCCCACTGCGCAATTTCTGGGAGAGAAAGCTTTGACAAAGAGCGGATTG 2340

DB 2389 AGGATTAAGTCCCCCACTGCGCAATTTCTGGGAGAGAAAGCTTTGACAAAGAGCGGATTG 2448
QY 2341 GCGATGCCCTGATGATGACATGACATGACAGGTGTGACCGATGAGAGACAACTGCC 2400
DB 2449 GCGATGCCCTGATGATGACATGACATGACAGGTGTGACCGATGAGAGACAACTGCC 2508
QY 2401 AGCTCTCTTCAATCCCGCAGAGCTGATGACAGAGATGAGTGGGGACCGCTGTG 2460
DB 2509 AGCTCTCTTCAATCCCGCAGAGCTGATGACAGAGATGAGTGGGGACCGCTGTG 2568
QY 2461 ACAAGTGCCTTACAGTGAACAACCTGCGCCGATGACAGACAAACAATGAGAGGTTG 2520
DB 2569 ACAAGTGCCTTACAGTGAACAACCTGCGCCGATGACAGACAAACAATGAGAGGTTG 2628
QY 2521 ACGGCTGCTCGGTGACATGATGGGAGAGATGCTTCAATGAACAGACAAATGCTCCT 2580
DB 2629 ACGGCTGCTCGGTGACATGATGGGAGAGATGCTTCAATGAACAGACAAATGCTCCT 2688
QY 2581 AGGTCTAACAACAGAGAGAGGAGACAGGATGATGAGGCTGGGGATCACTGTGA 2640
DB 2689 AGGTCTAACAACAGAGAGAGGAGACAGGATGATGAGGCTGGGGATCACTGTGA 2748
QY 2641 ACTGCCCTGCTGACAAACCTGACAGACCGAGTGAACATGACCTTGTGGGAGC 2700
DB 2749 ACTGCCCTGCTGACAAACCTGACAGACCGAGTGAACATGACCTTGTGGGAGC 2808
QY 2701 AGTGTGAACAACAAGAGACATGATGAGAGCGGACCAAGAACAAAGAGCAACTGCC 2760
DB 2809 AGTGTGAACAACAAGAGACATGATGAGAGCGGACCAAGAACAAAGAGCAACTGCC 2868
QY 2761 CTTACATCTCAACCCCAACAGGCTGACATGACAGAGACGCGCCAGGCGACGCTGTG 2820
DB 2869 CTTACATCTCAACCCCAACAGGCTGACATGACAGAGACGCGCCAGGCGACGCTGTG 2928
QY 2821 ACCCTGATGATGAACAAGATGAGCTCCCGATGACAGAGACAACTGCGGCTGTGTCA 2880
DB 2929 ACCCTGATGATGAACAAGATGAGCTCCCGATGACAGAGACAACTGCGGCTGTGTCA 2988
QY 2881 ACCAGACAGAGAGACTTGAAGGATGAGACGCGGATGATGATTTGTAAAGATGATTTG 2940
DB 2989 ACCAGACAGAGAGACTTGAAGGATGAGACGCGGATGATGATTTGTAAAGATGATTTG 3048
QY 2941 ACAATGACAACTCCAGATGATGATGTGTCTGAAACAAATGCTCATGATGAG 3000
DB 3049 ACAATGACAACTCCAGATGATGATGTGTCTGAAACAAATGCTCATGATGAG 3108
QY 3001 CAGACTTGAAGAACTTCCAGATGATGCTCCCTGATGCCAAAGGAGCAACCAATTGATC 3060
DB 3109 CAGACTTGAAGAACTTCCAGATGATGCTCCCTGATGCCAAAGGAGCAACCAATTGATC 3168
QY 3061 CCAACTGGGCTATTGGCATGAGAGAGAGAGCTGATGACAGACCACTTGACCCCG 3120
DB 3169 CCAACTGGGCTATTGGCATGAGAGAGAGAGCTGATGACAGACCACTTGACCCCG 3228
QY 3121 GCATGCTGAGGTTTGAAGATTTGGTGTGAGACTTCACTGAGGCACTTCACTGA 3180
DB 3229 GCATGCTGAGGTTTGAAGATTTGGTGTGAGACTTCACTGAGGCACTTCACTGA 3288
QY 3181 ACACTGACCGGAGAGAGAGCTATGCGGCTTGTCTTTGTGTTACAGTCAAGACCGCT 3240
DB 3289 ACACTGACCGGAGAGAGAGCTATGCGGCTTGTCTTTGTGTTACAGTCAAGACCGCT 3348
QY 3241 TCTATGATGATGATGAGAGAGGATGAGAGCAACCTGAGGAGAGCAAGCGCGG 3300
DB 3349 TCTATGATGATGATGAGAGAGGATGAGAGCAACCTGAGGAGAGCAAGCGCGG 3408
QY 3301 CTTATGACTACTCCGCGCTGTCTTCAAGTGTGAACTCAACAAGGAGAGCGGCGAGC 3360
DB 3409 CTTATGACTACTCCGCGCTGTCTTCAAGTGTGAACTCAACAAGGAGAGCGGCGAGC 3468
QY 3361 ACCTGAGGAACGCGCTGTGAGCAAGCGGAGAAACAGCGCGGAGAGGCTGCACTTATGCG 3420

QY 5580 TTATGTTTCACATGTCATAAATTTCACCACTGAAACCTGACTAGCTAGAACCTCAT 5639
DB 5680 TTATGTTTCACATGTCATAAATTTCACCACTGAAACCTGACTAGCTAGAACCTCAT 5739
QY 5640 TTTTAAAGATTAAACAAGAAATTAATTGTAAAGTTTCT 5684
DB 5740 TTTTAAAGATTAAACAAGAAATTAATTGTAAAGTTTCT 5784

RESULT 5
ABN95662
ID ABN95662 standard; DNA; 5784 BP.
ABN95662;
13-AUG-2002 (first entry)

DE Gene #2160 used to diagnose liver cancer.
XX Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
XX metastatic liver tumour; cytostatic; expression profile; disease state;
XX disease progression; drug toxicity; drug efficacy; drug metabolism.
OS Homo sapiens.
FN WO200229103-A2.
PD 11-APR-2002.
XX 02-OCT-2001; 2001WO-US030589.
PF 02-OCT-2000; 2000US-0237054P.
PR 02-OCT-2000; 2000US-0237054P.
XX (GENE-) GENE LOGIC INC.
PA Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
PI WPI; 2002-426119/45.
DR

PT Diagnosing and detecting the progression of liver cancer; hepatocellular
PT carcinoma or metastatic liver tumor in a patient, involves detecting the
PT level of expression of two or more genes in a liver tissue sample.
PS Claim 1; SEQ ID NO 2160; 298bp; English.

CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer; hepatocellular carcinoma or metastatic liver
CC tumor in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer; hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

QY Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;
SQ

Query Match 97.9%; Score 5576.6; DB 6; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

QY 1 GATACGCTGCACTGAGGCGGCTCTCCGCTCCAGCAGAGCCGCCCTTTGCAATC 60
DB 109 GAGCATCTGCACTGAGGCGGCTCTCCGCTCCAGCAGAGCCGCCCTTTGCAATC 168
QY 61 GATCCGGAACACTGAACAGATCATGCACTCTTTTGGCAACAGAGAGCTGAGCTG 120

DB 169 GGTCCGGAACACTGAACACGATCATGCACTCTTTTGGCAACAGAGAGCTGAGCTG 228
QY 121 CAGAGAGCAGATGCTCTGAGAGCGTGTCTGCTGCTGAGGCTGTGGCCACAGC 180
DB 229 CAGAGAGCAGATGCTCTGAGAGCGTGTCTGCTGCTGAGGCTGTGGCCACAGC 288
QY 181 AAGCTGTGTCACAGAGCAAGAGACAGACCTTGACCTTTTCAGTATCAGCAATCAAC 240
DB 289 AAGCTGTGTCACAGAGCAAGAGACAGACCTTGACCTTTTCAGTATCAGCAATCAAC 348
QY 241 GCAGAGCAATTTGGCCGCAAGCAGTTCCGCGGCGCCGACCCCGCGCTTACCGCT 300
DB 349 GCAGAGCAATTTGGCCGCAAGCAGTTCCGCGGCGCCGACCCCGCGCTTACCGCT 408
QY 301 TCGTGGCTTTGACTACATCCACGCGTGAACGAGATGACCTCAGCAAGATCACCAAG 360
DB 409 TCGTGGCTTTGACTACATCCACGCGTGAACGAGATGACCTCAGCAAGATCACCAAG 468
QY 361 TCATGCGGCAAGAGAGGCTTTCTCTCAGCGCCCAAGTCAAGCAGAGCGCAAGTCA 420
DB 469 TCATGCGGCAAGAGAGGCTTTCTCTCAGCGCCCAAGTCAAGCAGAGCGCAAGTCA 528
QY 421 GGGGACAGCTGTGGCTCTGAGAGGCGCGGTCTCTCCAGAGGAGTTCAGATGCTCT 480
DB 529 GGGGACAGCTGTGGCTCTGAGAGGCGCGGTCTCTCCAGAGGAGTTCAGATGCTCT 588
QY 481 CCAAGCGCCCGCGGACACGCTGATCTCACTGATGTAAGGACCCGCGCATGTGG 540
DB 589 CCAAGCGCCCGCGGACACGCTGATCTCACTGATGTAAGGACCCGCGCATGTGG 648
QY 541 TCTCCCTGAGAGACGTCGCGCTGCTGATCTCAGAGTGAAGAAAGCTCAAGTGTG 600
DB 649 TCTCCCTGAGAGACGTCGCGCTGCTGATCTCAGAGTGAAGAAAGCTCAAGTGTG 708
QY 601 CTGGCGAGACCTACAGCTTTCAGAGTGTGCTGAGCTCATAGACAGCTTCTGAGAGC 660
DB 709 CTGGCGAGACCTACAGCTTTCAGAGTGTGCTGAGCTCATAGACAGCTTCTGAGAGC 768
QY 661 AGCCCTTACAGAGACCTTCAGAGGCGGAAAGGCGGAGTACGTGCGCAAGGCTCTG 720
DB 769 AGCCCTTACAGAGACCTTCAGAGGCGGAAAGGCGGAGTACGTGCGCAAGGCTCTG 828
QY 721 CCAGAGAGATCACTTCAGAGGCTTTCAGAGCTTCACAGCTAGTGTGAAAACCTCTG 780
DB 829 CCAGAGAGATCACTTCAGAGGCTTTCAGAGCTTCACAGCTAGTGTGAAAACCTCTG 888
QY 781 TGAAGATATTTTACCAAGAAAGGCTTTCAGAGGCGGAGGAGGAGTCAACAGCGCA 840
DB 889 TGAAGATATTTTACCAAGAAAGGCTTTCAGAGGCGGAGGAGGAGTCAACAGCGCA 948
QY 841 TCAGTGAAGAACAGAGAGCTGCGCTGCGTCCGATGTCACACCGAGTACGTGGGCT 900
DB 949 TCAGTGAAGAACAGAGAGCTGCGCTGCGTCCGATGTCACACCGAGTACGTGGGCT 1008
QY 901 CCAGCTCAGAGAGAGAGGCGGAGTGTGGAAGCGCTCCGCGGAGAGGCTGGAAACATG 960
DB 1009 CCAGCTCAGAGAGAGAGGCGGAGTGTGGAAGCGCTCCGCGGAGAGGCTGGAAACATG 1068
QY 961 TCAGAGAGCTCTGCGGAGCTTCAGAGTCTCTGTCAGACAGCTCAGAGAACTCAAGAG 1020
DB 1069 TCAGAGAGCTCTGCGGAGCTTCAGAGTCTCTGTCAGACAGCTCAGAGAACTCAAGAG 1128
QY 1021 TGTGAAATGATTAACCAAGTTTCTTGTGGAAGCTCATTTGTGGCCCTCTTAAGACAAGAA 1080
DB 1129 TGTGAAATGATTAACCAAGTTTCTTGTGGAAGCTCATTTGTGGCCCTCTTAAGACAAGAA 1188
QY 1081 TGTGAGCTTCTGCGAGAGATGCGCGGTTCTTTGCGGAAATGAACGTGGGTGTGACA 1140
DB 1189 TGTGAGCTTCTGCGAGAGATGCGCGGTTCTTTGCGGAAATGAACGTGGGTGTGACA 1248
QY 1141 GCTGACACAGTGTACTGCAAGAAATTTAAACATTTTGCACCAATATCACTGCGCCG 1200
DB 1249 GCTGACACAGTGTACTGCAAGAAATTTAAACATTTTGCACCAATATCACTGCGCCG 1308

1201 CTGCAACCTGCGCCAGTCCATCCCTTTGTGGAAGCGGAATGCTGCCCCCTTCTCCTGCCCTCACT 1260
1309 CTGCAACCTGCGCCAGTCCATCCCTTTGTGGAAGCGGAATGCTGCCCTTCTCCTGCCCTCACT 1368
1261 CGGTGACGGTGAAGGAGGCTGCTCTCCGTGGGCAAGTGGACCCAGTGTCTCCGTGACGT 1320
1369 CGGTGACGGTGAAGGAGGCTGCTCTCCGTGGGCAAGTGGACCCAGTGTCTCCGTGACGT 1428
1321 GTGGCTGTGGGACCCAGCAGAGAGGCGGCTCTGTGACGTACACAGCAACACCTGCTTGG 1380
1429 GTGGCTGTGGGACCCAGCAGAGAGGCGGCTCTGTGACGTACACAGCAACACCTGCTTGG 1488
1381 GGCCCTCCATCCAGACACGGGCTTGACGTGAGCAAGTGTGACACCCGATCCGGCAGG 1440
1489 GGCCCTCGATCCAGACACGGGCTTGACGTGAGCAAGTGTGACACCCGATCCGGCAGG 1548
1441 ACGGCGCTGGAGCCACTGTGTCACTTGTGTCATGTCTGTGACCTGTGAGTGGCA 1500
1549 ACGGCGCTGGAGCCACTGTGTCACTTGTGTCATGTCTGTGACCTGTGAGTGGCA 1608
1501 ATATCACACGATCCGCTCTGCAACTCCCACTGCCAGTGGCCAGATGGGGGCAAGATTGCA 1560
1609 ATATCACACGATCCGCTCTGCAACTCCCACTGCCAGTGGCCAGATGGGGGCAAGATTGCA 1668
1561 AAGGGAGTGGCCGGGAGACCAAGACCTTGCAGGGCGCCCCATGCCCAATCGATGGCGCT 1620
1669 AAGGGAGTGGCCGGGAGACCAAGACCTTGCAGGGCGCCCCATGCCCAATCGATGGCGCT 1728
1621 GGAGCCCTTGGTCCCGTGTGCGGCTGTGACTGTCACTGTGCGGCTGGATCCGGGAGC 1680
1729 GGAGCCCTTGGTCCCGTGTGCGGCTGTGACTGTCACTGTGCGGCTGGATCCGGGAGC 1788
1681 GCACCCGGGCTGTCAACAGCCCTGAGCCTCAGTACGGAGGGAAGGCTGCGTGGGGGATG 1740
1789 GCACCCGGGCTGTCAACAGCCCTGAGCCTCAGTACGGAGGGAAGGCTGCGTGGGGGATG 1848
1741 TGCAGGAGCTCAGATGTGCAACAGAGGAGCTGCCCCGTGGATGCTTTATCCAAAC 1800
1849 TGCAGGAGCTCAGATGTGCAACAGAGGAGCTGCCCCGTGGATGCTTTATCCAAAC 1908
1801 CCTGCTTCCGGGAGCCAGTGCAGCAGCTTCCCGATGGGCTCTGGTATGCGGCTCT 1860
1909 CCTGCTTCCGGGAGCCAGTGCAGCAGCTTCCCGATGGGCTCTGGTATGCGGCTCT 1968
1861 GCCCTGTGGGCTTCTGGGCAATGGCAACCACTGTGAGGACCTGGACGAGTGTGCCCTGG 1920
1969 GCCCTGTGGGCTTCTGGGCAATGGCAACCACTGTGAGGACCTGGACGAGTGTGCCCTGG 2028
1921 TCCCGGACATCTGCTTCCACAGCAAGTGTGCTGCTGTCAACACTCAGCCTGGCT 1980
2029 TCCCGGACATCTGCTTCCACAGCAAGTGTGCTGCTGTCAACACTCAGCCTGGCT 2088
1981 TCCACTGCTGCCCTGCCCTGCCCGCCGATACAGAGGGAACAGCCCGTGGGGTGGCGCTGG 2040
2089 TCCACTGCTGCCCTGCCCGCCGATACAGAGGGAACAGCCCGTGGGGTGGCGCTGG 2148
2041 AAGCAGCCAGACGGGAAGCAAGTGTGAGCCCGGAACCCATCCAGGACAGACAC 2100
2149 AAGCAGCCAGACGGGAAGCAAGTGTGAGCCCGGAACCCATCCAGGACAGACAC 2208
2101 ACAATGCGCAACAAGCAGCGGAGTGCATCTACTTGGGCCACTTTCAGCGACCCCATGTACA 2160
2209 ACAATGCGCAACAAGCAGCGGAGTGCATCTACTTGGGTCACTTCAGCGACCCCATGTACA 2268
2161 AGTCGAGTGCACAGAGCTACCGGGGCGAGCGGCTCATCTGGGGGAGGACTCCGAGC 2220
2269 AGTCGAGTGCACAGAGCTACCGGGGCGAGCGGCTCATCTGGGGGAGGACTCCGAGC 2328
2221 TGGAGCGGCTGGCCCAACCTCAATCTGGTCTGCGGCCACCAACGCCACCTACCACTGCATCA 2280
2329 TGGAGCGGCTGGCCCAACCTCAATCTGGTCTGCGGCCACCAACGCCACCTACCACTGCATCA 2388

2281 AGGATACTGCCCCCTCTGCCAAATTTCTGGCAGGAGACTTTTGACAAGGACGGGATTG 2340
2389 AGGATACTGCCCCCTCTGCCAAATTTCTGGCAGGAGACTTTTGACAAGGACGGGATTG 2448
2341 CGGATGCTGTGATGATGACGATGACAATGACGCTGTGACCGATGAGAAGGACAACCTGCC 2400
2449 CGGATGCTGTGATGATGACGATGACAATGACGCTGTGACCGATGAGAAGGACAACCTGCC 2508
2401 AGCTCCTCTTCAATCCCGCCAGCTGACTATGACAAGGATGAGTTGGGGAACGCTGTG 2460
2509 AGCTCCTCTTCAATCCCGCCAGCTGACTATGACAAGGATGAGTTGGGGAACGCTGTG 2568
2461 ACAACTGCCCCCTTACGTTGACAAACCCCTGCCAGATCGACACAGACAACAATGGAGAGG 2520
2569 ACAACTGCCCCCTTACGTTGACAAACCCCTGCCAGATCGACACAGACAACAATGGAGAGG 2628
2521 ACGCTGCTCGTGGGACATTTGATGGGGAACGATGCTTCAATGACGAGACAATTTGCTCCT 2580
2629 ACGCTGCTCGTGGGACATTTGATGGGGAACGATGCTTCAATGACGAGACAATTTGCTCCT 2688
2581 ACGTCTCAACACACTGACACAGAGGACACGGATGTCAGCGTGTGGGGGATCACTGTGACA 2640
2689 ACGTCTCAACACACTGACACAGAGGACACGGATGTCAGCGTGTGGGGGATCACTGTGACA 2748
2641 ACTGCCCTCTGGTGCACAAACCTTGACACAGACCGACGTTGGACAATGACCTTGTGGGAC 2700
2749 ACTGCCCTCTGGTGCACAAACCTTGACACAGACCGACGTTGGACAATGACCTTGTGGGAC 2808
2701 AGTGTGACAAACAGAGGACATAGATGACGACGCGCCACAGACAACAACAGGACAACCTGCC 2760
2809 AGTGTGACAAACAGAGGACATAGATGACGACGCGCCACAGACAACAACAGGACAACCTGCC 2868
2761 CCTACATCTCAACCGCCAAACCGAGCTGACATGACAGACGGCCAGGGGACGACGCTGTG 2820
2869 CCTACATCTCAACCGCCAAACCGAGCTGACATGACAGACGGCCAGGGGACGACGCTGTG 2928
2821 ACCCTGATGATGACAAACGATGGGCTGCCGATGACAGGACAACCTGCCGCTTGTGTTCA 2880
2929 ACCCTGATGATGACAAACGATGGGCTGCCGATGACAGGACAACCTGCCGCTTGTGTTCA 2988
2881 ACCCAGACAGGAGGACTTGGACGCTGATGACGCGGCTGATTTGTAAAGATGATTTG 2940
2989 ACCCAGACAGGAGGACTTGGACGCTGATGACGCGGCTGATTTGTAAAGATGATTTG 3048
2941 ACAATGACAAACATCCAGATATTGATGATGCTCTCTGTAACAAACATGCCATCAGTGAGA 3000
3049 ACAATGACAAACATCCAGATATTGATGATGCTCTCTGTAACAAACATGCCATCAGTGAGA 3108
3001 CAGACTTCAGGAACCTCCAGATGGTCCCTTGGATCCCAAGGGACCAACCCAAATTTGATC 3060
3109 CAGACTTCAGGAACCTCCAGATGGTCCCTTGGATCCCAAGGGACCAACCCAAATTTGATC 3168
3061 CCAACTGGGTCAATTCGCCATCAAGCAAGGAGCTGTTTACAGACGCCNACTTCGACCCCG 3120
3169 CCAACTGGGTCAATTCGCCATCAAGCAAGGAGCTGTTTACAGACGCCNACTTCGACCCCG 3228
3121 GCATCGCTGTAGTGTGATGACGAGTTGGGTCTGTGGACTTCAGTGGGACATTTCTACGTAA 3180
3229 GCATCGCTGTAGTGTGATGACGAGTTGGGTCTGTGGACTTCAGTGGGACATTTCTACGTAA 3288
3181 ACATGACCGGGACGACGATATGCGGCTCTGCTTTTGGTTTACAGTCAAGGACGCGCT 3240
3289 ACATGACCGGGACGACGATATGCGGCTCTGCTTTTGGTTTACAGTCAAGGACGCGCT 3348
3241 TCTATGTGTTGATGTGGAAGCAGAGTGCAGACCTACTGGGAGGACCCAGGCCACGCGGG 3300
3349 TCTATGTGTTGATGTGGAAGCAGAGTGCAGACCTACTGGGAGGACCCAGGCCACGCGGG 3408
3301 CTTATGGCTACTCCGGGCTGTCCCTCAAGTGGTGAATCCACCAACCGGGACGGGCGAGC 3360
3409 CTTATGGCTACTCCGGGCTGTCCCTCAAGTGGTGAATCCACCAACCGGGACGGGCGAGC 3468
3361 ACCTGAGGACCGCGCTGTGGGCACACGGGGACACCGCGGGGACGCTGCGACCTTATGGC 3420

```
Db 3469 ACCTAGAGAACCGCTGTGTGGACACGGGGAAACCGCCGGGCAAGTGGAACTTATGGC 3528
Qy 3421 ACGACCCCAAGAACTTGGCTGGAGAACTACACGGCTTATAGTGGCACTGACTACA 3480
Db 3529 ACGACCCCAAGAACTTGGCTGGAGAACTACACGGCTTATAGTGGCACTGACTACA 3588
Qy 3481 GGGCCAAAGCTGGCTACATCAGAGCTTATAGCATGAAGAAACAGGTCACTGGCAGCT 3540
Db 3589 GGGCCAAAGCTGGCTACATCAGAGCTTATAGCATGAAGAAACAGGTCACTGGCAGCT 3648
Qy 3541 CAGACCTATCTATGACCAAACTTACGCTGGCGGGCGGCTGGCTCTATTTGTCTCTC 3600
Db 3649 CAGACCTATCTATGACCAAACTTACGCTGGCGGGCGGCTGGCTCTATTTGTCTCTC 3708
Qy 3601 AAGAAATGGTCTATTTCTCAGACCTCAGAGTGAAGATGAGAGATTTTAAACAAGATTG 3660
Db 3709 AAGAAATGGTCTATTTCTCAGACCTCAGAGTGAAGATGAGAGATTTTAAACAAGATTG 3768
Qy 3661 CTGATTTTCCGGCAATGCCCTGTGTGATGCCATGTCTCTAGACACCTCAGTTCAATGTGG 3720
Db 3769 CTGATTTTCCGGCAATGCCCTGTGTGATGCCATGTCTCTAGACACCTCAGTTCAATGTGG 3828
Qy 3721 TCCTGTGCTCTCTCTCTCTGACAGACCTCCTGTGCTTGAACCTTAACTGTAGTGTG 3780
Db 3829 TCCTGTGCTCTCTCTCTCTGACAGACCTCCTGTGCTTGAACCTTAACTGTAGTGTG 3888
Qy 3781 TTCACCTCTCTGACAGAACCCCAACCCAGAGTGCCTTCAAGAGATTAATCAATGGAAC 3840
Db 3889 TTCACCTCTCTGACAGAACCCCAACCCAGAGTGCCTTCAAGAGATTAATCAATGGAAC 3948
Qy 3841 GAGAGATGAACATCTAACCCCTAGAGAAACCGTTGGTGAATATGAGACTTTATG 3900
Db 3949 TCAGAGATGAACATCTAACCCCTAGAGAAACCGTTGGTGAATATGAGACTTTATG 4008
Qy 3901 TGGAGTGAATTAATGGGCAATGCCATTAATGCTTTTCTGTTTGTAAAAAGATGAC 3960
Db 4009 TGGAGTGAATTAATGGGCAATGCCATTAATGCTTTTCTGTTTGTAAAAAGATGAC 4068
Qy 3961 GTTTACATATAAATGTAATTAATCTATTTGATTTATGATATAGATTAAGAGAAATA 4020
Db 4069 GTTTACATATAAATGTAATTAATCTATTTGATTTATGATATAGATTAAGAGAAATA 4128
Qy 4021 CTGTGATTAAGCATTAATGATAATTAAGATGAATAAATATGCTGAATCTTCTTGGTG 4080
Db 4129 CTGTGATTAAGCATTAATGATAATTAAGATGAATAAATATGCTGAATCTTCTTGGTG 4188
Qy 4081 CTTAAAGTTGTCACTATTTCTTGAATTAAGATTGCTTCAATGACACCAATCCGCTA 4140
Db 4189 CTTAAAGTTGTCACTATTTCTTGAATTAAGATTGCTTCAATGACACCAATCCGCTA 4248
Qy 4141 AATTAATTAATAACAAGGCTCAATCAATTTGAAGTATGTTTATGAGAGAGATTA 4200
Db 4249 AATTAATTAATAACAAGGCTCAATCAATTTGAAGTATGTTTATGAGAGAGATTA 4308
Qy 4201 GAAAGACACAGGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTA 4260
Db 4309 GAAAGACACAGGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTA 4368
Qy 4261 CAGTTACAAATAAATAACAAGCTCTCTCTGTCTTCAATGAAGACCCCTCAATGTCAGTA 4320
Db 4369 CAGTTACAAATAAATAACAAGCTCTCTCTGTCTTCAATGAAGACCCCTCAATGTCAGTA 4428
Qy 4321 GAGATGAGTTTCAATCAAAAGAAACAACATCTTGTCAAAATGGGTGTGATGCGGTTCAAT 4380
Db 4429 GAGATGAGTTTCAATCAAAAGAAACAACATCTTGTCAAAATGGGTGTGATGCGGTTCAAT 4488
Qy 4381 GTGGATTGGCAAAACCTCATTTAATTAAGTAAAGTTAGCAGAGCAAAAGTGGGTTTAG 4440
Db 4489 GTGGATTGGCAAAACCTCATTTAATTAAGTAAAGTTAGCAGAGCAAAAGTGGGTTTAG 4548
Qy 4441 CTGCTCTTGTGCGGCTGTGTGTGCGGAGGCTCTGCTGAGCTTCTCTCCCAAGTT 4500
Db 4549 CTGCTCTTGTGCGGCTGTGTGTGCGGAGGCTCTGCTGAGCTTCTCTCCCAAGTT 4608
Qy 4501 TGCTGCTTAAGAGAAACCAAGACACACGACGCGGCAAAAGGGCAATCTTAACCGGAT 4560
Db 4609 TGCTGCTTAAGAGAAACCAAGACACACGACGCGGCAAAAGGGCAATCTTAACCGGAT 4668
Qy 4561 CTAGCTTTGTATCTGCGGACAAAGTGTCTTTTACCTGAATTTGATGATACATTTCAATTA 4620
Db 4669 CTAGCTTTGTATCTGCGGACAAAGTGTCTTTTACCTGAATTTGATGATACATTTCAATTA 4728
Qy 4621 GGTTCAGATTAAATATTTTGTATATTTTATTAAGTACATTAAGTAACTCCCAAT 4680
Db 4729 GGTTCAGATTAAATATTTTGTATATTTTATTAAGTACATTAAGTAACTCCCAAT 4788
Qy 4681 TACAGTAACTTATTTTAAATATGCTAGTAAACATATGATATTAATTTCTAGAAAACA 4740
Db 4789 TACAGTAACTTATTTTAAATATGCTAGTAAACATATGATATTAATTTCTAGAAAACA 4848
Qy 4741 AACATTAATAGTATATATCTCTGGAATAATGAGCTTGAATATATAGTTGTCAAC 4800
Db 4849 AACATTAATAGTATATATCTCTGGAATAATGAGCTTGAATATATAGTTGTGTCAAC 4908
Qy 4801 GATGAAGCATGCTAGAGCTGTATACAGATATCATAGAGATATAGAGAGTTATGATG 4860
Db 4909 GATGAAGCATGCTAGAGCTGTATACAGATATCATAGAGATATAGAGAGTTATGATG 4968
Qy 4861 AACCTTAATATATATATGTTGCAAGGATTTTATGTTCAATATTTGTACTGTATCTATC 4920
Db 4969 AACCTT-AATATATATATGTTGCAAGGATTTTATGTTCAATATTTGTACTGTATCTATC 5027
Qy 4921 TGCTGATATGGAATCTTTTATTAATCAACGCTGAAA- GAATCAGACATTTAGCTTGCC 4979
Db 5028 TGCTGATATGGAATCTTTTATTAATCAACGCTGAAA- GAATCAGACATTTAGCTTGCC 5087
Qy 4980 AGGACACCCCAATATACGATGATGATATATGACAAAGTTGTTTGTGTTT 5039
Db 5088 AGGACACCCCAATATACGATGATGATATATGACAAAGTTGTTTGTGTTT 5147
Qy 5040 TTTGTTGTTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 5099
Db 5148 TTTGTTGTTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 5203
Qy 5100 CTGATCCACTCCACATTAAGGGGTTTATGAGAGAAAGTGTGTGTGTGATGATGATG 5159
Db 5204 CTGATCCACTCCACATTAAGGGGTTTATGAGAGAAAGTGTGTGTGTGATGATGATG 5263
Qy 5160 GGGGCAAACTTTTCCCTTCTGTTTATATGATCAATCAATTTCTATGCAAAACAGAAAC 5219
Db 5264 GGGGCAAACTTTTCCCTTCTGTTTATATGATCAATCAATTTCTATGCAAAACAGAAAC 5323
Qy 5220 AATCATTAATCTTATGCTTATATGATCAATGATGATGATTAATTAATTTTGTGTTT 5279
Db 5324 AATCATTAATCTTATGCTTATATGATCAATGATGATGATTAATTAATTTTGTGTTT 5383
Qy 5280 CTTTGAAGTTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5339
Db 5384 CTTTGAAGTTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5440
Qy 5340 GCTGTATTTCCGAGCAACGAGAGCTTGGGATCTTCAATTAATGATGACGATGTCAC 5399
Db 5441 GCTGTATTTCCGAGCAACGAGAGCTTGGGATCTTCAATTAATGATGACGATGTCAC 5499
Qy 5400 AGGCTGAGGTTTCTGTTTCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5459
Db 5500 AGGCTGAGGTTTCTGTTTCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5559
Qy 5460 GATGATGATTAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5519
Db 5560 GATGATGATTAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5619
Qy 5520 AATTTATGATTAAGTTGATGAAAGTATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 5579
Db 5620 AATTTATGATTAAGTTGATGAAAGTATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 5679
```


QY	1081	TGTCAGCTTGTCTGACAGAGATGAGCGAGTCTTTTGCGGAAATATGAAAGCTGGTGGTGGACA	1140
Db	1189	TGTCAAGTTCTGTGACAGAGATGGCCGGTCTTTTGCGAATAATGAAAGCTGGTGGTGGACA	1248
QY	1141	GCTGCACCACTGTACTGTCAAGAAATTTAAACCAATTGGCCACCAATACACTGCCCGC	1200
Db	1249	GCTGCACCAAGTGTACTGTCAAGAAATTTAAACCAATTGGCCACCAATACACTGCCCGC	1308
QY	1201	CTGCACACTGTGCGCAGTCCATCTCTTTGTGAGAAAGCGAATGCTCACTCCCTCTGCCTCCACT	1260
Db	1309	CTGCACACTGTGCGCAGTCCATCTCTTTGTGAGAAAGCGAATGCTCACTCCCTCTGCCTCCACT	1368
QY	1261	CGGTGACCGGTGAGAGAGGCTGTGTCTCCGTGGGCGAGGTGGACCCCAATGTCTCCGTGACGT	1320
Db	1369	CGGTGACCGGTGAGAGAGGCTGTGTCTCCGTGGGCGAGGTGGACCCCAATGTCTCCGTGACGT	1428
QY	1321	GTGGCTCTGGAGACCCAGCAAGAGAGCGCGGTCTGTGACGTCAACAGCAACACTGTCTGG	1380
Db	1429	GTGGCTCTGGAGACCCAGCAAGAGAGCGCGGTCTGTGACGTCAACAGCAACACTGTCTGG	1488
QY	1381	GGCGCTCCCAATCCAGACACCGGGCTTGGAGCTGTGAGCAAGTGTGACACCCCGATCCGGAGG	1440
Db	1489	GGCGCTCCCAATCCAGACACCGGGCTTGGAGCTGTGAGCAAGTGTGACACCCCGATCCGGAGG	1548
QY	1441	ACGGCGGCTGGAGCCACTGTGTACACTTGTGTATGTCTGTGTGACCTGTGAGATTGGCA	1500
Db	1549	ACGGCGGCTGGAGCCACTGTGTACACTTGTGTATGTCTGTGTGACCTGTGAGATTGGCA	1608
QY	1501	ATTATCACAGCCATCCGTCTGTGAACTCCCAAGTCCCGCCAGATGGGGGGGCAAGAAATTGCA	1560
Db	1609	ATTATCACAGCCATCCGTCTGTGAACTCCCAAGTCCCGCCAGATGGGGGGGCAAGAAATTGCA	1668
QY	1561	AAGGAGTGTGCGCGGAGACCAAGCTTGCCAGGGCGCCCATGCTCCATGATGATGGCCGT	1620
Db	1669	AAGGAGTGTGCGCGGAGACCAAGCTTGCCAGGGCGCCCATGCTCCATGATGATGGCCGT	1728
QY	1621	GGAGCCCTCGTATCCCGTGTGGCTGTGCACTGTGCGAGTGTGCACTGTGCGGTGGGATCCGGAGC	1680
Db	1729	GGAGCCCTCGTATCCCGTGTGGCTGTGCACTGTGCGAGTGTGCACTGTGCGGTGGGATCCGGAGC	1788
QY	1681	GCACCCGGGTTGTGCAACAGCCTGTAGCTCAATAGGAGGGAAAGGCTGCTGTGGGGATG	1740
Db	1789	GCACCCGGGTTGTGCAACAGCCTGTAGCTCAATAGGAGGGAAAGGCTGCTGTGGGGATG	1848
QY	1741	TGCAGAGCGTCAATGTGCAACAAGAGAGCTCCCGTGTGATGTGTATTCCAAAC	1800
Db	1849	TGCAGAGCGTCAATGTGCAACAAGAGAGCTCCCGTGTGATGTGTATTCCAAAC	1908
QY	1801	CTGTCTTCCCGGAGGCCAATGTGACAGACTTCCCGATGGGTCTGTGTATGTGGGCTCTCT	1860
Db	1909	CTGTCTTCCCGGAGGCCAATGTGACAGACTTCCCGATGGGTCTGTGTATGTGGGCTCTCT	1968
QY	1861	GCCCTGTGGGTTTGTGGCAATGAGCAACCACTGTGAGCACTTGTGACGAGTGTGCCCTGG	1920
Db	1969	GCCCTGTGGGTTTGTGGCAATGAGCAACCACTGTGAGCACTTGTGACGAGTGTGCCCTGG	2028
QY	1921	TCCCGGCAATGTCTTTCACACAGCAAGTGTCTGCTGTGTAAACAATCAAGCTGGCT	1980
Db	2029	TCCCGGCAATGTCTTTCACACAGCAAGTGTCTGCTGTGTAAACAATCAAGCTGGCT	2088
QY	1981	TCCACTGTGCTTCCCTTGCCTCCGCTCCGATACAGAGGAAACAGCCCTGTGGGGTGGCTGG	2040
Db	2089	TCCACTGTGCTTCCCTTGCCTCCGCTCCGATACAGAGGAAACAGCCCTGTGGGGTGGCTGG	2148
QY	2041	AAGAGGCCAAGACGGAATAAGCAAGTGTGTGAGCCGGAATAACCAATGCAAGACAAAGCAC	2100
Db	2149	AAGAGGCCAAGACGGAATAAGCAAGTGTGTGAGCCGGAATAACCAATGCAAGACAAAGCAC	2208
QY	2101	ACAATCTGCACAGACACGGGAGTGTGATCTTACTGTGGGCACTTACAGGACCTCCATGTATCA	2160
Db	2209	ACAATCTGCACAGACACGGGAGTGTGATCTTACTGTGGGCACTTACAGGACCTCCATGTATCA	2268

QY	2161	AGTGGCAAGTGCAGACAGGCTTCAGGCGGGGACAGGGCTCATCTGCGGGAGCACTCGAGC	2220
Db	2269	AGTGCAGATGCCAGACAGGCTACGGGGGCGAGGGCTCATCTCGGGGAGGACCTCGAGC	2328
QY	2221	TGAGCGGCTGGCCCAACTCTAATCTGTCTGCGCACCAAGCCCACTTACCATCTGCATCA	2280
Db	2329	TGAGCGGCTGGCCCAACTCTAATCTGTGTGCGCACCAAGCCCACTTACCATCTGCATCA	2388
QY	2281	AGGATTAATGCCGCCCATCTGCCAAATTTCTGGGACAGAAAGCTTTTCAACAAGACGGGATTG	2340
Db	2389	AGGATTAATGCCGCCCATCTGCCAAATTTCTGGGACAGAAAGCTTTTCAACAAGACGGGATTG	2448
QY	2341	GCGATGCTGTGATGATGACATGACATGACGGTGTGACCGATGAGAAAGCAACTGCGC	2400
Db	2449	GCGATGCTGTGATGATGACATGACATGACGGTGTGACCGATGAGAAAGCAACTGCGC	2508
QY	2401	AGTCTCTTCAATCCCCGCGAGGCTGACATGACAAGATGAGGTTTGGGACCGCTGTG	2460
Db	2509	AGTCTCTTCAATCCCCGCGAGGCTGACATGACAAGATGAGGTTTGGGACCGCTGTG	2568
QY	2461	ACAATGCGCTTACGTGCAACCTGCGCAGATGACAACAACAACAATGAGAGGTTG	2520
Db	2569	ACAATGCGCTTACGTGCAACCTGCGCAGATGACAACAACAACAATGAGAGGTTG	2628
QY	2521	AGCGCTGCTCCGGGACATTGATGGGGAGCATGTCTTCAATGAGCAAGACAATTTGCTCCT	2580
Db	2629	AGCGCTGCTCCGGGACATTGATGGGGAGCATGTCTTCAATGAGCAAGACAATTTGCTCCT	2688
QY	2581	ACGCTTACAACTGACCAAGAGGACACGATGTGTACGGTGTGGGGGATCACTGTACACA	2640
Db	2689	ACGCTTACAACTGACCAAGAGGACACGATGTGTACGGTGTGGGGGATCACTGTACACA	2748
QY	2641	ACTGCCCCCTGGTGCACAACCTGTGACAGACCGAGCGTGGACATGACCTTGTGGGAGCC	2700
Db	2749	ACTGCCCCCTGGTGCACAACCTGTGACAGACCGAGCGTGGACATGACCTTGTGGGAGCC	2808
QY	2701	AGTGTGACAAACAAGAGCATATGATGACAGCGGCCACAGAACCAACAAGAGCAACTGCC	2760
Db	2809	AGTGTGACAAACAAGAGCATATGATGACAGCGGCCACAGAACCAACAAGAGCAACTGCC	2868
QY	2761	CCTACACTCTCCAAACGCAACCAAGGCTGACATGACAGAGACCGGCCAGGCGACTGTG	2820
Db	2869	CCTACACTCTCCAAACGCAACCAAGGCTGACATGACAGAGACCGGCCAGGCGACTGTG	2928
QY	2821	ACCCTGATGATGACAAACGATGGCGTCCCCCGATGACAGGAGCAACTGCGCGCTGTGTTCA	2880
Db	2929	ACCCTGATGATGACAAACGATGGCGTCCCCCGATGACAGGAGCAACTGCGCGCTGTGTTCA	2988
QY	2881	ACCAGACCAAGAGGACTTGGACCGGTGATGACCGGGGTGATATTTGTAAAGATGATTTTG	2940
Db	2989	ACCAGACCAAGAGGACTTGGACCGGTGATGACCGGGGTGATATTTGTAAAGATGATTTTG	3048
QY	2941	ACAATGACAAATCCCAAGATATTGATGATGTGTCTCGAAGAAACAATGCAATCAATGAGA	3000
Db	3049	ACAATGACAAATCCCAAGATATTGATGATGTGTCTCGAAGAAACAATGCAATCAATGAGA	3108
QY	3001	CAGACTTCAGAGAACTTCCAGATGCTCCCTTGGATCCAAAGGGACCAACCCAAATTTGATC	3060
Db	3109	CAGACTTCAGAGAACTTCCAGATGCTCCCTTGGATCCAAAGGGACCAACCCAAATTTGATC	3168
QY	3061	CCAACTGGGGTCAATTGCCCAATCCAAAGGACAGACCTGGTTACAGACGCAACTCGGACCCG	3120
Db	3169	CCAACTGGGGTCAATTGCCCAATCCAAAGGACAGACCTGGTTACAGACGCAACTCGGACCCG	3228
QY	3121	GCAATCGCTGATGATTTGACGAGTTTGGGTCTGTGACTTCAAGTGGCAATTCTACGTAA	3180
Db	3229	GCAATCGCTGATGATTTGACGAGTTTGGGTCTGTGACTTCAAGTGGCAATTCTACGTAA	3288
QY	3181	ACACTGACCGGGACAGACATGATGCGGGCTTGCTTTGGTTACCAAGTCAACACACCGCT	3240
Db	3289	ACACTGACCGGGACAGACATGATGCGGGCTTGCTTTGGTTACCAAGTCAACACACCGCT	3348
QY	3241	TCTATGTGTGATGTGGAGACAGTGAACGCAACCTTACTGGAGAGACAGCCACCGGGG	3300

3349 TCTATGTTGGTATGTGAAGCAGGTGACGACACCTTACTGGAGGACCGCCACCGCGG 3408
3301 CCTATGCTACTCGGGGTGTCTCCTCAGGTGTGACTCCACACGGGACGGCGAGC 3360
3409 CCTATGCTACTCGGGGTGTCTCCTCAGGTGTGAACTCCACACGGGACGGCGAGC 3468
3361 ACCTGAGGAACCGGCTGTGGCACAACGGGGAACACGGCGGGGAGGTGCGAACCTTATGGC 3420
3469 ACCTGAGGAACCGGCTGTGGCACAACGGGGAACACGGCGGGGAGGTGCGAACCTTATGGC 3528
3421 ACGACCCAGGACATTTGGCTGAGAGACTACACGGCTATAGTGGCACTGACATCACA 3480
3529 ACGACCCAGGACATTTGGCTGAGAGACTACACGGCTATAGTGGCACTGACATCACA 3588
3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGATGAAGAAACAGAGTCAATGGCAGACT 3540
3589 GGCCCAAGACCGGCTACATCAGAGTCTTAGTGATGAAGAAACAGAGTCAATGGCAGACT 3648
3541 CAGACCTATCTATGACAAACCTACGCTGGGGGGGCTGGGTCTATTTGCTCTCTC 3600
3649 CAGACCTATCTATGACAAACCTACGCTGGGGGGGCTGGGTCTATTTGCTCTCTC 3708
3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATCGAGAGATATTTAAACAAGATTG 3660
3709 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATCGAGAGATATTTAAACAAGATTG 3768
3661 CTGCAATTCGGGCAATGCCGTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTTGG 3720
3769 CTGCAATTCGGGCAATGCCGTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTTGG 3828
3721 TCCCTTGGCTTCTCTCTAGACAGACCTCTCTGCTGCTTACCTTAACCTCAGTGGTTC 3780
3829 TCCCTTGGCTTCTCTCTAGACAGACCTCTCTGCTGCTTACCTTAACCTCAGTGGTTC 3888
3781 TTACCTCTCTGAGCAACCCCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
3889 TTACCTCTCTGAGCAACCCCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948
3841 GCAGAGATGACATCTACCCACTAGAGGAACCCAGTTTGGTATATATGAGACTTTATG 3900
3949 TCAGAGATGACATCTACCCACTAGAGGAACCCAGTTTGGTATATATGAGACTTTATG 4008
3901 TGGAGTGAAATTTGGGATGCCATTCATATGCTTTTCTTTTGTGTTTAAAAAGAAATGAC 3960
4009 TGGAGTGAAATTTGGGATGCCATTCATATGCTTTTCTTTTGTGTTTAAAAAGAAATGAC 4068
3961 GTTTACATATAAATGTAATTTACTTATTTATTTATGTTATATGAGTTGAAGGAAATA 4020
4069 GTTTACATATAAATGTAATTTACTTATTTATTTATGTTATATGAGTTGAAGGAAATA 4128
4021 CTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATATGCTGAACCTACTTTTGGTG 4080
4129 CTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATATGCTGAACCTACTTTTGGTG 4188
4081 CTTAAAGTTGTCACTATTTCTTGAATTAGAGTTGCTCTACAAATGACACAAATCCCGCTA 4140
4189 CTTAAAGTTGTCACTATTTCTTGAATTAGAGTTGCTCTACAAATGACACAAATCCCGCTA 4248
4141 AATAAATTTATAACAAGGTCATTTCAATTTGAAGTAAATGTTTACTTAAGGAGAGATTA 4200
4249 AATAAATTTATAACAAGGTCATTTCAATTTGAAGTAAATGTTTACTTAAGGAGAGATTA 4308
4201 GAAGACACAGGCTAGCAAAATGACATGACTACGATTAACCTAATCGGAACATGTAATA 4260
4309 GAAGACACAGGCTAGCAAAATGACATGACTACGATTAACCTAATCGGAACATGTAATA 4368
4261 CAGTTACAAAATAAAGCACT 4320
4369 CAGTTACAAAATAAAGCACT 4428
4321 CAGATGCAAGTTTCATCAAGAAACAAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4380

4429 GAGATGCAGTTTCTATCAAGAAACAAACATCTCTGCAATGGGTGTGACGGTTCAGAT 4488
4381 GTGGATTTGGCAAAACCTTCATTTAAGTAAAAAGTTTAGCAGAGCAAAAGTGCAGTCTTAG 4440
4489 GTGGATTTGGCAAAACCTTCATTTAAGTAAAAAGTTTAGCAGAGCAAAAGTGCAGTCTTAG 4548
4441 CTGTGCTTTGTGCGCTGTGTGTGCGGAGGCTCTGCTGCTGAGCTTCTTCCCGAGTT 4500
4549 CTGTGCTTTGTGCGCTGTGTGTGCGGAGGCTCTGCTGCTGAGCTTCTTCCCGAGTT 4608
4501 TGCTCCCTGAGAGGAACACAGAGCAGACACAGCGCGGAAAAAGCGCATCTAAAGCGGTAT 4560
4609 TGCTCCCTGAGAGGAACACAGAGCAGACACAGCGCGGAAAAAGCGCATCTAAAGCGGTAT 4668
4561 CTAGCTTTGTGTAACCTGCGGACAAAGTTGCTTTTACCTGATTTGATGATACATTTCAITAA 4620
4669 CTAGCTTTGTGTAACCTGCGGACAAAGTTGCTTTTACCTGATTTGATGATACATTTCAITAA 4728
4621 GGTTCAGTATAAATATTTTGTAAATTTTAAAGTACTATAGAAATCAACTCCATT 4680
4729 GGTTCAGTATAAATATTTTGTAAATTTTAAAGTACTATAGAAATCAACTCCATT 4788
4681 TACCAAGTAACTTATTTTAAATATGCTAGTAAACACATATGATGATATAATTTCTAGAAACA 4740
4789 TACCAAGTAACTTATTTTAAATATGCTAGTAAACACATATGATGATATAATTTCTAGAAACA 4848
4741 AACTCTAATAAGTATATAATCTCTGGAATAATGAGCTTGATAATATAGTTGTCTAC 4800
4849 AACTCTAATAAGTATATAATCTCTGGAATAATGAGCTTGATAATATAGTTGTCTAC 4908
4801 GATGAAGCATGCTAGAGCTGTAAAGCAATACATAGAGAAATAGAGAGTTTATGATGG 4860
4909 GATGAAGCATGCTAGAGCTGTAAAGCAATACATAGAGAAATAGAGAGTTTATGATGG 4968
4861 AACCTTAATAATATGATGCTGCGAGGATTTTGTGCTCAATATTTGTTACTGTTACTATC 4920
4969 AACCTT-AAATATAATGTTGCCAGGATTTAGTTCAATATTTGTTACTGTTACTATC 5027
4921 TGCTGTATATGAAATCTTTTAAATCAAAACGCTGAAAAA-GAATCAGCAATTTAGTCTTCCC 4979
5028 TGCTGTATATGAAATCTTTTAAATCAAAACGCTGAAAAACGAATCAGCAATTTAGTCTTCCC 5087
4980 AGGCACACCCAAATATCAGTCATGTAATATGTAATGCAAGTTTGTGTTTGTGTTTGT 5039
5088 AGGCACACCCAAATATCAGTCATGTAATATGTAATGCAAGTTTGTGTTTGTGTTTGT 5147
5040 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5099
5148 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5203
5100 CTCTCCCACTCCACATAGAGGTTTATAGAGAGTCTGCTGCTCTGATGATGATGATGATG 5159
5204 CTCTCCCACTCCACATAGAGGTTTATAGAGAGTCTGCTGCTCTGATGATGATGATGATG 5263
5160 GGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCATTTCTATGCCAAACAGGAAC 5219
5264 GGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCATTTCTATGCCAAACAGGAAC 5323
5220 AATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGTATAAAATTAATTTGTGTTT 5279
5324 GATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGTATAAAATTAATTTGTGTTT 5383
5280 CTTTGTAGGTTGATCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5339
5384 CTTTGTAGGTTGATCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5440
5340 GCTGTATTTCCCGAGACCAACGAAGGTTGGGATCTTCAATTAATGTAGCGACTGTCAAC 5399
5441 GCTGTATTTCCCGAGACCAACGAAGGTTGGGATCTTCAATTAATGTAGCGACTGTCAAC 5499
5400 AGCGTGCAGGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5459
5500 AGCGTGCAGGTTTCTGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5559

901 CCAGCTCAGAGAGAGGCGCCGAGGTTGGGAAACGCTCTGTGAGAGAGCTGGGAAACATGG 960
 1009 CCAGCTCGAGAGAGAGGCGCCGAGGTTGGGAAACGCTCTGTGAGAGAGCTGGGAAACATGG 1068
 961 TCCAGAGAGCTCTCGGAGGCTCCAGCTCTGTGAAACAGCTCTAGCGAGAACTCAAGAGAG 1020
 1069 TCCAGAGAGCTCTCGGAGGCTCCAGCTCTGTGAAACAGCTCTAGCGAGAACTCAAGAGAG 1128
 1021 TGTGGAATGATGAACCAAGTTTCTCTGGAGAGCTATTTGGTGGCCCTCTTAAGAGAAAGAA 1080
 1129 TGTGGAATGATGAACCAAGTTTCTCTGGAGAGCTATTTGGTGGCCCTCTTAAGAGAAAGAA 1188
 1081 TGTGAGAGCTCTCGGAGGCTCCAGCTCTGTGAAACAGCTCTAGCGAGAACTCAAGAGAG 1140
 1189 TGTGAGAGCTCTCGGAGGCTCCAGCTCTGTGAAACAGCTCTAGCGAGAACTCAAGAGAG 1248
 1141 GCTGCAACCAAGTGTACCTGAAGAAATTTAAACCAATTTGGCCACCAAAATCACCTGCCCCG 1200
 1249 GCTGCAACCAAGTGTACCTGAAGAAATTTAAACCAATTTGGCCACCAAAATCACCTGCCCCG 1308
 1201 CTGCAACCTGGCCAGTCCATCTTTGTGGAAGGCGAATGCTGCCCTTCTGCTCCACT 1260
 1309 CTGCAACCTGGCCAGTCCATCTTTGTGGAAGGCGAATGCTGCCCTTCTGCTCCACT 1368
 1261 CGGTGAGAGGCTGTGCTCTCGGTGGGAGAGTGGACCCCAAGTGTCTCGGTGACGT 1320
 1369 CGGTGAGAGGCTGTGCTCTCGGTGGGAGAGTGGACCCCAAGTGTCTCGGTGACGT 1428
 1321 GTGCTCTGGGACCCAGAGAGGCGGTCTGTGACGTCTAGCGAGAACTCAAGAGAG 1380
 1429 GTGCTCTGGGACCCAGAGAGGCGGTCTGTGACGTCTAGCGAGAACTCAAGAGAG 1488
 1381 GGCCTCTCATCAGACAGGCGTGTGAGTCTGAGCAAGTGTGACCCGATCCGGCAGG 1440
 1489 GGCCTCTCATCAGACAGGCGTGTGAGTCTGAGCAAGTGTGACCCGATCCGGCAGG 1548
 1441 ACGCGCTGTGAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 1549 ACGCGCTGTGAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1608
 1501 ATATCACAGCATCCGCTCTGTGCACTCCCGAGTCCCGAGAGTGGGGGGCAAGATTGCA 1560
 1609 ATATCACAGCATCCGCTCTGTGCACTCCCGAGTCCCGAGAGTGGGGGGCAAGATTGCA 1668
 1561 AAGGAGTGGCGGAGCAACAAAGCTGTGCAAGGCGGCCATGCGCAATCGATGGCGCT 1620
 1669 AAGGAGTGGCGGAGCAACAAAGCTGTGCAAGGCGGCCATGCGCAATCGATGGCGCT 1728
 1621 GGAGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 1729 GGAGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1788
 1681 GCACCCGGGTCTGCAACAGCCCTGAGCTCAGTACGAGAGGAGGCGCTGCTGCTGCTGCTGCT 1740
 1789 GCACCCGGGTCTGCAACAGCCCTGAGCTCAGTACGAGAGGAGGCGCTGCTGCTGCTGCTGCT 1848
 1741 TGCAGGAGCTCAGATGTGCAACAGAGGAGCTGCGCGCTGAGTGGCTGTTTCCAAACC 1800
 1849 TGCAGGAGCTCAGATGTGCAACAGAGGAGCTGCGCGCTGAGTGGCTGTTTCCAAACC 1908
 1801 CTTGCTTCCCGGAGCCAGTGTGAGAGCTTCCCGATGGGTCTGCTGCTGCTGCTGCTGCTGCT 1860
 1909 CTTGCTTCCCGGAGCCAGTGTGAGAGCTTCCCGATGGGTCTGCTGCTGCTGCTGCTGCTGCT 1968
 1861 GCTGCTGGGCTTCTTGGGCAATGGCAACCACTGTGAGAGCTGAGAGTGGCTGCTGCTGCTGCT 1920
 1969 GCTGCTGGGCTTCTTGGGCAATGGCAACCACTGTGAGAGCTGAGAGTGGCTGCTGCTGCTGCT 2028
 1921 TCCCGGATCTGCTTCTCCACAGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 2029 TCCCGGATCTGCTTCTCCACAGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2088
 1981 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040

2089 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2148
 2041 AAGCAGCAAGAGAGAGGAAAGCAAGTGTGTGAGCCGAAAGCCCATGCAAGAGAGAG 2100
 2149 AAGCAGCAAGAGAGAGGAAAGCAAGTGTGTGAGCCGAAAGCCCATGCAAGAGAGAG 2208
 2101 ACAACTGCCAACAGCAGCGAGTGCATCTACCTGGGCCCACTTTCAGCGAGCCCACTGATCA 2160
 2209 ACAACTGCCAACAGCAGCGAGTGCATCTACCTGGGGTCACTTTCAGCGAGCCCACTGATCA 2268
 2161 AGTCGAGTCCAGACAGGCTACCGGGCGAGCGGCTCATCTGCGGGAGAGACTTCGGAGC 2220
 2269 AGTCGAGTCCAGACAGGCTACCGGGCGAGCGGCTCATCTGCGGGAGAGACTTCGGAGC 2328
 2221 TGGAGCGTGGCCCAACCTCAATCTGTGCGCCACCAACCGCCACTTACCACTGCAATCA 2280
 2329 TGGAGCGTGGCCCAACCTCAATCTGTGCGCCACCAACCGCCACTTACCACTGCAATCA 2388
 2281 AGGATAAATGCGCCCATCTGCAAAATTTCTGGGAGGAGACTTTTGACAAGGACGGGATTG 2340
 2389 AGGATAAATGCGCCCATCTGCAAAATTTCTGGGAGGAGACTTTTGACAAGGACGGGATTG 2448
 2341 GCGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
 2449 GCGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2508
 2401 AGCTCTCTTCAATCCCGCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
 2509 AGCTCTCTTCAATCCCGCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2568
 2461 ACAATGCGCTTTCGTGCAAACTTCTGCGGAGGAGTGCACAGACAACTTGGAGAGGATG 2520
 2569 ACAATGCGCTTTCGTGCAAACTTCTGCGGAGGAGTGCACAGACAACTTGGAGAGGATG 2628
 2521 ACGCTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2580
 2629 ACGCTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2688
 2581 ACGCTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2640
 2689 ACGCTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2748
 2641 ACGCTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2700
 2749 ACGCTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2808
 2701 ACGCTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2760
 2809 ACGCTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2868
 2761 CCGTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2820
 2869 CCGTGTGTCTGTGAGACTTGTGAGGAGGAGTGTCTTCAATGAAAGGAGCAATTTGCTCCT 2928
 2821 ACCCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
 2929 ACCCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2988
 2881 ACCCAGACAGGAGAGCTTGGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
 2989 ACCCAGACAGGAGAGCTTGGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3048
 2941 ACAATGACAACTCCAGATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
 3049 ACAATGACAACTCCAGATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3108
 3001 CAGACTTTCAGGAACTTCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
 3109 CAGACTTTCAGGAACTTCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3168
 3061 CCAACTGGGTCTTTCGCTCATCAAGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 3120

Db 3169 CCAACTGGGTCAATTCGCCATCAAGCAGAGGAGCTGGTTTCAGACAGCCAACTCGGACCCCG 3228
Qy 3121 GCATCGCTGTAGTTTGAACGAGTTTGGCTGTGGACTTCAGTGGCACAATTTACGTAA 3180
Db 3229 GCATCGCTGTAGTTTGAACGAGTTTGGCTGTGGACTTCAGTGGCACAATTTACGTAA 3288
Qy 3181 ACACGTGACCGGACGACGACTATGCCGCTTCGTCCTTTGGTTTACAGTCAAGCAGCGCGCT 3240
Db 3289 ACACGTGACCGGACGACGACTATGCTGCTTCGTCCTTTGGTTTACAGTCAAGCAGCGCGCT 3348
Qy 3241 TCTATGTGGTGAATGGGAAGAGGAGTGAACGAGACTACTGGGAGGACGAGCCGCGGG 3300
Db 3349 TCTATGTGGTGAATGGGAAGAGGAGTGAACGAGACTACTGGGAGGAGCAGCCGCGGG 3408
Qy 3301 CCTATGGCTACTCCGCGCTGCTCCCTCAAGTGGTGAACCTCCACACGCGGAGCGGCGAGC 3360
Db 3409 CCTATGGCTACTCCGCGCTGCTCCCTCAAGTGGTGAACCTCCACACGCGGAGCGGCGAGC 3468
Qy 3361 ACCTGAGGAACGCGTGTGGCACACGGGGAACACGCCGGGACGAGTGGGAACCTTTATGGC 3420
Db 3469 ACCTGAGGAACGCGTGTGGCACACGGGGAACACGCCGGGACGAGTGGGAACCTTTATGGC 3528
Qy 3421 AGGACCCAGGAACATTTGGCTGGAGGACTACAGGCTTATAGTGGCAGCTGACTCACA 3480
Db 3529 AGGACCCAGGAACATTTGGCTGGAGGACTACAGGCTTATAGTGGCAGCTGACTCACA 3588
Qy 3481 GGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAACAGGTCTATGGCAGACT 3540
Db 3589 GGCCCAAGACGCGTACATCAGAGTCTTAGTGCATGAAGGAAACAGGTCTATGGCAGACT 3648
Qy 3541 CAGGACCTATCTATGACCAACCTAGCTGGGGGGGCTGGGTCTATTTGCTCTCTCTC 3600
Db 3649 CAGGACCTATCTATGACCAACCTAGCTGGGGGGGCTGGGTCTATTTGCTCTCTCTC 3708
Qy 3601 AAGAAATGCTCTATTTCTCAGACCTCAAGTACGAATGAGAGATATTTAAACAAGATTG 3660
Db 3709 AAGAAATGCTCTATTTCTCAGACCTCAAGTACGAATGAGAGATATTTAAACAAGATTG 3768
Qy 3661 CTGCAATTCGGCAATGCGCTGTGATGCGATGCTGCTCCCTAGACACCTCAGTTCATTTGG 3720
Db 3769 CTGCAATTCGGCAATGCGCTGTGATGCGATGCTGCTCCCTAGACACCTCAGTTCATTTGG 3828
Qy 3721 TCCCTGTGGCTTCTCTCTACGACGACCTCCTGCTGCCCTTGACCTTAACTCTGATGGTTC 3780
Db 3829 TCCCTGTGGCTTCTCTCTACGACGACCTCCTGCTGCCCTTGACCTTAACTCTGATGGTTC 3888
Qy 3781 TTCACCTCTGCGAGAACCCCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAAAC 3840
Db 3889 TTCACCTCTGCGAGAACCCCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAAAC 3948
Qy 3841 GCAGAGATCAACATCTAACCCACTAGAGGAACCAAGTTCGTTGATATGAGACTTTATG 3900
Db 3949 TCAGAGATCAACATCTAACCCACTAGAGGAACCAAGTTCGTTGATATGAGACTTTATG 4008
Qy 3901 TGGAGTGAATAATGGGCATGCCATTAATGCTTTTCTGTTTCTGTTTAAAGAAATGAC 3960
Db 4009 TGGAGTGAATAATGGGCATGCCATTAATGCTTTTCTGTTTCTGTTTAAAGAAATGAC 4068
Qy 3961 GTTTACATATAAATGCTAATTAATGATTTATGTTATGTTATGAGTTCGAGGGAATA 4020
Db 4069 GTTTACATATAAATGCTAATTAATGATTTATGTTATGTTATGAGTTCGAGGGAATA 4128
Qy 4021 CTGTGCATTAAGCCATTAATTAATTAAGCATGAATAATTTGCTGAACACTACTTTGGTG 4080
Db 4129 CTGTGCATTAAGCCATTAATTAATTAAGCATGAATAATTTGCTGAACACTACTTTGGTG 4188
Qy 4081 CTTTAAGTGTCACTATTTCTGAATTAAGTGTGCTCAATGACACACAATCCCGCTA 4140
Db 4189 CTTTAAGTGTCACTATTTCTGAATTAAGTGTGCTCAATGACACACAATCCCGCTA 4248
Qy 4141 AATAAATTAACAAGGGTCAATTAATTAAGTGTGCTCAATGACACACAATCCCGCTA 4200
Db 4249 AATAAATTAACAAGGGTCAATTAATTAAGTGTGCTCAATGACACACAATCCCGCTA 4308

Qy 4201 GAAGACACAGGCATAGCAATGACATTAAGCTTACCGATTAACTAATCGACATCTAATA 4260
Db 4309 GAAGACACAGGCATAGCAATGACATTAAGCTTACCGATTAACTAATCGACATCTAATA 4368
Qy 4261 CAGTTACAAAATAAAGCAACTCTCTCTTGTCTTCAATGAAGCCCTCATGTGCAGTA 4320
Db 4369 CAGTTACAAAATAAAGCAACTCTCTCTTGTCTTCAATGAAGCCCTCATGTGCAGTA 4428
Qy 4321 GAGATGAGTTTCAATCAAGAACAAACATCTTGCATATGGGTGTGATGCGGTCCAGAT 4380
Db 4429 GAGATGAGTTTCAATCAAGAACAAACATCTTGCATATGGGTGTGATGCGGTCCAGAT 4488
Qy 4381 GTGGAATTTGCGCAAAACCTCATTTAAGTAAAGGTTAGCAGAGCAAAAGTCCGGTGTCTTAG 4440
Db 4489 GTGGAATTTGCGCAAAACCTCATTTAAGTAAAGGTTAGCAGAGCAAAAGTCCGGTGTCTTAG 4548
Qy 4441 CTGCTGCTTGTGCGCTGTGGTGTGGGGAGGCTCCTGCTGAGCTTCTTCCGCCAGCTT 4500
Db 4549 CTGCTGCTTGTGCGCTGTGGTGTGGGGAGGCTCCTGCTGAGCTTCTTCCGCCAGCTT 4608
Qy 4501 TGCTGCTCAGAGGAACACAGAGCAGACGACAGCGCGGAAAGGGGCGCATCTAACCGTAT 4560
Db 4609 TGCTGCTCAGAGGAACACAGAGCAGACGACAGCGCGGAAAGGGGCGCATCTAACCGTAT 4668
Qy 4561 CTAGGCTTTGGTAACTGCGGACAAAGTTGCTTTTACTGATTTGATGATACATTTCAATTA 4620
Db 4669 CTAGGCTTTGGTAACTGCGGACAAAGTTGCTTTTACTGATTTGATGATACATTTCAATTA 4728
Qy 4621 GGTTCAGTTTAAATATTTTGTAAATATTTAATTAAGTGACTATAGAAATGCAATCCCAT 4680
Db 4729 GGTTCAGTTTAAATATTTTGTAAATATTTAATTAAGTGACTATAGAAATGCAATCCCAT 4788
Qy 4681 TACAGTAATCTATTTTAAATATGCTAGTAAACATATGATAGTATTAATTTCTAGAAACA 4740
Db 4789 TACAGTAATCTATTTTAAATATGCTAGTAAACATATGATAGTATTAATTTCTAGAAACA 4848
Qy 4741 AACATCTAATAGTATATAATCTCTGTAATAATGAGGCTTCATATAATTTAGTGTGTAC 4800
Db 4849 AACATCTAATAGTATATAATCTCTGTAATAATGAGGCTTCATATAATTTAGTGTGTAC 4908
Qy 4801 GATGAAGCATGCTAGAGCTGTAAACAGAAATACATAGAGAAATATGAGGAGTTTATGATGG 4860
Db 4909 GATGAAGCATGCTAGAGCTGTAAACAGAAATACATAGAGAAATATGAGGAGTTTATGATGG 4968
Qy 4861 AACCTTAAATATATATATGCTGACGATTTTGCAGGATTTTCAATATTTGTTACTGTATCTATC 4920
Db 4969 AACCTT-AAATATATATATGCTGACGATTTTGCAGGATTTTCAATATTTGTTACTGTATCTATC 5027
Qy 4921 TGCTGTATATGGAATTTCTTTTAAATCAACCGCTGAAA- GAATCAGCATTTAGTCTTGCC 4979
Db 5028 TGCTGTATATGGAATTTCTTTTAAATCAACCGCTGAAAACGAATCAGCATTTAGTCTTGCC 5087
Qy 4980 AGGCACACCAATATCAGTCATGTATATGCAAGTTTGTGTTTGTGTTTGTGTTT 5039
Db 5088 AGGCACACCAATATCAGTCATGTATATGCAAGTTTGTGTTTGTGTTTGTGTTT 5147
Qy 5040 TTTGTTGGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 5099
Db 5148 TTTGTTGGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 5203
Qy 5100 CTGATCCCACTCCACATAGAGGTTTAGTAAAGAGAGTCTGCTCTGATGATGATAG 5159
Db 5204 CTGATCCCACTCCACATAGAGGTTTAGTAAAGAGAGTCTGCTCTGATGATGATAG 5263
Qy 5160 GGGGCAAACTTTTCCCTTTCTGTTTAAATAGTCAATCAATTTCTATGCAACAGGAAC 5219
Db 5264 GGGGCAAACTTTTCCCTTTCTGTTTAAATAGTCAATCAATTTCTATGCAACAGGAAC 5323
Qy 5220 AATCCATTAATTTAGTCTTAAATGATACATTTGATGATTTGATTAATTTGTTGTTT 5279
Db 5324 GATCCCAATTTAGTCTTAAATGATACATTTGATGATTTGATTAATTTGTTGTTT 5383

QY 661 AGCCCTTACAGACCTGACAGCGGAAAGAGCGGATGTACGTGGCCAAAGGCTGTG 720
Db 769 AGCCCTTACAGACCTGACAGCGGAAAGAGCGGATGTACGTGGCCAAAGGCTGTG 828
QY 721 CCAGAGAGAGTCACTTCAAGGGTTTGGCTTCAAGAGTCCACTTAAGTTTGAACCTGTG 780
Db 829 CCAGAGAGAGTCACTTCAAGGGTTTGGCTTCAAGAGTCCACTTAAGTTTGAACCTGTG 888
QY 781 TGAAGATATTTCTAAGCAAGAGGTTGCGACAGAGCGGAGAGCTGAGATCAACGCCA 840
Db 889 TGAAGATATTTCTAAGCAAGAGGTTGCGACAGAGCGGAGAGCTGAGATCAACGCCA 948
QY 841 TCAGTAGAAACACAGAGAGCTGCGCTGAGTCCGAGTTCACCAACCGAGTACGTGGGCC 900
Db 949 TCAGTAGAAACACAGAGAGCTGCGCTGAGTCCGAGTTCACCAACCGAGTACGTGGGCC 1008
QY 901 CCAGCTCAGAGAGAGCGGAGGTTGTGGAACGCTCGTGGAGAGAGCTGGGAAACATGG 960
Db 1009 CCAGCTCAGAGAGAGCGGAGGTTGTGGAACGCTCGTGGAGAGAGCTGGGAAACATGG 1068
QY 961 TCCAGAGAGCTCTCGGGGCTTCCAGTCTGTGAACGACTCAGCGAGAACTTCAAGAGAG 1020
Db 1069 TCCAGAGAGCTCTCGGGGCTTCCAGTCTGTGAACGACTCAGCGAGAACTTCAAGAGAG 1128
QY 1021 TGTGATATATTAACAGTTTCTGTGGAGCTCATTTGGGCGCTCTTAAGACAGAGAA 1080
Db 1129 TGTGATATATTAACAGTTTCTGTGGAGCTCATTTGGGCGCTCTTAAGACAGAGAA 1188
QY 1081 TGTGATATATTAACAGTTTCTGTGGAGCTCATTTGGGCGCTCTTAAGAGTGTGACA 1140
Db 1189 TGTGATATATTAACAGTTTCTGTGGAGCTCATTTGGGCGCTCTTAAGAGTGTGACA 1248
QY 1141 GCTGACACAGTGTACTGTGAGAAATTTAAACCTTTGGCAACCAATCACTCCGCGC 1200
Db 1249 GCTGACACAGTGTACTGTGAGAAATTTAAACCTTTGGCAACCAATCACTCCGCGC 1308
QY 1201 CTGCAACCTGCGCAGATCCATCTTTGTGAAGGCGAATGTCTGCTTCTGCTCTCACT 1260
Db 1309 CTGCAACCTGCGCAGATCCATCTTTGTGAAGGCGAATGTCTGCTTCTGCTCTCACT 1368
QY 1261 CGGTGACGAGTGAAGAGGCTGTGCTTCCGTGGCAAGTGGAGCCGAGTCTCCGTGACT 1320
Db 1369 CGGTGACGAGTGAAGAGGCTGTGCTTCCGTGGCAAGTGGAGCCGAGTCTCCGTGACT 1428
QY 1321 GTGAGCTGTGGAGCCAGCAGAGAGGCGGCTGTGAGCTCACACAGCAACACTGCTTGG 1380
Db 1429 GTGAGCTGTGGAGCCAGCAGAGAGGCGGCTGTGAGCTCACACAGCAACACTGCTTGG 1488
QY 1381 GGCCCTTCATCCAGACAGCGGCTTGCAGTGTGACAAAGTGTGACACCCGAGTCCGAGAG 1440
Db 1489 GGCCCTTCATCCAGACAGCGGCTTGCAGTGTGACAAAGTGTGACACCCGAGTCCGAGAG 1548
QY 1441 ACCGCGGCTGAGAGCACTGTGCACTTGGTCTTCACTGTGTGACCTGTGAGATTGACA 1500
Db 1549 ACCGCGGCTGAGAGCACTGTGCACTTGGTCTTCACTGTGTGACCTGTGAGATTGACA 1608
QY 1501 ATATACACAGCATCCGTCTGTGCACTCCCAAGTCCCAAGTGGGAGGAGATTTGCA 1560
Db 1609 ATATACACAGCATCCGTCTGTGCACTCCCAAGTCCCAAGTGGGAGGAGATTTGCA 1668
QY 1561 AAGGAGATGGCCGGGAGACCAAAAGCTGACAGGAGCGGCCCATGCCAATGTAGTGGCGCT 1620
Db 1669 AAGGAGATGGCCGGGAGACCAAAAGCTGACAGGAGCGGCCCATGCCAATGTAGTGGCGCT 1728
QY 1621 GAGAGCCCTGTGCTCCGCTGTGCTGCACTGTCACTGTGCTGTGCTGGGATCCGAGAGC 1680
Db 1729 GAGAGCCCTGTGCTCCGCTGTGCTGCACTGTCACTGTGCTGTGCTGGGATCCGAGAGC 1788
QY 1681 GCACCCGAGTCTGCAAGCCGCTGAGCTTCAAGTACGAGAGGAGAGGCTGTGGGGAGATG 1740
Db 1789 GCACCCGAGTCTGCAAGCCGCTGAGCTTCAAGTACGAGAGGAGAGGCTGTGGGGAGATG 1848

QY 1741 TGAAGAGCGTCAATGTGCAACAGAGAGAGCTGCCCGTGTGATGCTGTTATCCAAAC 1800
Db 1849 TGAAGAGCGTCAATGTGCAACAGAGAGAGCTGCCCGTGTGATGCTGTTATCCAAAC 1908
QY 1801 CCGTCTCCCGGAGGCGCAATGTGAGAGCTTCCCGATGAGTCTGTGATGCGGCTCT 1860
Db 1909 CCGTCTCCCGGAGGCGCAATGTGAGAGCTTCCCGATGAGTCTGTGATGCGGCTCT 1968
QY 1861 GCGCTGTGGCTTCTTGGCAATGGAACCACTGTGAGAGCTTGAACAGTGTGCTTGG 1920
Db 1969 GCGCTGTGGCTTCTTGGCAATGGAACCACTGTGAGAGCTTGAACAGTGTGCTTGG 2028
QY 1921 TCCCGGACATGTCTTCCACAGAGAGTGTGCTGTGTGCAACACTGAGCTGCTGCT 1980
Db 2029 TCCCGGACATGTCTTCCACAGAGAGTGTGCTGTGTGCAACACTGAGCTGCTGCT 2088
QY 1981 TCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 2089 TCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2148
QY 2041 AAGAGGCAAGAGGAAAGCAAGTGTGAGGCGGAGAAACCAATGCAAGAGCAAGAC 2100
Db 2149 AAGAGGCAAGAGGAAAGCAAGTGTGAGGCGGAGAAACCAATGCAAGAGCAAGAC 2208
QY 2101 ACAACTGCAAGAGAGCGGAGTGTGATCTTCTGAGGCACTTCAAGGAGCCCATGTACA 2160
Db 2209 ACAACTGCAAGAGAGCGGAGTGTGATCTTCTGAGGCACTTCAAGGAGCCCATGTACA 2268
QY 2161 AGTGCAGTGTGCAAGAGGCTTACGGGAGCAAGGCTCATTTCCGGGGAGAGACTCGAGAC 2220
Db 2269 AGTGCAGTGTGCAAGAGGCTTACGGGAGCAAGGCTCATTTCCGGGGAGAGACTCGAGAC 2328
QY 2221 TGAAGGCTGAGGCAACCTCAATGTGTGCTGCGCAACAGCGCACCTTACACTGTAC 2280
Db 2329 TGAAGGCTGAGGCAACCTCAATGTGTGCTGCGCAACAGCGCACCTTACACTGTAC 2388
QY 2281 AGGATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
Db 2389 AGGATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2448
QY 2341 GCGATGCTGTGATGATGAGCAATGATGATGATGATGATGATGATGATGATGATGATG 2400
Db 2449 GCGATGCTGTGATGATGAGCAATGATGATGATGATGATGATGATGATGATGATGATG 2508
QY 2401 AGCTCTCTTCAATCCCGGCAAGGCTGTGATGATGATGATGATGATGATGATGATGATG 2460
Db 2509 AGCTCTCTTCAATCCCGGCAAGGCTGTGATGATGATGATGATGATGATGATGATGATG 2568
QY 2461 ACAACTGCGCTTACGTGCAACACCTGCGCAGATGCAACAGACCAATGAGAGAGG 2520
Db 2569 ACAACTGCGCTTACGTGCAACACCTGCGCAGATGCAACAGACCAATGAGAGAGG 2628
QY 2521 ACAGCTGCTGCTGAGCAATGTGAGAGCAATGTTCAATGAAACGAGCAATTTGCTCT 2580
Db 2629 ACAGCTGCTGCTGAGCAATGTGAGAGCAATGTTCAATGAAACGAGCAATTTGCTCT 2688
QY 2581 ACAGCTGCAACATGCAACAGAGGAGCAAGATGTGAGGCTGTGAGGAGGATCACTGTG 2640
Db 2689 ACAGCTGCAACATGCAACAGAGGAGCAAGATGTGAGGCTGTGAGGAGGATCACTGTG 2748
QY 2641 ACTGCGCCCTGTGCAACACCTGACCAAGACGAGCTGTGCAATGATCACTTTGTTGGAG 2700
Db 2749 ACTGCGCCCTGTGCAACACCTGACCAAGACGAGCTGTGCAATGATCACTTTGTTGGAG 2808
QY 2701 AGTGTGAACAAGAGAGCAATGATGAGAGCGGCAACAGAACCAAGAGCAACAGCTGCC 2760
Db 2809 AGTGTGAACAAGAGAGCAATGATGAGAGCGGCAACAGAACCAAGAGCAACAGCTGCC 2868
QY 2761 CCTACATCTCCAAAGCAACAGGCTGATGACAGAGAGCGGCAAGGCTGCTGTG 2820
Db 2869 CCTACATCTCCAAAGCAACAGGCTGATGACAGAGAGCGGCAAGGCTGCTGTG 2928
QY 2821 ACCGTGATGATGACAGATGCGCTGCCAGTGAACAGGCAACACTGCGGCTGTGTCTA 2880

Chr	Position	Ref	Alt	Gene	Feature	Score	Strand	Quality	Filter	Variant Type	Annotation
2Y	5040	TTTGTGGTGGTTTGGTTTGGTTTGGTTTAAAGTTGCAATGATCTTTCTGCAGGAATAAGTCA		THBS2	coding	5099	+	30	0	SNP	5099
Db	5148	TTTGTGGTGGTTG-----GTTTTTTTGGTTTAAAGTTGCAATGATCTTTCTGCAGGAATAAGTCA		THBS2	coding	5203	+	30	0	SNP	5203
QY	5100	CTCATCCCACTCCACATCAAGGGGTTTAGTAAAGAGAAGTCTGTCTGCTCATGATGATGATAG		THBS2	coding	5159	+	30	0	SNP	5159
Db	5204	CTCATCCCACTCCACATCAAGGGGTTTAGTAAAGAGAAGTCTGTCTGCTCATGATGATGATAG		THBS2	coding	5263	+	30	0	SNP	5263
QY	5160	GGGGCAAACTTTTCCCTTCTCTGTTAATAGTACATCAAGTTTCTATGCGCAACACGGAAC		THBS2	coding	5219	+	30	0	SNP	5219
Db	5264	GGGGCAAACTTTTCCCTTCTCTGTTAATAGTACATCAAGTTTCTATGCGCAACACGGAAC		THBS2	coding	5323	+	30	0	SNP	5323
QY	5220	AAATCCATAACTTTAGTCTTAATGTACACATTCGATCTTTGTATAAAATAAATTTTGTGTTT		THBS2	coding	5279	+	30	0	SNP	5279
Db	5324	GATCCATAACTTTAGTCTTAATGTACACATTCGATCTTTGTATAAAATAAATTTTGTGTTT		THBS2	coding	5383	+	30	0	SNP	5383
QY	5280	CCTTTCAGGTTGATCGTTGTTGTTGTTTGTGTTGTTGTTGTTTACCTTTTTCGCTGTTGA		THBS2	coding	5339	+	30	0	SNP	5339
Db	5384	CCTTTCAGGTTGATCGTTGTTGTTGTTTGTGTTGTTGTTTACCTTTTTCGCTGTTGA		THBS2	coding	5440	+	30	0	SNP	5440
QY	5340	GCTGTATTCCGAGACCAACGAAGCGTTGGGATACCTTCAATAATGTAGCGACTGTCAAC		THBS2	coding	5399	+	30	0	SNP	5399
Db	5441	GCTGTATTCCGAGACCAACGAAGCGTTGGGATACCTTCAATAATGTAGCGACTGTCAAC		THBS2	coding	5499	+	30	0	SNP	5499
QY	5400	AGCGTCAGGTTTCTGTTTCTGTTGTTGGGTCACCGTCAAGTGGTGGGAGTGAC		THBS2	coding	5459	+	30	0	SNP	5459
Db	5500	AGCGTCAGGTTTCTGTTTCTGTTGTTGGGTCACCGTCAAGTGGTGGGAGTGAC		THBS2	coding	5559	+	30	0	SNP	5559
QY	5460	GATGATGTGAATATTAGAAATGACCAATATTTTGTGAAATATTTATGTTTCTTAAAC		THBS2	coding	5519	+	30	0	SNP	5519
Db	5560	GATGATGTGAATATTAGAAATGACCAATATTTTGTGAAATATTTATGTTTCTTAAAC		THBS2	coding	5619	+	30	0	SNP	5619
QY	5520	AAATTTATCGTATAGTTGATGAACGTCATGTTTTCGCAAGACTGTAAATATTTAT		THBS2	coding	5579	+	30	0	SNP	5579
Db	5620	AAATTTATCGTATAGTTGATGAACGTCATGTTTTCGCAAGACTGTAAATATTTAT		THBS2	coding	5679	+	30	0	SNP	5679
QY	5580	TTATGTTTCACATGTTCAAAATTTCCACCTGAAACCCCTGCCTTAGCTAGTAGAACCTCAT		THBS2	coding	5639	+	30	0	SNP	5639
Db	5680	TTATGTTTCACATGTTCAAAATTTCCACCTGAAACCCCTGCCTTAGCTAGTAGAACCTCAT		THBS2	coding	5739	+	30	0	SNP	5739
QY	5640	TTTTAAAGATTACACACAGGAATAAATTTGTAATAAAGGTTTTCT 5684		THBS2	coding	5684	+	30	0	SNP	5684
Db	5740	TTTTAAAGATTACACACAGGAATAAATTTGTAATAAAGGTTTTCT 5784		THBS2	coding	5784	+	30	0	SNP	5784

XX	13-MAR-2003.
PD	04-SEP-2002; 2002MO-US028113.
XX	05-SEP-2001; 2001US-0317178P.
XX	16-OCT-2001; 2001US-0329958P.
PR	14-DEC-2001; 2001US-0001772A.
XX	(VITI-) VITIVITY INC.
PA	Mccarthy J;
PI	WPI; 2003-300816/29.
XX	P-PSDB; AA36411.
DR	Identifying polymorphisms in thrombospondin 2, angiotensin converting
XX	enzyme and/or beta-fibrinogen genes in nucleic acid sample of subject, by
PT	contacting the nucleic acid with a complementary probe or primer.
PT	Claim 2; Fig 1; 194pp; English.
XX	The invention relates to a method for determining the identity of one or
XX	more allelic variants of a polymorphic region of a thrombospondin 2
CC	(THBS2), angiotensin converting enzyme (ACE)-1 and/or beta-fibrinogen
CC	(FGB) genes in a nucleic acid obtained from a subject. The method
CC	involves contacting the nucleic acid with a complementary probe or
CC	primer. The method is useful for diagnosing or aiding in the diagnosis of
CC	vascular disease or disorder in a subject e.g. myocardial infarction,
CC	coronary artery disease, atherosclerosis, ischaemia, stroke, peripheral
CC	vascular disease, venous thromboembolism and pulmonary embolism. The
CC	present sequence is human THBS2 reference DNA
XX	Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 U; 0 Other;
SQ	Query Match 97.9%; Score 5576.6; DB 8; Length 5784;
	Best Local Similarity 99.4%; Pred. No. 0;
	Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;
QY	1 GACTACGTCGCTGACGAGGCGCGGTCTCTCGCTCCAGCAGAGCCTGCGCCTTCTGAGTC 60
Db	109 GAGCATCTCGCTGCTGACGAGGCGCGGTCTCTCGCTCCAGCAGAGCCTGCGCCTTCTGAGTC 168
QY	61 GGTCGGAACTGTAAACCACTACATCACTGCATCTTTTGGCAACCAAGGAGCTCAGCTG 120
Db	169 GGTCGGAACTGTAAACCACTATCACTGCATCTTTTGGCAACCAAGGAGCTCAGCTG 228
QY	121 CAGGAGGCAGAGTGTCTGAGAGCTGGTCTCTGCTGGCTCTGTGGGTGTGGCCAGCAGC 180
Db	229 CAGGAGGCAGAGTGTCTGAGAGCTGGTCTCTGCTGGCTCTGTGGGTGTGGCCAGCAGC 288
QY	181 AAGTGTGTCAACGAGCAAGACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACC 240
Db	289 AAGTGTGTCAACGAGCAAGACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACC 348
QY	241 GCAAGACCATTTGGCGCCGCAAGCAGTTCCGCGGGCCCGAACCCCGGCTGCGGCTTACCGCT 300
Db	349 GCAAGACCATTTGGCGCCGCAAGCAGTTCCGCGGGCCCGAACCCCGGCTGCGGCTTACCGCT 408
QY	301 TCGTGGCTTTTGACTACATCCACCGGTGAAACGCAAGATGACCTCAGCAAGATCAACCAAGA 360
Db	409 TCGTGGCTTTTGACTACATCCACCGGTGAAACGCAAGATGACCTCAGCAAGATCAACCAAGA 468
QY	361 TCATGCGGCAAGAGGGGCTTTCTTCTCAACCGCCAGCTCAAGCAGGACGGCAAGTCCA 420
Db	469 TCATGCGGCAAGAGGGGCTTTCTTCTCAACCGCCAGCTCAAGCAGGACGGCAAGTCCA 528
QY	421 GGGGACGCTGTGGCTCTGGAGGGCCCGGCTCTCTCCAGAGGAGGTTCCAGATCGTCT 480
Db	529 GGGGACGCTGTGGCTCTGGAGGGCCCGGCTCTCTCCAGAGGAGGTTCCAGATCGTCT 588
QY	481 CCAACGGCCCGCGGACACGCTGGATCTCACTACTGGATTGACGGCACCGGCGATGGG 540

WO2003020118-A2.

589 CCAACGGCCCCGGGACACGCTGGATCTACCTACTGGATTGACGGCACCCCGGCATGTGG 648
541 TCTCCCTGGAGGACGTCGGGCTCGCTGACTCGCAGTGGAGAACGTCACCGTGCAGCTGG 600
649 TCTCCCTGGAGGACGTCGGGCTCGCTGACTCGCAGTGGAGAACGTCACCGTGCAGCTGG 708
601 CTGGCGAGACCTACAGCTTCGACGTGGGCTGGGCTGACCTCATAGACAGCTTCGCTCTGGAGC 660
709 CTGGCGAGACCTACAGCTTCGACGTGGGCTGGGCTGACCTCATAGACAGCTTCGCTCTGGAGC 768
661 AGCCCTTCTACGAGACCTCGACGCGGAAAGAGCGGATGTACGTGGCCCAAGGCTCTG 720
769 AGCCCTTCTACGAGACCTCGACGCGGAAAGAGCGGATGTACGTGGCCCAAGGCTCTG 828
721 CCAGAGAGAGCTACCTTCAGGGGTTTGTTCAGAAAGCTGCACCTAGTGTGTTGAAAACTCTG 780
829 CCAGAGAGAGCTACCTTCAGGGGTTTGTTCAGAAAGCTGCACCTAGTGTGTTGAAAACTCTG 888
781 TGGAGATATTTCTAAGCAAGAGGGTTGCCAGCAAGGCCAGGAGCTGAGATCAACGCCA 840
889 TGGAGATATTTCTAAGCAAGAGGGTTGCCAGCAAGGCCAGGAGCTGAGATCAACGCCA 948
841 TCAGTGAGAACACAGAGACGCTCGGCTCCGATGTCACCAAGGAGTACGTGGGCC 900
949 TCAGTGAGAACACAGAGACGCTCGGCTCCGATGTCACCAAGGAGTACGTGGGCC 1008
901 CCAGCTCAGAGAGGAGCCCGAGGTGCGAAGCTGCTGCGAGGAGCTGGGAAACATGS 960
1009 CCAGCTCAGAGAGGAGCCCGAGGTGCGAAGCTGCTGCGAGGAGCTGGGAAACATGS 1068
961 TCCAGGAGCTCTCGGGCTCCAGCTCTGTAACCCAGCTCAGCGAGAACCTCAAGAGAG 1020
1069 TCCAGGAGCTCTCGGGCTCCAGCTCTGTAACCCAGCTCAGCGAGAACCTCAAGAGAG 1128
1021 TGTGTAATGTAACAGTTCTCTGGAGCTCATTTGGTGCCCTCTAGACAGGAAACA 1080
1129 TGTGTAATGTAACAGTTCTCTGGAGCTCATTTGGTGCCCTCTAGACAGGAAACA 1188
1081 TGTGAGCTTGTGTCAGGATGGCGGTTCTTTGGGAAATGAAAGTGAGGTGGTGGACA 1140
1189 TGTGAGCTTGTGTCAGGATGGCGGTTCTTTGGGAAATGAAAGTGAGGTGGTGGACA 1248
1141 GCTGCACACGCTGACTGCAAGAAATTTAAACCAATTTGCCAACCAATCACCTGCGCCG 1200
1249 GCTGCACACGCTGACTGCAAGAAATTTAAACCAATTTGCCAACCAATCACCTGCGCCG 1308
1201 CTGCAACCTGCGCCAGTCCATCTTTGTGAAGCGGAATGCTGCGCTTCCTGCTCCACT 1260
1309 CTGCAACCTGCGCCAGTCCATCTTTGTGAAGCGGAATGCTGCGCTTCCTGCTCCACT 1368
1261 CGGTGAGCGGTGAGAGGGCTGCTCCGTGGGAGAGTGAGCCAGTGTCTCGTGACGT 1320
1369 CGGTGAGCGGTGAGAGGGCTGCTCCGTGGGAGAGTGAGCCAGTGTCTCGTGACGT 1428
1321 GTGGCTCTGGGACCCAGCAGAGAGGCGGCTCTGTGACGTCACAGCAACACCTGCTGG 1380
1429 GTGGCTCTGGGACCCAGCAGAGAGGCGGCTCTGTGACGTCACAGCAACACCTGCTGG 1488
1381 GGCCCTCCATCCAGACACGGGCTTGCAGTGTGACAAAGTGTGACCCGATCCGGCAGG 1440
1489 GGCCCTCCATCCAGACACGGGCTTGCAGTGTGACAAAGTGTGACCCGATCCGGCAGG 1548
1441 ACGGGCTGTGAGCCACTGCTACCTTGTGCTTCTATGCTCTGTGACCTGTGAGATTGGCA 1500
1549 ACGGGCTGTGAGCCACTGCTACCTTGTGCTTCTATGCTCTGTGACCTGTGAGATTGGCA 1608
1501 ATATCACACGATCCGTCTCTGCAACTCCCGAGTGGCCCGAGATGGGGGGCAAGATTGCA 1560
1609 ATATCACACGATCCGTCTCTGCAACTCCCGAGTGGCCCGAGATGGGGGGCAAGATTGCA 1668
1561 AAGGAGTGGCGGAGACCAAGGCTTGCAGGCGCCCGATCCCAATCGATGGCGGCT 1620
1669 AAGGAGTGGCGGAGACCAAGGCTTGCAGGCGCCCGATCCCAATCGATGGCGGCT 1728

QY 1621 GAGACCCCTGTCTCCCGTGTGGCTCGCTGCACTGTCACTGTGCTCCGCTGGATCCGGAGC 1680
Db 1729 GAGACCCCTGTCTCCCGTGTGGCTCGCTGCACTGTCACTGTGCTCCGCTGGATCCGGAGC 1788
QY 1681 GCACCCGGTCTGCAACAGCCCTGAGCTCAGTACGGAGGAGGAGCCCTGCTGGGGGATG 1740
Db 1789 GCACCCGGTCTGCAACAGCCCTGAGCTCAGTACGGAGGAGGAGCCCTGCTGGGGGATG 1848
QY 1741 TCCAGGACGCTCAGATGTGCAACAGAGGAGCTGCCCGCTGGATGGCTGTTTATCCAAAC 1800
Db 1849 TCCAGGACGCTCAGATGTGCAACAGAGGAGCTGCCCGCTGGATGGCTGTTTATCCAAAC 1908
QY 1801 CCTGCTCCCGGAGCCAGTGCAGAGCTTCCCGATGGTCTGCTGCTCATGCGGCTCT 1860
Db 1909 CCTGCTCCCGGAGCCAGTGCAGAGCTTCCCGATGGTCTGCTGCTCATGCGGCTCT 1968
QY 1861 GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGACGAGTGTGCCCTGG 1920
Db 1969 GCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGACGAGTGTGCCCTGG 2028
QY 1921 TCCCGGACATCTGCTTCTCCACCAAGAGTGCCTGCTGTGTCAACACTCAGCTGGCT 1980
Db 2029 TCCCGGACATCTGCTTCTCCACCAAGAGTGCCTGCTGTGTCAACACTCAGCTGGCT 2088
QY 1981 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 2089 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2148
QY 2041 AAGCAGCAGACGAGAAAGCAAGTGTGTGAGCCGCAAAACCCATGCAAGGACAGACAC 2100
Db 2149 AAGCAGCAGACGAGAAAGCAAGTGTGTGAGCCGCAAAACCCATGCAAGGACAGACAC 2208
QY 2101 ACACTGCTCACAAGCAGCAGGAGTGTCTACTGCGGCACTTCAAGGACCCCACTGTACA 2160
Db 2209 ACACTGCTCACAAGCAGCAGGAGTGTCTACTGCGGCACTTCAAGGACCCCACTGTACA 2268
QY 2161 AGTGCAGTGTGACAGAGCTTACGCGGCGAGCGGCTCATCTGCGGGGAGAGCTCGGACC 2220
Db 2269 AGTGCAGTGTGACAGAGCTTACGCGGCGAGCGGCTCATCTGCGGGGAGAGCTCGGACC 2328
QY 2221 TGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2329 TGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2388
QY 2281 AGGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
Db 2389 AGGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2448
QY 2341 GCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2449 GCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2508
QY 2401 AGCTCCTCTTCAATCCCGCAGGCTGACTATGACAGGATGAGGTTGGGACCCGCTGTG 2460
Db 2509 AGCTCCTCTTCAATCCCGCAGGCTGACTATGACAGGATGAGGTTGGGACCCGCTGTG 2568
QY 2461 ACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
Db 2569 ACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2628
QY 2521 AGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Db 2629 AGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2688
QY 2581 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
Db 2689 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2748
QY 2641 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
Db 2749 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2808

QY 2701 AGTGTGACAAACGAGGACATAGATGACGACGCGCCACAGAAACAACCGAGCAACTGCC 2760
 Db 2809 AGTGTGACAAACGAGGACATAGATGACGACGCGCCACAGAAACAACCGAGCAACTGCC 2868
 QY 2761 CCTACATCTCCAAACGCGCAACGAGCTGACCATGACAGAGCGCGCCAGGCGAGCGCTGTG 2820
 Db 2869 CCTACATCTCCAAACGCGCAACGAGCTGACCATGACAGAGCGCGCCAGGCGAGCGCTGTG 2928
 QY 2821 ACCCTGATGATGACAAACGATGGCGTCCCGATGACAGGGAACAACGCGCTTGTGTCA 2880
 Db 2929 ACCCTGATGATGACAAACGATGGCGTCCCGATGACAGGGAACAACGCGCTTGTGTCA 2988
 QY 2881 ACCCAGACCGAGGACTTGGACCGGTGATGAGCGGGGTGATTTGTAAGATGATTTTG 2940
 Db 2989 ACCCAGACCGAGGACTTGGACCGGTGATGAGCGGGGTGATTTGTAAGATGATTTTG 3048
 QY 2941 ACAATGACAAACATCCAGATATTGATGATGTGTCTCTGMAAAACAATGCCATCAGTGAGA 3000
 Db 3049 ACAATGACAAACATCCAGATATTGATGATGTGTCTCTGMAAAACAATGCCATCAGTGAGA 3108
 QY 3001 CAGACTTCAGGAACCTTCAGATGTCCTCCCTTGGATCCCAAGGAGCACCCCAATTCATC 3060
 Db 3109 CAGACTTCAGGAACCTTCAGATGTCCTCCCTTGGATCCCAAGGAGCACCCCAATTCATC 3168
 QY 3061 CCAACTGGGTGATTCGCCCATCAAGCGCAAGGAGCTGGTTTCAGACAGCCAACTCGGACCCCG 3120
 Db 3169 CCAACTGGGTGATTCGCCCATCAAGCGCAAGGAGCTGGTTTCAGACAGCCAACTCGGACCCCG 3228
 QY 3121 GCATCGCTGTAGTTTGAACAGATTTGGGTCTGTGGACTTCAGTGGGACATTCACGTAA 3180
 Db 3229 GCATCGCTGTAGTTTGAACAGATTTGGGTCTGTGGACTTCAGTGGGACATTCACGTAA 3288
 QY 3181 ACACCTGACCGGACGACGACTATGCGCGCTTCGTCTTTGGTTACAGTCAAGCAGCGCGCT 3240
 Db 3289 ACACCTGACCGGACGACGACTATGCGCGCTTCGTCTTTGGTTACAGTCAAGCAGCGCGCT 3348
 QY 3241 TCTATGCGGTGATGTGAAGCAGGTGAACGACACTCTAGGAGGACACGCCACGCGGG 3300
 Db 3349 TCTATGCGGTGATGTGAAGCAGGTGAACGACACTCTAGGAGGACACGCCACGCGGG 3408
 QY 3301 CCTATGGCTACTCCCGCGTGTCCCTCAAGGTGGTGAACCTCCACACCGGGGACGGCGAGC 3360
 Db 3409 CCTATGGCTACTCCCGCGTGTCCCTCAAGGTGGTGAACCTCCACACCGGGGACGGCGAGC 3468
 QY 3361 ACCTGAGGAAACGCGTGTGGACACGCGGAAACAGCGCGGGGACGGTGGCAACCTTATGGC 3420
 Db 3469 ACCTGAGGAAACGCGTGTGGACACGCGGAAACAGCGCGGGGACGGTGGCAACCTTATGGC 3528
 QY 3421 ACGACCCAGGAAACATTCGCTGGAAGGACTACCGGCTTATAGTGGCACTGACTCACA 3480
 Db 3529 ACGACCCAGGAAACATTCGCTGGAAGGACTACCGGCTTATAGTGGCACTGACTCACA 3588
 QY 3481 GGGCCAAAGCTGGCTACATCAGAGCTTTAGTGCATGAAGGAAACAGGTCAATGGCAGACT 3540
 Db 3589 GGGCCAAAGCTGGCTACATCAGAGCTTTAGTGCATGAAGGAAACAGGTCAATGGCAGACT 3648
 QY 3541 CAGGACCTATCTATGACCAACCTAGCTGGCGGGCGCTGGTCTATTTCTCTCTC 3600
 Db 3649 CAGGACCTATCTATGACCAACCTAGCTGGCGGGCGCTGGTCTATTTCTCTCTC 3708
 QY 3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGAGAGATATTTAAACAAGATTG 3660
 Db 3709 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGAGAGATATTTAAACAAGATTG 3768
 QY 3661 CTGCAATTCGGCAATGCCCTGTGATGCCATGGTCCCTAGACACCTCAGTTCATTTGG 3720
 Db 3769 CTGCAATTCGGCAATGCCCTGTGATGCCATGGTCCCTAGACACCTCAGTTCATTTGG 3828
 QY 3721 TCCCTGTGGCTTCTCTCTAGCAGACCTCCTGTGCTCCCTTGACCTTAACCTCTGATGTTTC 3780
 Db 3829 TCCCTGTGGCTTCTCTCTAGCAGACCTCCTGTGCTCCCTTGACCTTAACCTCTGATGTTTC 3888
 QY 3781 TTCACCTCTCGCAGCAACCCCAAGTGGCTTCAGAGGATAAATATCAATGGAC 3840

Db 3889 TTCACTCTCTCGCAGCAACCCCAACCCCAAGTGGCTTCAGAGGATAAATATCAATGGAC 3948
 QY 3841 GCAGAGATGAACATCTAAACCCACTAGAGAAACAGTTTGGTGATATATGAGACTTTATG 3900
 Db 3949 TCAGAGATGAACATCTAAACCCACTAGAGAAACAGTTTGGTGATATATGAGACTTTATG 4008
 QY 3901 TGGAGTGAATAATTTGGGCATGCCATTAATTCCTTTCTCTCTTTTGTGTTTAAAGAGATGAC 3960
 Db 4009 TGGAGTGAATAATTTGGGCATGCCATTAATTCCTTTCTCTCTTTTGTGTTTAAAGAGATGAC 4068
 QY 3961 GTTTACATATAAATGTAAATTTACTATTATTTATGTATATGAGCTTGAAGGGATA 4020
 Db 4069 GTTTACATATAAATGTAAATTTACTATTATTTATGTATATGAGCTTGAAGGGATA 4128
 QY 4021 CTGTGCATAGGCATATGATAAATTAAGCATGAAATAATTTGCTGAACACTTTTGGTG 4080
 Db 4129 CTGTGCATAGGCATATGATAAATTAAGCATGAAATAATTTGCTGAACACTTTTGGTG 4188
 QY 4081 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTTACAAATGACACACAATCCCGCTA 4140
 Db 4189 CTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTTACAAATGACACACAATCCCGCTA 4248
 QY 4141 AATAAATTATAAACAAGGCTCAATTTCAAAATTTGAAGTAAATGTTTTAGTAAGAGATTA 4200
 Db 4249 AATAAATTATAAACAAGGCTCAATTTCAAAATTTGAAGTAAATGTTTTAGTAAGAGATTA 4308
 QY 4201 GAAGACACAGCATAGCAAAATGACATAAGCTACCGATTAACTAAATCGAAATGTAATAA 4260
 Db 4309 GAAGACACAGCATAGCAAAATGACATAAGCTACCGATTAACTAAATCGAAATGTAATAA 4368
 QY 4261 CAGTTACAAAATAAACAAGACTCTCTCTTGTCTTAAAGTTAGCAGAAAGCCCTCATGTGAGTA 4320
 Db 4369 CAGTTACAAAATAAACAAGACTCTCTCTTGTCTTAAAGTTAGCAGAAAGCCCTCATGTGAGTA 4428
 QY 4321 GAGATGCGAGTTTCATCAAGAAACAACATCTCTGCAAAATGGGTGTGATCGCGTTCCAGAT 4380
 Db 4429 GAGATGCGAGTTTCATCAAGAAACAACATCTCTGCAAAATGGGTGTGATCGCGTTCCAGAT 4488
 QY 4381 GTGGATTTGGCAAAACCTCAATTTAAGTAAAGTTAGCAGAAAGTTGCGGTGCTTTAG 4440
 Db 4489 GTGGATTTGGCAAAACCTCAATTTAAGTAAAGTTAGCAGAAAGTTGCGGTGCTTTAG 4548
 QY 4441 CTGCTGCTTGTGCGCTGTGCTGCGGGAGCTCTCTGCTGAGCTTCTCTCCCGAGCTT 4500
 Db 4549 CTGCTGCTTGTGCGCTGTGCTGCGGGAGCTCTCTGCTGAGCTTCTCTCCCGAGCTT 4608
 QY 4501 TGTGCTCTGAGAGGAAACAGAGCAGACGCGCGGAAAGGCGCATCTAAACCGCTAT 4560
 Db 4609 TGTGCTCTGAGAGGAAACAGAGCAGACGCGCGGAAAGGCGCATCTAAACCGCTAT 4668
 QY 4561 CTAGGCTTTGGTAACTGCGGCAAGTTGCTTTTACTGATTTGATGATACATTTCCATTAA 4620
 Db 4669 CTAGGCTTTGGTAACTGCGGCAAGTTGCTTTTACTGATTTGATGATACATTTCCATTAA 4728
 QY 4621 GGTTCCAGTTATAAATAATTTGTTAATATTTAATTAAGTACATATAGAATGCAACTCCATT 4680
 Db 4729 GGTTCCAGTTATAAATAATTTGTTAATATTTAATTAAGTACATATAGAATGCAACTCCATT 4788
 QY 4681 TACCAGTAACTTATTTAAATATGCTAGTAAACATATGTTAGTATATTTCTAGAAACA 4740
 Db 4789 TACCAGTAACTTATTTAAATATGCTAGTAAACATATGTTAGTATATTTCTAGAAACA 4848
 QY 4741 AACATCTAATAGTATATAATCTGTGAAATAATGAGGCTTCATATAATTTAGTTGTCAAC 4800
 Db 4849 AACATCTAATAGTATATAATCTGTGAAATAATGAGGCTTCATATAATTTAGTTGTCAAC 4908
 QY 4801 GATGAAGCATGCTAGAGCTGTAAACAGAAATACATAGAGAAATAGAGGAGTTTATGAGG 4860
 Db 4909 GATGAAGCATGCTAGAGCTGTAAACAGAAATACATAGAGAAATAGAGGAGTTTATGAGG 4968
 QY 4861 AACCTTAAATATATAATTTGCCAGCGATTTTGTAGTTCAATATTTGTACTGTATCTATC 4920

Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;			
QY	1	GACTACGTCGACCTGACGGCGGGTCTCTCGCTCCAGCAGCGCTGGCGCTTCTGACTC	60
Db	109	GAGCATCTGACCTGACGCGCGGTCTCTGCTCCAGCAGAGCTGGCGCTTCTGACTC	168
QY	61	GGTCGGAACTGAAACCACTGATCATCTGATCTTTTGGCAACCAAGAGCTCAGCTG	120
Db	169	GGTCGGAACTGAAACCACTGATCATCTGATCTTTTGGCAACCAAGAGCTCAGCTG	228
QY	121	CAGGAGGAGGATGGTCTGGAGGGTGGTCTGCTGGCTCTGTGGCTGTGGCCAGCAGC	180
Db	229	CAGGAGGAGGATGGTCTGGAGGGTGGTCTGCTGGCTCTGTGGCTGTGGCCAGCAGC	288
QY	181	AAGCTGGTCAACAGAGCAAAAGACAGCTTCGACCTTTTCAGTATCAGCAATCAACC	240
Db	289	AAGCTGGTCAACAGAGCAAAAGACAGCTTCGACCTTTTCAGTATCAGCAATCAACC	348
QY	241	GCAAGACATTTGGCGCCCAAGCAGTTCCGCGGCGCGACCCCGGGTTCGCGCTTACCGCT	300
Db	349	GCAAGACATTTGGCGCCCAAGCAGTTCCGCGGCGCGACCCCGGGTTCGCGCTTACCGCT	408
QY	301	TCGTGCGCTTTGACTACATCCCAACCGGTGAACGAGATGACCTCAGCAAGATCAACGA	360
Db	409	TCGTGCGCTTTGACTACATCCCAACCGGTGAACGAGATGACCTCAGCAAGATCAACGA	468
QY	361	TCATCGCGCAGAGAGAGGCTTCTTCCTCAGCGGCCAGCTCAAGCAGAGCGCAAGTCCA	420
Db	469	TCATCGCGCAGAGAGAGGCTTCTTCCTCAGCGGCCAGCTCAAGCAGAGCGCAAGTCCA	528
QY	421	GGGGCAGCTGTGTGCTCTGAGAGGCGCGGTCTCTCCAGAGCAGTTCGAGATCGTCT	480
Db	529	GGGGCAGCTGTGTGCTCTGAGAGGCGCGGTCTCTCCAGAGCAGTTCGAGATCGTCT	588
QY	481	CCAGCGGCGCGGACAGCTGATGATCTCACTCTGATTTGAGCGACCGCGCATGTGG	540
Db	589	CCAGCGGCGCGGACAGCTGATGATCTCACTCTGATTTGAGCGACCGCGCATGTGG	648
QY	541	TCCTCCTGGAGACGTGCGCTGGTGTGACTCGCAGTGGAAAGACGTCAACGTGACGTGG	600
Db	649	TCCTCCTGGAGACGTGCGCTGGTGTGACTCGCAGTGGAAAGACGTCAACGTGACGTGG	708
QY	601	CTGGCGACCTACAGCTTGACAGTGGCTGGACCTCATAGACAGCTTCGCTCTGACG	660
Db	709	CTGGCGACCTACAGCTTGACAGTGGCTGGACCTCATAGACAGCTTCGCTCTGACG	768
QY	661	AGCCCTTCTACAGACCTGACGCGGAAAGAGCCGGATGATCGTGGCCAAAGGCTCTG	720
Db	769	AGCCCTTCTACAGACCTGACGCGGAAAGAGCCGGATGATCGTGGCCAAAGGCTCTG	828
QY	721	CCAGAGAGTCACTTACAGGGTTTCTTCAGAGCTCCACTAGTGTTCGAAACTCTG	780
Db	829	CCAGAGAGTCACTTACAGGGTTTCTTCAGAGCTCCACTAGTGTTCGAAACTCTG	888
QY	781	TGGAAGATATTCTAAGCAAGAGGGTTGCCAGCAAGGCGGAGCTGAGATCAACGCCA	840
Db	889	TGGAAGATATTCTAAGCAAGAGGGTTGCCAGCAAGGCGGAGCTGAGATCAACGCCA	948
QY	841	TCAGTGAAGACACAGAGAGCTGGCCCTGGTTCGATGTCAACCGAGTACGTGGCC	900
Db	949	TCAGTGAAGACACAGAGAGCTGGCCCTGGTTCGATGTCAACCGAGTACGTGGCC	1008
QY	901	CCAGCTCAGAGAGGAGGCGGAGGTGTGCAACGCTCGTGGAGAGCTGGGAAACATGG	960
Db	1009	CCAGCTCAGAGAGGAGGCGGAGGTGTGCAACGCTCGTGGAGAGCTGGGAAACATGG	1068
QY	961	TCAGAGGCTTCGGGGTTCACGTCTCGTGAACCAAGCTCAGCGAGAACCTCAAGAGAG	1020
Db	1069	TCAGAGGCTTCGGGGTTCACGTCTCGTGAACCAAGCTCAGCGAGAACCTCAAGAGAG	1128
QY	1021	TGTCGAATGATTAACAGTTCTCTGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGAACA	1080
Db	1129	TGTCGAATGATTAACAGTTCTCTGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGAACA	1188

QY	1081	TGTACGTTGTGCGCAGGATGCGCGTTCTTTTGGGAAAAATGAAACGTGGGTGTGGACA	1140
Db	1189	TGTACGTTGTGCGCAGGATGCGCGTTCTTTTGGGAAAAATGAAACGTGGGTGTGGACA	1248
QY	1141	GCTGCACACAGTGTACCTGCAAGAAATTTAAACCATTTGCCACCAATACCTTCCCGC	1200
Db	1249	GCTGCACACAGTGTACCTGCAAGAAATTTAAACCATTTGCCACCAATACCTTCCCGC	1308
QY	1201	CTGCAACCTGCGCCAGTCCATCTTTTGGAGGCAATGTGCGCTTCTTCCCTCCACT	1260
Db	1309	CTGCAACCTGCGCCAGTCCATCTTTTGGAGGCAATGTGCGCTTCTTCCCTCCACT	1368
QY	1261	CGGTGACCGGTGAGAGGGCTTCTCGTGGGAGAGTGGACCCAGTCTCCGTGACGT	1320
Db	1369	CGGTGACCGGTGAGAGGGCTTCTCGTGGGAGAGTGGACCCAGTCTCCGTGACGT	1428
QY	1321	GTGGCTCTGGGACCCAGCAGAGAGCGGTCTCTGTGACGTCAACAGCAACACCTCTTGG	1380
Db	1429	GTGGCTCTGGGACCCAGCAGAGAGCGGTCTCTGTGACGTCAACAGCAACACCTCTTGG	1488
QY	1381	GGCCTTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGATCCGGCAGG	1440
Db	1489	GGCCTTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGATCCGGCAGG	1548
QY	1441	ACGGGGCTTGGAGCCACTGGTCACTTGTCTCTTCAATGTGTGACCTGTGGAGTTGCA	1500
Db	1549	ACGGGGCTTGGAGCCACTGGTCACTTGTCTCTTCAATGTGTGACCTGTGGAGTTGCA	1608
QY	1501	ATATCACAGCATCGTCTCTGCAACTCCCGAGTCCCGAGTGGGGGGCAAGATTGCA	1560
Db	1609	ATATCACAGCATCGTCTCTGCAACTCCCGAGTCCCGAGTGGGGGGCAAGATTGCA	1668
QY	1561	AAGGGAGTGGCGGAGACCAAGAGCTTGCAGGGGCGCCCATGSCCAATTCGATGGCGCT	1620
Db	1669	AAGGGAGTGGCGGAGACCAAGAGCTTGCAGGGGCGCCCATGSCCAATTCGATGGCGCT	1728
QY	1621	GAGGCCCTTGGTCCCGTGGTCCGCTGCACTGTCACTGTGCGGTGGGATCCGGGAGC	1680
Db	1729	GAGGCCCTTGGTCCCGTGGTCCGCTGCACTGTCACTGTGCGGTGGGATCCGGGAGC	1788
QY	1681	GACACCGGCTGTGCAACAGCCCTGAGCCTCAGTAGCGGAGGAGGCTTCCGTGGGGATG	1740
Db	1789	GACACCGGCTGTGCAACAGCCCTGAGCCTCAGTAGCGGAGGAGGCTTCCGTGGGGATG	1848
QY	1741	TGACAGAGCGTCAGATGTGCAACAGAGAGCTGCCCCGTGATGCTGTTTATCAACC	1800
Db	1849	TGACAGAGCGTCAGATGTGCAACAGAGAGCTGCCCCGTGATGCTGTTTATCAACC	1908
QY	1801	CCTGTCTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTTGGTCATGCGCTCT	1860
Db	1909	CCTGTCTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTTGGTCATGCGCTCT	1968
QY	1861	GCCCTGTGGCTTCTTGGGCAATGGCAACCACTGTGAGGACCTGACAGTGTGCCCTGG	1920
Db	1969	GCCCTGTGGCTTCTTGGGCAATGGCAACCACTGTGAGGACCTGACAGTGTGCCCTGG	2028
QY	1921	TCCCGACATCTGCTTCTCCACAGCAGGCTGCTGCTGTGCTCAACTCAGCTTGGCT	1980
Db	2029	TCCCGACATCTGCTTCTCCACAGCAGGCTGCTGCTGTGCTCAACTCAGCTTGGCT	2088
QY	1981	TCCACTTGCCTTCCCGCCCGCCGATACAGAGGAAACACGCCCTGCGGGTGGCGCTGG	2040
Db	2089	TCCACTTGCCTTCCCGCCCGCCGATACAGAGGAAACACGCCCTGCGGGTGGCGCTGG	2148
QY	2041	AAGCAGCAAGCGGAAGCAAGTGTGTGAGCCGGAACCCATGCAAGGCAAGACAC	2100
Db	2149	AAGCAGCAAGCGGAAGCAAGTGTGTGAGCCGGAACCCATGCAAGGCAAGACAC	2208
QY	2101	ACAACCTGCCACAGCAGCGGAGTGCATCTACTGGGCGCACTTACGCGACCCCATGTACA	2160
Db	2209	ACAACCTGCCACAGCAGCGGAGTGCATCTACTGGGCGCACTTACGCGACCCCATGTACA	2268

2161 AGTGGAGTCCAGACAGGCTACGCGGGGACGGGCTCATCTGCGGGGAGGACTCGGACC 2220 Db
2269 AGTGGAGTCCAGACAGGCTACGCGGGGACGGGCTCATCTGCGGGGAGGACTCGGACC 2328 Qy
2221 TGGACGGCTGGCCCAACCTCAATCTGGTCTGCGCCACCAACGCACTTACCACTGCAATCA 2280 Db
2329 TGGACGGCTGGCCCAACCTCAATCTGGTCTGCGCCACCAACGCACTTACCACTGCAATCA 2388 Qy
2281 AGGATAACTGCCCCCACTCCGCAAACTCTGGGAGGAGGACTTTGACAGGAGCGGATG 2340 Db
2389 AGGATAACTGCCCCCACTCCGCAAACTCTGGGAGGAGGACTTTGACAGGAGCGGATG 2448 Qy
2341 GCGATGCTGTGATGATGACGATGACAAATGACGATGACCGGATGAGAAAGCAACTGCC 2400 Db
2449 GCGATGCTGTGATGATGACGATGACAAATGACGATGACCGGATGAGAAAGCAACTGCC 2508 Qy
2401 AGCTCTCTTTCAATCCCGGACGCTGACTATGACAGGATGAGGTTGGGGACCGCTGG 2460 Db
2509 AGCTCTCTTTCAATCCCGGACGCTGACTATGACAGGATGAGGTTGGGGACCGCTGG 2568 Qy
2461 ACAACTGCCCTTACGTGCACAAACCTGCCAGATCGACACAGACAAATGGAGAGGGTG 2520 Db
2569 ACAACTGCCCTTACGTGCACAAACCTGCCAGATCGACACAGACAAATGGAGAGGGTG 2628 Qy
2521 ACGCTGCTCGTGGACATTTGATGGGACAGATGTCTTCAATGACAGACAAATGTCCT 2580 Db
2629 ACGCTGCTCGTGGACATTTGATGGGACAGATGTCTTCAATGACAGACAAATGTCCT 2688 Qy
2581 ACGTCTAACACTGACACAGGAGACAGGATGGTGACGGTGTGGGGATCACTGTGACA 2640 Db
2689 ACGTCTAACACTGACACAGGAGACAGGATGGTGACGGTGTGGGGATCACTGTGACA 2748 Qy
2641 ACTGCCCTCGTGGACAAACCTGACACAGACCGACGCTGGGACCTTTGTTGGGGACC 2700 Db
2749 ACTGCCCTCGTGGACAAACCTGACACAGACCGACGCTGGGACCTTTGTTGGGGACC 2808 Qy
2701 AGTGTGACAAACAGGACATGATGACAGCGGCCACCAAGAACACAGGACAACTGCC 2760 Db
2809 AGTGTGACAAACAGGACATGATGACAGCGGCCACCAAGAACACAGGACAACTGCC 2868 Qy
2761 CCTACATCTCCAAACGCAACAGGCTGACCAATGACAGACCGGCGAGCGCTGGT 2820 Db
2869 CCTACATCTCCAAACGCAACAGGCTGACCAATGACAGACCGGCGAGCGCTGGT 2928 Qy
2821 ACCCTGATGATGACAAAGATGGCTGCCGATGACAGGCACTGCCGCTGTGTGTTCA 2880 Db
2929 ACCCTGATGATGACAAAGATGGCTGCCGATGACAGGCACTGCCGCTGTGTGTTCA 2988 Qy
2881 ACCCAGACCCAGGAGCTTGGACGGTGTGATGACGGGGTGATTTGTAAGATGATTTG 2940 Db
2989 ACCCAGACCCAGGAGCTTGGACGGTGTGATGACGGGGTGATTTGTAAGATGATTTG 3048 Qy
2941 ACAATGACAACTCCAGATATTGATGATGATGCTGCTGAAACAATGCCATCAGTGAGA 3000 Db
3049 ACAATGACAACTCCAGATATTGATGATGATGCTGCTGAAACAATGCCATCAGTGAGA 3108 Qy
3001 CAGACTTCAGGAACTTCAGATGGTCCCTTGGATCCCAAGGAGCACCCCAATTTGATC 3060 Db
3109 CAGACTTCAGGAACTTCAGATGGTCCCTTGGATCCCAAGGAGCACCCCAATTTGATC 3168 Qy
3061 CCACTGGGTGATTCGCCATCAAGCAAGGAGCTGGTTGACAGAGCCAACTCGGACCCCG 3120 Db
3169 CCACTGGGTGATTCGCCATCAAGCAAGGAGCTGGTTGACAGAGCCAACTCGGACCCCG 3228 Qy
3121 GCATCGCTGTAGTTTTCAGAGTTTGGGTCTGGACTTCAGTGGGACATTTCTACGTAA 3180 Db
3229 GCATCGCTGTAGTTTTCAGAGTTTGGGTCTGGACTTCAGTGGGACATTTCTACGTAA 3288 Qy
3181 ACACCTGACGGGACGACGACTATGCGCGCTTCGCTTTGGTTTACAGTCAAGCAGCGCT 3240 Db
3289 ACACCTGACGGGACGACGACTATGCGCGCTTCGCTTTGGTTTACAGTCAAGCAGCGCT 3348 Qy
3241 TCTATGTGTGATGTGGAAGAGGAGGACGACGACCTACTGCGGAGGACCAAGCCACGCGGG 3300

3349 TCTATGTGTGATGTGGAAGCAGAGTGACGAGCTACTTGGAGGACCAAGCCACGCGGG 3408 Db
3301 CCTATGCTACTCCGGGCTGTCCTCAAGTGGTGAACCTCCACCACGGGACGGCGAGC 3360 Qy
3409 CCTATGCTACTCCGGGCTGTCCTCAAGTGGTGAACCTCCACCACGGGACGGCGAGC 3468 Db
3361 ACCTGAGGAAACGCGCTGTGGCACACGGGGAACACGCGGGGACAGGTGCGAACCTTTATGGC 3420 Qy
3469 ACCTGAGGAAACGCGCTGTGGCACACGGGGAACACGCGGGGACAGGTGCGAACCTTTATGGC 3528 Db
3421 ACGACCCAGGAAACATTTGGCTGGAAGGACTACAGGCGCTATAGTGGCAGCTGACTCACA 3480 Qy
3529 ACGACCCAGGAAACATTTGGCTGGAAGGACTACAGGCGCTATAGTGGCAGCTGACTCACA 3588 Db
3481 GGCCCAAGACTTGGCTTACATCAGAGTCTTAGTGCAATGAAGGAAAAACAGGTGATGCGAGCT 3540 Qy
3589 GGCCCAAGACTTGGCTTACATCAGAGTCTTAGTGCAATGAAGGAAAAACAGGTGATGCGAGCT 3648 Db
3541 CAGGACCTTATCTATGACCAAAACCTACGCTGGCGGGCGGCTGGGTCTATTTGCTCTCTC 3600 Qy
3649 CAGGACCTTATCTATGACCAAAACCTACGCTGGCGGGCGGCTGGGTCTATTTGCTCTCTC 3708 Db
3601 AAGAAATGCTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTG 3660 Qy
3709 AAGAAATGCTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTG 3768 Db
3661 CTGCAATTCGGGCAATGCGCTGTGATGCGCATGGTCCCTAGACACCTCAGTTCATTTGGG 3720 Qy
3769 CTGCAATTCGGGCAATGCGCTGTGATGCGCATGGTCCCTAGACACCTCAGTTCATTTGGG 3828 Db
3721 TCCTTGTGGCTTCTCTCTAGCAGCCTCCTGTGCTTACCTTACCTTAACTCTGATGGTTC 3780 Qy
3829 TCCTTGTGGCTTCTCTCTAGCAGCCTCCTGTGCTTACCTTAACTCTGATGGTTC 3888 Db
3781 TTCACTCTCTGCCAGCAACCCCAACCCCAAGTGCCTCAGAGGATAAATATCAATGGAAC 3840 Qy
3889 TTCACTCTCTGCCAGCAACCCCAACCCCAAGTGCCTCAGAGGATAAATATCAATGGAAC 3948 Db
3841 GCAGAGATGACATCTTAAACCACTAGAGGAAACAGTTTGGTGATATATGAGACTTTATG 3900 Qy
3949 TCAGAGATGACATCTTAAACCACTAGAGGAAACAGTTTGGTGATATATGAGACTTTATG 4008 Db
3901 TGGAGTGAATTTGGGCAATGCAATTTACATTTCTTTCTTTCTTTTAAAGAAATGAC 3960 Qy
4009 TGGAGTGAATTTGGGCAATGCAATTTACATTTCTTTCTTTCTTTTAAAGAAATGAC 4068 Db
3961 GTTTACATATAAATGTAATTTACTTTTGTATTTATGTTATATGAGTTGAGGGAATA 4020 Qy
4069 GTTTACATATAAATGTAATTTACTTTTGTATTTATGTTATGTTATGAGTTGAGGGAATA 4128 Db
4021 CTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATATTGCTGAACACTACTTTTGGTG 4080 Qy
4129 CTGTGCATAAGCCATTATGATAAATTAAGCATGAAAAATATTGCTGAACACTACTTTTGGTG 4188 Db
4081 CTTAAAGTTGCACTATTCTTGAATTAGAGTTGCTCTCAATGACACACAATCCCGTA 4140 Qy
4189 CTTAAAGTTGCACTATTCTTGAATTAGAGTTGCTCTCAATGACACACAATCCCGTA 4248 Db
4141 AATAAATTATAACCAAGGTCATTTCAAAATTGAAGTAATGTTTGTAGTAAGGAGATTA 4200 Qy
4249 AATAAATTATAACCAAGGTCATTTCAAAATTGAAGTAATGTTTGTAGTAAGGAGATTA 4308 Db
4201 GAAGCAACAGGCAATAGCAATGACATGCTAACCGATTAACTAATCGGAACATGTAAAA 4260 Qy
4309 GAAGCAACAGGCAATAGCAATGACATGCTAACCGATTAACTAATCGGAACATGTAAAA 4368 Db
4261 CAGTTACAAAAATAACGAACCTCTCTTGTCTTCAATGAAGCCCTCATGTGCACTA 4320 Qy
4369 CAGTTACAAAAATAACGAACCTCTCTTGTCTTCAATGAAGCCCTCATGTGCACTA 4428 Db
4321 GAGATGCAATTTTCAATCAAGAAACAAACATCTTGCATAATGGGTGTGATGCGGTTCCAGAT 4380 Qy

QY 1 GACTACGCTGCACTGACGGCGGCTCTCTCGCTCCAGCAGAGCCTGGCCCTTCTGACTC 60
 DB 109 GAGCATCTGCACTGACGGCGGCTCTCTCGCTCCAGCAGAGCCTGGCCCTTCTGACTC 168
 QY 61 GGTCCGGAACACTGAAACAGTCACTGATCTTTTGGCAAAACAGAGACTCAGCTG 120
 DB 169 GGTCCGGAACACTGAAACAGTCACTGATCTTTTGGCAAAACAGAGACTCAGCTG 228
 QY 121 CAGGAGGAGGATGGTCTGGAAGGCTGGTCTCTGCTGGCTCTCTGGGTGTGGCCACAGCAGC 180
 DB 229 CAGGAGGAGGATGGTCTGGAAGGCTGGTCTCTGCTGGCTCTCTGGGTGTGGCCACAGCAGC 288
 QY 181 AAGCTGGTCAACAGAAAGACAGAGCTTTCGACCTTTTTCAGTATCAGGAAATCAACC 240
 DB 289 AAGCTGGTCAACAGAAAGACAGAGCTTTCGACCTTTTTCAGTATCAGGAAATCAACC 348
 QY 241 GCAAGACATTGGGCGCAAGCAGTTCCGCGGCGCGACCCCGGGCTGCGGCTTACCGCT 300
 DB 349 GCAAGACATTGGGCGCAAGCAGTTCCGCGGCGCGACCCCGGGCTGCGGCTTACCGCT 408
 QY 301 TCGTGGCTTTGACTATACATCCACCGGTGAACGAGATGACTCAGCAAGATCAACGA 360
 DB 409 TCGTGGCTTTGACTATACATCCACCGGTGAACGAGATGACTCAGCAAGATCAACGA 468
 QY 361 TCATGCGCAGAGAGAGGCTTCTCTCAGCGCCAGCTCAAGCAGAGCGGCAAGTCCA 420
 DB 469 TCATGCGCAGAGAGAGGCTTCTCTCAGCGCCAGCTCAAGCAGAGCGGCAAGTCCA 528
 QY 421 GGGCAGCCTGTGGCTCTGAGAGGCGCCGCTCTCTCCAGAGCAGTTCGAGATCGTCT 480
 DB 529 GGGCAGCCTGTGGCTCTGAGAGGCGCCGCTCTCTCCAGAGCAGTTCGAGATCGTCT 588
 QY 481 CCAGCGCCCGCGGACACGCTGATCTCACTACTGATGAGCGGACCGGCAATGTGG 540
 DB 589 CCAGCGCCCGCGGACACGCTGATCTCACTACTGATGAGCGGACCGGCAATGTGG 648
 QY 541 TCTCCCTGGAGAGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 DB 649 TCTCCCTGGAGAGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
 QY 601 CTGGGAGACCTACAGCTTGACGCTGGCTGCGACCTCATAGACAGCTTCTGCTCTGACG 660
 DB 709 CTGGGAGACCTACAGCTTGACGCTGGCTGCGACCTCATAGGACCAAGTCTCTGACG 768
 QY 661 AGCCCTTCTAGCAGACCTGACGCGGAAAGAGCCGATGTAGCTGGCCAAAGGCTCTG 720
 DB 769 AGCCCTTCTAGCAGACCTGACGCGGAAAGAGCCGATGTAGCTGGCCAAAGGCTCTG 828
 QY 721 CCAGAGAGTCACTTACAGGCTTGTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 DB 829 CCAGAGAGTCACTTACAGGCTTGTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
 QY 781 TGGAGATATTCTAAGCAAGAGGTTGCCAGCAAGGCGGAGCTGAGATCAAGCCCA 840
 DB 889 TGGAGATATTCTAAGCAAGAGGTTGCCAGCAAGGCGGAGCTGAGATCAAGCCCA 948
 QY 841 TCAGTGAGAACACAGAGAGCTGCGCTGGTCCGCAATGTACACCCAGTACGTGGGCC 900
 DB 949 TCAGTGAGAACACAGAGAGCTGCGCTGGTCCGCAATGTACACCCAGTACGTGGGCC 1008
 QY 901 CCAGCTCAGAGAGGAGGCGGAGGCTGCGAAAGCTGCTGGAGGAGCTGGGAACATGG 960
 DB 1009 CCAGCTCAGAGAGGAGGCGGAGGCTGCGAAAGCTGCTGGAGGAGCTGGGAACATGG 1068
 QY 961 TCCAGGAGCTCTCGGGGCTCCAGCTCTCTGTAACCAAGCTCAGCGAGAACTCAAGAGAG 1020
 DB 1069 TCCAGGAGCTCTCGGGGCTCCAGCTCTCTGTAACCAAGCTCAGCGAGAACTCAAGAGAG 1128
 QY 1021 TGTCAAGTAAACAGATTTCTTGGAGGCTCATTTGTTGGCCCTTCAAGCAAGGAACA 1080
 DB 1129 TGTCAAGTAAACAGATTTCTTGGAGGCTCATTTGTTGGCCCTTCAAGCAAGGAACA 1188
 QY 1081 TGTCAAGTGTGGCAGGATGGCGGCTTCTTTGGGGAATAAGAAAGTGGGTGGTGACA 1140

DB 1189 TGTCAAGTGTGGCAGGATGGCGGTTCTTTTGGGAAATGAACGCTGGGTGGTGACA 1248
 QY 1141 GCTGCACACGCTGACCTGCAAGAAATTTAAACCAATTTGCCACCAATCAGCTGCCGCG 1200
 DB 1249 GCTGCACACGCTGACCTGCAAGAAATTTAAACCAATTTGCCACCAATCAGCTGCCGCG 1308
 QY 1201 CTGCAACCTTGCCGCAAGTCCATCTTTTGGAGGGAATGCTGCGCTTCTCTGCTCCACT 1260
 DB 1309 CTGCAACCTTGCCGCAAGTCCATCTTTTGGAGGGAATGCTGCGCTTCTCTGCTCCACT 1368
 QY 1261 CGGTGACGCTGAGGAGGCTGGTCTCGGTGGGAGAGTGGACCCAGTCTCGGTGACGT 1320
 DB 1369 CGGTGACGCTGAGGAGGCTGGTCTCGGTGGGAGAGTGGACCCAGTCTCGGTGACGT 1428
 QY 1321 GTGGCTCTGGGACCCAGCAGAGAGGCGGCTCTGTGAGCTCACCAGCAACACCTCTTGG 1380
 DB 1429 GTGGCTCTGGGACCCAGCAGAGAGGCGGCTCTGTGAGCTCACCAGCAACACCTCTTGG 1488
 QY 1381 GGGCTCTCATCCAGACACAGGCTTTCAGTCTGAGCAAGTGTGACACCCGATCCGGCAGG 1440
 DB 1489 GGGCTCTCATCCAGACACAGGCTTTCAGTCTGAGCAAGTGTGACACCCGATCCGGCAGG 1548
 QY 1441 ACGCGGCTGGAGGCACTGGTCACTTGGTCTTCTGATCTCTGTGACCTGTGGAGTTGCA 1500
 DB 1549 ACGCGGCTGGAGGCACTGGTCACTTGGTCTTCTGATCTCTGTGACCTGTGGAGTTGCA 1608
 QY 1501 ATATCAGACGATCCGCTCTGTCAACTCCCAAGTCCCAAGTGGGGGCAAGAAATGCA 1560
 DB 1609 ATATCAGACGATCCGCTCTGTCAACTCCCAAGTCCCAAGTGGGGGCAAGAAATGCA 1668
 QY 1561 AAGGAGTGGCGGAGAGCAAGGCTTCCAGGGGCGCCCATGCCCAATCATGATGCCGCT 1620
 DB 1669 AAGGAGTGGCGGAGAGCAAGGCTTCCAGGGGCGCCCATGCCCAATCATGATGCCGCT 1728
 QY 1621 GAGGCCCTTGGTCCCGCTGGTGGCTTGCAGTCTCACTGTCACTGTGCTGCTGGGATCCGGGAGC 1680
 DB 1729 GAGGCCCTTGGTCCCGCTGGTGGCTTGCAGTCTCACTGTCACTGTGCTGCTGGGATCCGGGAGC 1788
 QY 1681 GCACCGGCTTGCACACGCTTGCAGCTTGCAGTACGAGGAGGAGGCTGCTGCTGGGGATG 1740
 DB 1789 GCACCGGCTTGCACACGCTTGCAGCTTGCAGTACGAGGAGGAGGCTGCTGCTGGGGATG 1848
 QY 1741 TCCAGGAGCTCAGATGTGCAACAGAGAGGAGCTGCTGCTGGTGGATGGCTTATCAAACC 1800
 DB 1849 TCCAGGAGCTCAGATGTGCAACAGAGAGGAGCTGCTGCTGGTGGATGGCTTATCAAACC 1908
 QY 1801 CTTGCTTCCGGAGGCGCAGTGCAGAGCTTCCCGATGGGTCTGCTGCTGCTGCTGCTGCT 1860
 DB 1909 CTTGCTTCCGGAGGCGCAGTGCAGAGCTTCCCGATGGGTCTGCTGCTGCTGCTGCTGCT 1968
 QY 1861 GGCCTGTGGGCTTCTTGGGCAATGCAACCTGAGAGGAGCTGCTGCTGCTGCTGCTGCTGCT 1920
 DB 1969 GGCCTGTGGGCTTCTTGGGCAATGCAACCTGAGAGGAGCTGCTGCTGCTGCTGCTGCTGCT 2028
 QY 1921 TCCCGACATCTGCTTCTCACCAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 DB 2029 TCCCGACATCTGCTTCTCACCAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2088
 QY 1981 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
 DB 2089 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2148
 QY 2041 AAGCAGCCAAAGCGAAAGCAAGTGTGTGAGGCTCGGAAACCCATGCAAGGAGCAAGAC 2100
 DB 2149 AAGCAGCCAAAGCGAAAGCAAGTGTGTGAGGCTCGGAAACCCATGCAAGGAGCAAGAC 2208
 QY 2101 ACAACTGCCACAAGCAGCAGGAGTGCATCTTACCTGGGCTTCTGAGGACCCCATGTACA 2160
 DB 2209 ACAACTGCCACAAGCAGCAGGAGTGCATCTTACCTGGGCTTCTGAGGACCCCATGTACA 2268
 QY 2161 AGTGGAGTGGCAGACAGGCTACCGGCGGAGGCTCATCTGCGGGGAGGAGCTCGGACC 2220

2269 AGTCGAGTGCAGACAGGCTACGCGGCGACGGGCTCATCTCGGGGAGGACTCGGACC 2328
2221 TGGACGCTGGCCCAACCTCAATCTGGTCTGCGCCACCAACGCCACCTACCACCTGCATCA 2280
2329 TGGACGCTGGCCCAACCTCAATCTGGTCTGCGCCACCAACGCCACCTACCACCTGCATCA 2388
2281 AGGATAACTGCCCCCACTCTGCCAAATCTCGGGCAGGAAGACTTTGACAAGGACGGGATTG 2340
2389 AGGATAACTGCCCCCACTCTGCCAAATCTCGGGCAGGAAGACTTTGACAAGGACGGGATTG 2448
2341 GCGATGCTGTGATGATGACGATGACGAATGACCGGTGACCGTGTACCGATGAGAGGACAACTGCC 2400
2449 GCGATGCTGTGATGATGACGATGACGAATGACCGGTGACCGTGTGACCGATGAGAGGACAACTGCC 2508
2401 AGCTTCCTCTTCAATCCCCCGCCAGGCTCACTATGACAAGGATGAGTTGGGGACCGCTGTG 2460
2509 AGCTTCCTCTTCAATCCCCCGCCAGGCTCACTATGACAAGGATGAGTTGGGGACCGCTGTG 2568
2461 ACAACTGCCCTTACGTGACAAACCTGCCAGATGACACAGACAAATGAGAGGGTG 2520
2569 ACAACTGCCCTTACGTGACAAACCTGCCAGATGACACAGACAAATGAGAGGGTG 2628
2521 ACGCTGCTCCGTGACAACTGATGGGACGATGTCTTCAATGAACGAGACAAATGTGCCCT 2580
2629 ACGCTGCTCCGTGACAACTGATGGGACGATGTCTTCAATGAACGAGCAATGTGCCCT 2688
2581 ACGTCTAACAACACTGACAGAGGACACGGATGGTGAAGGTGGGGATCACTGTGACA 2640
2689 ACGTCTAACAACACTGACAGAGGACACGGATGGTGAAGGTGGGGATCACTGTGACA 2748
2641 ACTGCCCTCGTGCACAACTGATGGGACGATGTCTTCAATGAACGAGACAAATGTGCCCT 2700
2749 ACTGCCCTCGTGCACAACTGATGGGACGATGTCTTCAATGAACGAGCAATGTGCCCT 2808
2701 AGTGTGACAAACAGGACATAGATGACAGCGCCACCAAGAAACAAACAGGACAACTGCC 2760
2809 AGTGTGACAAACAGGACATAGATGACAGCGCCACCAAGAAACAAACAGGACAACTGCC 2868
2761 CTTACATCTCCAGCCCAACAGGCTGACCATGACAGAGCGCCAGGCGAGCGCTGTG 2820
2869 CTTACATCTCCAGCCCAACAGGCTGACCATGACAGAGCGCCAGGCGAGCGCTGTG 2928
2821 ACCCTGATGATGACAAACAGTGGGCTCCCGATGACAGGACAACTGCCGCTGTGTTCA 2880
2929 ACCCTGATGATGACAAACAGTGGGCTCCCGATGACAGGACAACTGCCGCTGTGTTCA 2988
2881 ACCCAGACAGGAGACTTGGACGGTATGACAGCGGGGTGATTTGTAAGATGATTTG 2940
2989 ACCCAGACAGGAGACTTGGACGGTATGACAGCGGGGTGATTTGTAAGATGATTTG 3048
2941 ACAATGACAAATCCAGATATTGATGATGTGTCTGAAACAAATGCCATCAGTGAGA 3000
3049 ACAATGACAAATCCAGATATTGATGATGTGTCTGAAACAAATGCCATCAGTGAGA 3108
3001 CAGACTTCAGGAACTTCAGATGCTCCCTTGGATCCCAAGGGACCAACCAATTTGATC 3060
3109 CAGACTTCAGGAACTTCAGATGCTCCCTTGGATCCCAAGGGACCAACCAATTTGATC 3168
3061 CCAACTGGCTCATTTCCGCACTCAAGCAAGAGCTGTTTCAGACAGCCAACTCCGGACCCCG 3120
3169 CCAACTGGCTCATTTCCGCACTCAAGCAAGAGCTGTTTCAGACAGCCAACTCCGGACCCCG 3228
3121 GCATGCTGTAGTTTGAACGATTTGGGTCTGGAACCTTCAGTGGCAATTTCTACGTAA 3180
3229 GCATGCTGTAGTTTGAACGATTTGGGTCTGGAACCTTCAGTGGCAATTTCTACGTAA 3288
3181 ACATGACCGGAGCAGACTATCCCGCTTCGCTTTTGGTTACAGTCAAGCAGCGCT 3240
3289 ACATGACCGGAGCAGACTATCCCGCTTCGCTTTTGGTTACAGTCAAGCAGCGCT 3348
3241 TCTATGTGGTGTAGTGAAGCAGGTGACGACGACTACTGGGAGCAGCCACCGCGG 3300
3349 TCTATGTGGTGTAGTGAAGCAGGTGACGACGACTACTGGGAGCAGCCACCGCGG 3408

3301 CCTATGGCTACTCCGGCGTGTCCCTCAAGTGGTGAACCTCACACACGGGACGGCGGAGC 3360
3409 CCTATGGCTACTCCGGCGTGTCCCTCAAGTGGTGAACCTCACACACGGGACGGCGGAGC 3468
3361 ACCTGAGGAAACGCGCTGTGGCACAACGGGGAACCGCGGGCAGGTCCGAACCTTTATGGC 3420
3469 ACCTGAGGAAACGCGCTGTGGCACAACGGGGAACCGCGGGCAGGTCCGAACCTTTATGGC 3528
3421 ACGACCCAGGAAACATTTGGCTTGGAGGACTACACGGCTTATAGTGGCAGCTGACTCACA 3480
3529 ACGACCCAGGAAACATTTGGCTTGGAGGACTACACGGCTTATAGTGGCAGCTGACTCACA 3588
3481 GGCCCAAGACTGGCTACATCAGACTCTTAGTGCATGAAGGAAACACAGTCAATGCGAGCT 3540
3589 GGCCCAAGACTGGCTACATCAGACTCTTAGTGCATGAAGGAAACACAGTCAATGCGAGCT 3648
3541 CAGACCTATCTATGACCAACCTACGCTGGCGGGCGCTGGGTCTATTTGTCTTCTCTC 3600
3649 CAGACCTATCTATGACCAACCTACGCTGGCGGGCGCTGGGTCTATTTGTCTTCTCTC 3708
3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATCAGAGATATTTAAACAAGATTTG 3660
3709 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATCAGAGATATTTAAACAAGATTTG 3768
3661 CTGCATTTCCGGCAATGCGCTGTCATGCCATGCTCCCTAGACACCTCAGTTCATTTGG 3720
3769 CTGCATTTCCGGCAATGCGCTGTCATGCCATGCTCCCTAGACACCTCAGTTCATTTGG 3828
3721 TCCCTGTGGCTTCTCTCTAGCAGCACCTCCTCTGCTCCCTGACCTTAACCTGATGGTTC 3780
3829 TCCCTGTGGCTTCTCTCTAGCAGCACCTCCTCTGCTCCCTGACCTTAACCTGATGGTTC 3888
3781 TTCACCTCTCCAGGAAACCCCAACCCAGTGCCTTCAGAGGATTAATATCAATGGAAC 3840
3889 TTCACCTCTCCAGGAAACCCCAACCCAGTGCCTTCAGAGGATTAATATCAATGGAAC 3948
3841 CAGAGATGAAATCTTAAACCACTAGAGGAAACCAAGTTTGGTGATATATGAGACTTTATG 3900
3949 TCAGAGATGAAATCTTAAACCACTAGAGGAAACCAAGTTTGGTGATATATGAGACTTTATG 4008
3901 TGGAGTGAATTTGGGCAATGCCATTAATGCTCTTTTCTGTTTGTAAAGAAATGAC 3960
4009 TGGAGTGAATTTGGGCAATGCCATTAATGCTCTTTTCTGTTTGTAAAGAAATGAC 4068
3961 GTTACATATATAATGTAATTAATTTGTTATTTATGTTATATGAGAGTGAAGGGAATA 4020
4069 GTTACATATATAATGTAATTAATTTGTTATTTATGTTATATGAGAGTGAAGGGAATA 4128
4021 CTGTGCATPAAGCCATTAATGTAATTAATTAAGCATGAAATAATTTGCTGAACCTACTTTGGTG 4080
4129 CTGTGCATPAAGCCATTAATGTAATTAATTAAGCATGAAATAATTTGCTGAACCTACTTTGGTG 4188
4081 CTTAAAGTTGTCATTTCTTGAATTTAGAGTTGCTCTACAAATGACACAAATCCCGCTA 4140
4189 CTTAAAGTTGTCATTTCTTGAATTTAGAGTTGCTCTACAAATGACACAAATCCCGCTA 4248
4141 AATAAATTTATAACAAGGGTCAATTTCAAAATTTGAAGTAATTTTAGTGAAGAGATTA 4200
4249 AATAAATTTATAACAAGGGTCAATTTCAAAATTTGAAGTAATTTTAGTGAAGAGATTA 4308
4201 GAAGACACAGGATGACAAATGACATGACCTGAGTAACTAACTAACTGACACATGTAATA 4260
4309 GAAGACACAGGATGACAAATGACATGACCTGAGTAACTAACTAACTGACACATGTAATA 4368
4261 CAGTTACAAAATTAACGAACTCTCTCTTGTCTCAATGAAAGCCCTCATGTGCAATA 4320
4369 CAGTTACAAAATTAACGAACTCTCTCTTGTCTCAATGAAAGCCCTCATGTGCAATA 4428
4321 GAGATGCGATTTTCATCAAGAGACAAACATCTTCTGCAATGAGTGTGATGCGGTTCCAGAT 4380
4429 GAGATGCGATTTTCATCAAGAGACAAACATCTTCTGCAATGAGTGTGATGCGGTTCCAGAT 4488

QY 4381 GTGGATTTGGCAACCTCATTTTAAGTAARAGGTAGCAGAGCAAGTGGCGTCTTTAG 4440
DB |||||
QY 4489 GTGGATTTGGCAACCTCATTTTAAGTAARAGGTAGCAGAGCAAGTGGCGTCTTTAG 4548
DB |||||
QY 4441 CTGCTGCTTGTGCGGCTGTGCTGCGGAGGCGCTCTGCTGCTGCTGCTTCCCGAGCTT 4500
DB |||||
QY 4549 CTGCTGCTTGTGCGGCTGTGCTGCGGAGGCGCTCTGCTGCTGCTTCCCGAGCTT 4608
DB |||||
QY 4501 TGCTGCTGAGAGGACAGAGGACAGACAGCGCGGAGGCGCATCTAAGCGGTAT 4560
DB |||||
QY 4609 TGCTGCTGAGAGGACAGAGGACAGACAGCGCGGAGGCGCATCTAAGCGGTAT 4668
DB |||||
QY 4561 CTAGGCTTTGTGTAACCTGCGGACAGCTTCTTACCTGATTTGATGATACATTTTCATTAA 4620
DB |||||
QY 4669 CTAGGCTTTGTGTAACCTGCGGACAGCTTCTTACCTGATTTGATGATACATTTTCATTAA 4728
DB |||||
QY 4621 GGTTCAGTTATTAATATTTTGTAAATTTTAAAGTGACTATAGATGCACTCCATT 4680
DB |||||
QY 4729 GGTTCAGTTATTAATATTTTGTAAATTTTAAAGTGACTATAGATGCACTCCATT 4788
DB |||||
QY 4681 TACCAGTAACCTTATTTTAAATATGCTTAGTAAACATATGATGATATTTCTAGAAACA 4740
DB |||||
QY 4789 TACCAGTAACCTTATTTTAAATATGCTTAGTAAACATATGATGATATTTCTAGAAACA 4848
DB |||||
QY 4741 ACATCTTAATAGTATATATCTCTGTGAAATATGAGCGCTTGATATTTAGTTGTAC 4800
DB |||||
QY 4849 AACATCTTAATAGTATATATCTCTGTGAAATATGAGCGCTTGATATTTAGTTGTAC 4908
DB |||||
QY 4801 GATGAAGCATGCTGAAGCTGTAAACAGATACATAGAGAAATAGGAGTTTATGATGG 4860
DB |||||
QY 4909 GATGAAGCATGCTGAAGCTGTAAACAGATACATAGAGAAATAGGAGTTTATGATGG 4968
DB |||||
QY 4861 AACCTTAATATATATGTTGCGGAGGATTTAGTTCAATATTTGTTACGTTTATCATT 4920
DB |||||
QY 4969 AACCTT-AATATATATGTTGCGGAGGATTTAGTTCAATATTTGTTACGTTTATCATT 5027
DB |||||
QY 4921 TGCTGATATGAATTTCTTTAAATTTCAACGCTGAAA- GAATCAGCATTTAGCTTGCC 4979
DB |||||
QY 5028 TGCTGATATGAATTTCTTTAAATTTCAACGCTGAAAACGATCAGCATTTAGCTTGCC 5087
DB |||||
QY 4980 AGGCACACCAATATACGTATGTTAAATATGACAAAGTTGTTTGTGTTTGTGTTT 5039
DB |||||
QY 5088 AGGCACACCAATATACGTATGTTAAATATGACAAAGTTGTTTGTGTTTGTGTTT 5147
DB |||||
QY 5040 TTTGTTGTTGTTGTTTGTGTTTAAAGTTGCTGATGCTTCTGCGAGAAATAGTCA 5099
DB |||||
QY 5148 TTTGTTGTTGTTGTTTGTGTTTAAAGTTGCTGATGCTTCTGCGAGAAATAGTCA 5203
DB |||||
QY 5100 CTCATCCCACTCCACATAGGGGTTTAGTAAAGAGAGTCTGCTGCTGATGATGATAG 5159
DB |||||
QY 5204 CTCATCCCACTCCACATAGGGGTTTAGTAAAGAGAGTCTGCTGCTGATGATGATAG 5263
DB |||||
QY 5160 GGGGCAATCTTTTCCCTTCTGTTAAATAGTATGATCAGATTTCTGCGAGAAAGTCA 5219
DB |||||
QY 5264 GGGGCAATCTTTTCCCTTCTGTTAAATAGTATGATCAGATTTCTGCGAGAAAGTCA 5323
DB |||||
QY 5220 AATCCATAACTTTAGTCTTAATGATACATGCAATTTTGTAAATTAATTTTCTGTTT 5279
DB |||||
QY 5324 GATCCATAACTTTAGTCTTAATGATACATGCAATTTTGTAAATTAATTTTCTGTTT 5383
DB |||||
QY 5280 CTTTGGAGTTGATGTTGTTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5339
DB |||||
QY 5384 CTTTGGAGTTGATGTTGTTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5440
DB |||||
QY 5340 GCTGTATTTCCGAGACCAAGAGGTTGGGATCTTCAATTAATAGTGGAGCTGTCAAC 5399
DB |||||
QY 5441 GCTGTATTTCCGAGACCAAGAGGTTGGGATCTTCAATTAATAGTGGAGCTGTCAAC 5499
DB |||||
QY 5400 AGCGTGCAGGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5459
DB |||||
QY 5500 AGCGTGCAGGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5559
DB |||||
QY 5460 GATGATGTGAATATTTAGATGTACCATATTTTGTAAATTAATTTTATGTTTCTTAAC 5519
DB |||||

DB 5560 GATGATGTGAATATTTAGATGTACCATATTTTGTAAATTAATTTTCTTAAC 5619
QY 5520 AATTTATCGTATAGTGTGATGAAAGCGTCAATGTTTGTCCAAAGACTGTAATATTTAT 5579
DB 5620 AATTTATCGTATAGTGTGATGAAAGCGTCAATGTTTGTCCAAAGACTGTAATATTTAT 5679
QY 5580 TTATGTTTCAATGCTCAAAATTTTCAACACTGAAACCTGCACTAGCTAGCACTCAT 5639
DB 5680 TTATGTTTCAATGCTCAAAATTTTCAACACTGAAACCTGCACTAGCTAGCACTCAT 5739
QY 5640 TTTTAAAGATTAAACACAGGAAATTAATTTGTAAAAAGGTTTCT 5684
DB 5740 TTTTAAAGATTAAACACAGGAAATTAATTTGTAAAAAGGTTTCT 5784

RESULT 12
AAC77795
ID AAC77795 standard; cDNA; 3787 BP.
XX AAC77795;
XX AC
XX DT
XX 08-FEB-2001 (first entry)
XX Human cancer associated gene sequence SEQ ID NO:189.
DE Human; cancer associated gene; cancer antigen; detection; cancer;
XX diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
KW antidiabetic; antilasthmatic; antirheumatic; antiallergic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
KW dermatological; neuroprotective; thrombolytic; coagulant; nocotropic;
KW vasotropic; antiproliferative; antidiabetic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disease;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening; ss.
XX Homo sapiens.
OS
XX WO200055350-A1.
XX 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US005882.
XX 12-MAR-1999; 99US-0124270P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI: 2000-587533/55.
XX P-PSDB; AAB43586.
XX Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer.
XX Claim 1; Page 765-766; 2352pp; English.
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in
CC AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnery; immunomodulator;
CC antidiabetic; antilasthmatic; antirheumatic; antiallergic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
CC nocotropic; vasotropic; antiproliferative and angiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders from
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune

3923 ATTACATTGCTTTTCTTGTGTTTAAAGAAATGACGTTTACATATAAAATGTAATTA 3982
 Db
 2014 ATTACATTGCTTTTCTTGTGTTTAAAGAAATGACGTTTACATATAAAATGTAATTA 2073
 Qy
 3983 CTTATTGTATTATGTGTAATAGGAGTTGAAGGAATACCTGTGTCATTAAGCCATTAATGATA 4042
 Db
 2074 CTTATTGTATTATGTGTAATAGGAGTTGAAGGAATACCTGTGTCATTAAGCCATTAATGATA 2133
 Qy
 4043 AATTAAAGCATGAAATAATCTGCTGAACCTACTTTTGGTGTCTTAAAGTTGTCACTATTCTTG 4102
 Db
 2134 AATTAAAGCATGAAATAATCTGCTGAACCTACTTTTGGTGTCTTAAAGTTGTCACTATTCTTG 2193
 Qy
 4103 AATTAAAGTTGCTCTACAAATGACACACAAATCCGCTAAATAAATAAACAAGGTCAC 4162
 Db
 2194 AATTAAAGTTGCTCTACAAATGACACACAAATCCGCTAAATAAATAAACAAGGTCAC 2253
 Qy
 4163 ATTCAAATTTCAAGTTAAATGTTTAAAGGAGAGATTAGAGACCAACAGGCATAGCAAT 4222
 Db
 2254 ATTCAAATTTCAAGTTAAATGTTTAAAGGAGAGATTAGAGACCAACAGGCATAGCAAT 2313
 Qy
 4223 GACATAAGCTACCGATTAACTAAATCGGAACATGTAACACAGTTTCAAAAAATAAACAAGT 4282
 Db
 2314 GACATAAGCTACCGATTAACTAAATCGGAACATGTAACACAGTTTCAAAAAATAAACAAGT 2373
 Qy
 4283 CTCCTCTGCTACCAATGAAGCCCTCATGTGCGAGTAGAGATGCACTTTTCATCAAGAA 4342
 Db
 2374 CTCCTCTGCTACCAATGAAGCCCTCATGTGCGAGTAGAGATGCACTTTTCATCAAGAA 2433
 Qy
 4343 CAACATCTCTGCAAAATGGGTGTGATGCGGTTCAGATGTGGAATTTGGCAAAACCTCAT 4402
 Db
 2434 CAACATCTCTGCAAAATGGGTGTGATGCGGTTCAGATGTGGAATTTGGCAAAACCTCAT 2493
 Qy
 4403 TAAGTAAAGTTAGCAGACAAAGTGGGTGCTTAAAGTGTGCTGCTGCTGCTGCTGCTGCT 4462
 Db
 2494 TAAGTAAAGTTAGCAGACAAAGTGGGTGCTTAAAGTGTGCTGCTGCTGCTGCTGCTGCT 2553
 Qy
 4463 GTCGGGAGGCTCCTGCTGAGTCTTCCCTGAGTCTTCCCTGAGTCTGAGAGGAAACAGAG 4522
 Db
 2554 GTCGGGAGGCTCCTGCTGAGTCTTCCCTGAGTCTTCCCTGAGTCTGAGAGGAAACAGAG 2613
 Qy
 4523 CAGACGACAGCGCGGAAAGGCGATCTAACCGGTATCTAGGCTTTGGTAACTGGCGAC 4582
 Db
 2614 CAGACGACAGCGCGGAAAGGCGATCTAACCGGTATCTAGGCTTTGGTAACTGGCGAC 2673
 Qy
 4583 AAGTTGCTTTTACCTGATTCATGATGATATTTTCAATTAAGTTTCCAGTTTAAATATTTTG 4642
 Db
 2674 AAGTTGCTTTTACCTGATTCATGATGATATTTTCAATTAAGTTTCCAGTTTAAATATTTTG 2733
 Qy
 4643 TTAATATTATTAAGTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4702
 Db
 2734 TTAATATTATTAAGTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2793
 Qy
 4703 TGCCTAGTAAACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4762
 Db
 2794 TGCCTAGTAAACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2853
 Qy
 4763 CTGTGAAATATGAGGCTTGATATATTTAGTGTGTGATGATGATGATGATGATGATGATGATGAT 4822
 Db
 2854 CTGTGAAATATGAGGCTTGATATATTTAGTGTGTGATGATGATGATGATGATGATGATGATGAT 2913
 Qy
 4823 AACAGATACATAGGATATGAGGCTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 4882
 Db
 2914 AACAGATACATAGGATATGAGGCTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 2972
 Qy
 4883 CAGCGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4942
 Db
 2973 CAGCGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3032
 Qy
 4943 ATTCAAAGCTGAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5001
 Db
 3033 ATTCAAAGCTGAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3092
 Qy
 5002 TGTGTAATATGACAAAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 5061

3093 TGTGTAATATGACAAAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 3152
 Qy
 5062 TGTGTAATATGACAAAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 5121
 Db
 3153 TGTGTAATATGACAAAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 3212
 Qy
 5122 GTTTAGTAAAGAAAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5181
 Db
 3213 GTTTAGTAAAGAAAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3272
 Qy
 5182 GTTTAGTAAAGAAAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5241
 Db
 3273 GTTTAGTAAAGAAAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3332
 Qy
 5242 GTACACATGCAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5301
 Db
 3333 GTACACATGCAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3392
 Qy
 5302 TGTGTTTGTGCTGCACTTTTACCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 5361
 Db
 3393 TGTGTTTGTGCTGCACTTTTACCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 3452
 Qy
 5362 AGCGTTGGGATACCTTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5421
 Db
 3453 AGCGTTGGGATACCTTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3512
 Qy
 5422 GTGTTGTGGGTCACCGTACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5481
 Db
 3513 GTGTTGTGGGTCACCGTACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3572
 Qy
 5482 TACCATATTTTGTGTAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5541
 Db
 3573 TACCATATTTTGTGTAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3632
 Qy
 5542 AAACGTCATGTTTGTGCAAGCTGTAATATTTTATGATGATGATGATGATGATGATGATGATGATGAT 5601
 Db
 3633 AAACGTCATGTTTGTGCAAGCTGTAATATTTTATGATGATGATGATGATGATGATGATGATGATGAT 3692
 Qy
 5602 TTTCCACCTGAAACCTGCACTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 5661
 Db
 3693 TTTCCACCTGAAACCTGCACTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 3752
 Qy
 5662 ATAAATTTGTAATAAAGGTTTCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5696
 Db
 3753 ATAAATTTGTAATAAAGGTTTCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3787

RESULT 13
 AAA88669
 ID AAA88669 standard; cDNA; 3596 BP.
 XX
 AC AAA88669;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Human thrombospondin-2 cDNA.
 XX
 KW Thrombospondin-2; TSP-2; human; angiogenesis; cell proliferation;
 KW melanoma; tumour; cancer; squamous cell carcinoma; antiangiogenic;
 KW prostate cancer; psoriasis; rosecea dermatosis; antitumour; gene therapy;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 CDS 26..3544
 FT /*tag= a
 XX
 XX WO200057899-A1.
 XX 05-OCT-2000.
 XX

QY 1607 AATCGATGGCGCTGGAGCCCTGGTCCCGTGGTTCGGCTGCACTGTCACTGTGCGG 1666
 Db 1501 AATCGATGGCGCTGGAGCCCTGGTCCCGTGGTTCGGCTGCACTGTCACTGTGCGG 1560
 QY 1667 TGGGATCCGGAGCCGACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGGAAGC 1726
 Db 1561 TGGGATCCGGAGCCGACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGGAAGC 1620
 QY 1727 CTGCGTGGGGATGTGACAGGAGCGTCAGATGTGCAACAGAGGAGCTGCCCGCTGGATGG 1786
 Db 1621 CTGCGTGGGGATGTGACAGGAGCGTCAGATGTGCAACAGAGGAGCTGCCCGCTGGATGG 1680
 QY 1787 CTGTTTATCCAAACCCCTGCTCCCGGAGCCGACGTGACAGAGCTTCCCGATGGGTCTG 1846
 Db 1681 CTGTTTATCCAAACCCCTGCTCCCGGAGCCGACGTGACAGAGCTTCCCGATGGGTCTG 1740
 QY 1847 GTCATGCGGCTCTGCGCTGTGGGCTTCTGGGCAATGSCACCCACATGTGAGGACCTGGA 1906
 Db 1741 GTCATGCGGCTCTGCGCTGTGGGCTTCTGGGCAATGSCACCCACATGTGAGGACCTGGA 1800
 QY 1907 CGAGTGTCCCTGTGCTCCCGACATCTGCTTCTCCACAGCAAGTGTGCTCGCTGTCAA 1966
 Db 1801 CGAGTGTCCCTGTGCTCCCGACATCTGCTTCTCCACAGCAAGTGTGCTCGCTGTCAA 1860
 QY 1967 CACTCAGCTGTGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2026
 Db 1861 CACTCAGCTGTGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
 QY 2027 CGGGTTCGGCTTGAAGCAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2086
 Db 1921 CGGGTTCGGCTTGAAGCAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1980
 QY 2087 CAGGACACGAC 2146
 Db 1981 CAGGACACGAC 2040
 QY 2147 CGACCCCATGTACAAAGTGGAGTGCAGACAGGCTACCGGGGCGACAGGCTCATCTGCGG 2206
 Db 2041 CGACCCCATGTACAAAGTGGAGTGCAGACAGGCTACCGGGGCGACAGGCTCATCTGCGG 2100
 QY 2207 GGAGACTCGGACCTGGAAGGTGGCCCAACCTCAATCTGTCTGGCCACCAAGCGCAC 2266
 Db 2101 GGAGACTCGGACCTGGAAGGTGGCCCAACCTCAATCTGTCTGGCCACCAAGCGCAC 2160
 QY 2267 CTACCACTGCATCAAGGATAACTGCCCCCATCTGCCAAATCTGGGCAAGGACTTTGA 2326
 Db 2161 CTACCACTGCATCAAGGATAACTGCCCCCATCTGCCAAATCTGGGCAAGGACTTTGA 2220
 QY 2327 CAAAGCGGGATTTGGCGATGCTGTGATGATGACATGACAAATGACGCTGTGACCGATGA 2386
 Db 2221 CAAAGCGGGATTTGGCGATGCTGTGATGATGACATGACAAATGACGCTGTGACCGATGA 2280
 QY 2387 GAAAGCAACCTGCCAGCTCCTCTCAATCCCGCGAGCTGACATATGACAAAGGATGAGGT 2446
 Db 2281 GAAAGCAACCTGCCAGCTCCTCTCAATCCCGCGAGCTGACATATGACAAAGGATGAGGT 2340
 QY 2447 TGGGACCGCTGTGACAACTGCTTACGTCAGCAACCCCTGCCAGATCGACACAGACAA 2506
 Db 2341 TGGGACCGCTGTGACAACTGCTTACGTCAGCAACCCCTGCCAGATCGACACAGACAA 2400
 QY 2507 CAATGGAGGGTGAAGCTGCTGCTGCGGACATTTGATGGGACGATGCTTCAATGAACG 2566
 Db 2401 CAATGGAGGGTGAAGCTGCTGCTGCGGACATTTGATGGGACGATGCTTCAATGAACG 2460
 QY 2567 AGACAATTTGCCCTACGCTACAACTGACACACCTGACAGAGGACACGATGCTGCGGTGG 2626
 Db 2461 AGACAATTTGCCCTACGCTACAACTGACACACCTGACAGAGGACACGATGCTGCGGTGG 2520
 QY 2627 GGATCACTGTGACACTGCCCTGGTGGACAAACCTGACAGACCGACCTGGGCAATGA 2686
 Db 2521 GGATCACTGTGACACTGCCCTGGTGGACAAACCTGACAGACCGACCTGGGCAATGA 2580

QY 2687 CCTTGTGGGGACCACTGTGTCACAAACAGGACATAGATGACGACGGCCACCAAGACAA 2746
 Db 2581 CCTTGTGGGGACCACTGTGTCACAAACAGGACATAGATGACGACGGCCACCAAGACAA 2640
 QY 2747 CAGGACAACTGGCCCTACATCTCCAAACGCAACAGGCTGACCATGACAGAGAGGCA 2806
 Db 2641 CAGGACAACTGGCCCTACATCTCCAAACGCAACAGGCTGACCATGACAGAGAGGCA 2700
 QY 2807 GGGCGACGGCTGTGACCCCTGATGATGACAAACGATGGCGTCCCGATGACAGGGAACAATG 2866
 Db 2701 GGGCGACGGCTGTGACCCCTGATGATGACAAACGATGGCGTCCCGATGACAGGGAACAATG 2760
 QY 2867 CGGCTTGTGTTCAACCCAGACAGGAGACCTTGGACGGTATGACGCGGTGATATTG 2926
 Db 2761 CGGCTTGTGTTCAACCCAGACAGGAGACCTTGGACGGTATGACGCGGTGATATTG 2820
 QY 2927 TAAAGATGATTTGACATGACAAATCCACATATGATGATGATGATGATGATGATGATGAT 2986
 Db 2821 TAAAGATGATTTGACATGACAAATCCACATATGATGATGATGATGATGATGATGATGAT 2880
 QY 2987 TGCATCAGTGAACAGACTTCAGGAACTTCCAGATGCTCCCTTGGATCCCAAGGGAC 3046
 Db 2881 TGCATCAGTGAACAGACTTCAGGAACTTCCAGATGCTCCCTTGGATCCCAAGGGAC 2940
 QY 3047 CACCCAAATTTGATCCCACTGGTCAATTCGCAATCAAGCAAGGAGCTGTTTCAGACAGC 3106
 Db 2941 CACCCAAATTTGATCCCACTGGTCAATTCGCAATCAAGCAAGGAGCTGTTTCAGACAGC 3000
 QY 3107 CAACTCGGACCCCGCATCGCTGTAGTGTGATGATGATGATGATGATGATGATGATGATGAT 3166
 Db 3001 CAACTCGGACCCCGCATCGCTGTAGTGTGATGATGATGATGATGATGATGATGATGATGAT 3060
 QY 3167 CAACTCTACGTAACACACTGACCGGACGACGACTATGCCGCTTCCCTTGGTGTATACCA 3226
 Db 3061 CAACTCTACGTAACACACTGACCGGACGACGACTATGCCGCTTCCCTTGGTGTATACCA 3120
 QY 3227 GTCAAGCAGCCGCTTCTATGTGTGATGTGGAAGCAGGTTGACGACAGACCTACTTGGAGGA 3286
 Db 3121 GTCAAGCAGCCGCTTCTATGTGTGATGTGGAAGCAGGTTGACGACAGACCTACTTGGAGGA 3180
 QY 3287 CAGACCCACGCGGCTTATGCTATCTCCGCGTGTCCCTCAAGTGGTGAATCCACCCAC 3346
 Db 3181 CAGACCCACGCGGCTTATGCTATCTCCGCGTGTCCCTCAAGTGGTGAATCCACCCAC 3240
 QY 3347 GGGGACGGGCGAGCAGCTGAGGAAACGCTGTGGACACGCGGGAACACGCGGGGCGAGT 3406
 Db 3241 GGGGACGGGCGAGCAGCTGAGGAAACGCTGTGGACACGCGGGAACACGCGGGGCGAGT 3300
 QY 3407 GCGAACCTTATGACAGACCCAGGAAACATTTGGCTGGAAGGACTACAGGCTTATAGGTG 3466
 Db 3301 GCGAACCTTATGACAGACCCAGGAAACATTTGGCTGGAAGGACTACAGGCTTATAGGTG 3360
 QY 3467 GCACTGTACTCAGGCGCCCAAGACTGGCTTACATCAGAGTCTTGTGATGAAAGGAAACA 3526
 Db 3361 GCACTGTACTCAGGCGCCCAAGACTGGCTTACATCAGAGTCTTGTGATGAAAGGAAACA 3420
 QY 3527 GGTATGGCAGACTCAGGACCTTATGACAAACCTTACGCTGGGCGGCGCTGGTCT 3586
 Db 3421 GGTATGGCAGACTCAGGACCTTATGACAAACCTTACGCTGGGCGGCGCTGGTCT 3480
 QY 3587 ATTTGTCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGATAT 3646
 Db 3481 ATTTGTCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGATAT 3540
 QY 3647 TTAACAAGATTTGTGCAATTTCCGCAATGCGCTGTGATGCCATGGTCCCTAGA 3702
 Db 3541 TTAACAAGATTTGTGCAATTTCCGCAATGCGCTGTGATGCCATGGTCCCTAGA 3596

RESULT 14
 ABX14061
 ID ABX14061 standard; cDNA; 3596 BP.
 XX

1141 TTCTCGCTCCACTCGGTGAGCGGTGAGGAGGCTGGTCTCCGTGGCGCAGAGTGGACCCA 1200
1307 GTGCTCCGTGACGCTGTGGCTCTGGGACCCAGCAGAGAGGCGGTCTCTGTGACGCTCACACG 1366
1201 GTGCTCCGTGACGCTGTGGCTCTGGGACCCAGCAGAGAGGCGGTCTCTGTGACGCTCACACG 1260
1367 CAACACCTGTTGGGGCCCTCCATCCAGACACAGGCTTGCAGTCTGAGCAAGTGTGACAC 1426
1261 CAACACCTGTTGGGGCCCTCCATCCAGACACAGGCTTGCAGTCTGAGCAAGTGTGACAC 1320
1427 CCGCATCCGGCAGGACCGCGCTGGAGCCACTGGTCACTTGTCTTCTCATGTCTGTGAC 1486
1321 CCGCATCCGGCAGGACCGCGCTGGAGCCACTGGTCACTTGTCTTCTCATGTCTGTGAC 1380
1487 CTGTGGAGTTGGCAATATCACGCATCCCTCTCTGCACTCCCGAGTGCCCGCAGATGGG 1546
1381 CTGTGGAGTTGGCAATATCACGCATCCCTCTCTGCACTCCCGAGTGCCCGCAGATGGG 1440
1547 GGGCAAGAAATTGCAAGGGAGTGCCCGGGAGACCAAGCCCTGCGAGGGCCGCCATGCC 1606
1441 GGGCAAGAAATTGCAAGGGAGTGCCCGGGAGACCAAGCCCTGCGAGGGCCGCCATGCC 1500
1607 AATCGATGGCGCTGGAGCCCTGGTCCCGTGGTGGCCCTGCACTGTCACTGTGCCCG 1666
1501 AATCGATGGCGCTGGAGCCCTGGTCCCGTGGTGGCCCTGCACTGTCACTGTGCCCG 1560
1667 TGGGATCCGGAGCGCACCGCGGTCTGCAACAGCCCTGAGCCCTCAGTACGAGGGAGGC 1726
1561 TGGGATCCGGAGCGCACCGCGGTCTGCAACAGCCCTGAGCCCTCAGTACGAGGGAGGC 1620
1727 CTGCGTGGGGATGTGAGAGCGTCAAGAGCTGATGTGCAACAGAGAGCTGCCCGCTGATGG 1786
1621 CTGCGTGGGGATGTGAGAGCGTCAAGAGCTGATGTGCAACAGAGAGCTGCCCGCTGATGG 1680
1787 CTGTTTATCCAAACCCCTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTTG 1846
1681 CTGTTTATCCAAACCCCTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTTG 1740
1847 GTCATGGGCTCTGCGCTGTGGCTCTTGGGCAATGGCAACCCAGCTGTGAGACCTTGA 1906
1741 GTCATGGGCTCTGCGCTGTGGCTCTTGGGCAATGGCAACCCAGCTGTGAGACCTTGA 1800
1907 CGAGTGTGCTGCTGCCGACATCTGCTTCTCCACAGCAAGTGCTGCTGCTGTGTCAA 1966
1801 CGAGTGTGCTGCTGCCGACATCTGCTTCTCCACAGCAAGTGCTGCTGCTGTGTCAA 1860
1967 CACTCAGCCTGGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2026
1861 CACTCAGCCTGGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
2027 CGGGGTGGCTGGAAGCAGCAGCAAGCGGAAGCAAGTGTGTGAGCCCGAAGCCCATG 2086
1921 CGGGGTGGCTGGAAGCAGCAGCAAGCGGAAGCAAGTGTGTGAGCCCGAAGCCCATG 1980
2087 CAAGGACAAGACACAACTGCCACAAAGCAGCGGAGTGATCTACCTGGGCACTTCAG 2146
1981 CAAGGACAAGACACAACTGCCACAAAGCAGCGGAGTGATCTACCTGGGCACTTCAG 2040
2147 CGACCCCATGTACAAAGTGGAGTCCAGACAGGCTACCGGGGACCGGGCTCATCTGCGG 2206
2041 CGACCCCATGTACAAAGTGGAGTCCAGACAGGCTACCGGGGACCGGGCTCATCTGCGG 2100
2207 GGAGGACTCGGACCTTGGACCGCTGGCCCAACCTCAATCTGGTCTGCGCCACCAAGCCAC 2266
2101 GGAGGACTCGGACCTTGGACCGCTGGCCCAACCTCAATCTGGTCTGCGCCACCAAGCCAC 2160
2267 CTACCACTGATCAAGTACTGCGCCCATCTGCGCAANTCTGGGCAAGGAGCTTGA 2326
2161 CTACCACTGATCAAGTACTGCGCCCATCTGCGCAANTCTGGGCAAGGAGCTTGA 2220
2327 CAAGGACGGGATGGCGGATGCTGTGATGATGAGATGACAAATGACGGTGTGACCGGATGA 2386

2221 CAAGGACGGGATTGGCGATGCTGTGATGATGACGATGACAAATGACGGTGTGACCGATGA 2280
2387 GAAGGACAACTGCCAGCTCTCTTCAATCCCGGCGCAGGCTGACTATGACAAAGGATGAGGT 2446
2281 GAAGGACAACTGCCAGCTCTCTTCAATCCCGGCGCAGGCTGACTATGACAAAGGATGAGGT 2340
2447 TGGGACCGCTGTGACAACTGCTTACGTGCACAAACCCCTGCCAGATCGACAGACAA 2506
2341 TGGGACCGCTGTGACAACTGCTTACGTGCACAAACCCCTGCCAGATCGACAGACAA 2400
2507 CAATGGAGAGGATGACGCTGCTCGTGGACATTTGATGGGAGCATGTCTTCAATGAACG 2566
2401 CAATGGAGAGGATGACGCTGCTCGTGGACATTTGATGGGAGCATGTCTTCAATGAACG 2460
2567 AGACAAATTTGCTTACGTCTCAACACTGACCAAGAGGACACGGATGCTGACGGTGTGGG 2626
2461 AGACAAATTTGCTTACGTCTCAACACTGACCAAGAGGACACGGATGCTGACGGTGTGGG 2520
2627 GGATCACTGTGACAACTGCTCCCTGCTGGTGCACAAACCTGACAGACCGGCTGGCAATGA 2686
2521 GGATCACTGTGACAACTGCTCCCTGCTGGTGCACAAACCTGACAGACCGGCTGGCAATGA 2580
2687 CCTTGTGGGACACAGTGTGACAAACAGAGGACATAGATGACAGCGCCACCAAGAACAA 2746
2581 CCTTGTGGGACACAGTGTGACAAACAGAGGACATAGATGACAGCGCCACCAAGAACAA 2640
2747 CCAGGACAACTGCTCCCTACATCTCCAAACCGCAACAGGCTGACCATGACAGACGGCCA 2806
2641 CCAGGACAACTGCTCCCTACATCTCCAAACCGCAACAGGCTGACCATGACAGACGGCCA 2700
2807 GGGCGACCGCTGTGACCGCTGATGACAAACAGTGGCTGCCCGATGACAGGACCACTG 2866
2701 GGGCGACCGCTGTGACCGCTGATGACAAACAGTGGCTGCCCGATGACAGGACCACTG 2760
2867 CCGGCTGTGTTAAACCCAGACCGAGGAGACTTGGACCGTGTATGACAGCGGGTGATATTG 2926
2761 CCGGCTGTGTTAAACCCAGACCGAGGAGACTTGGACCGTGTATGACAGCGGGTGATATTG 2820
2927 TAAAGATGATTTGACAAATGACATCCAGATATTGATGATGTGTCTCTGTAAGAACAA 2986
2821 TAAAGATGATTTGACAAATGACATCCAGATATTGATGATGTGTCTCTGTAAGAACAA 2880
2987 TGCCATGATGAGACAGACTTCCAGAACTTCCAGATGTGCTCCCTTGGATGCCAAAGGAC 3046
2881 TGCCATGATGAGACAGACTTCCAGAACTTCCAGATGTGCTCCCTTGGATGCCAAAGGAC 2940
3047 CACCCAAATTTGATCCAACTGGGTCAATTCGCCATCCAGGCAAGGAGCTGTTCAGACAGC 3106
2941 CACCCAAATTTGATCCAACTGGGTCAATTCGCCATCCAGGCAAGGAGCTGTTCAGACAGC 3000
3107 CAACTCGGACCCCGGCATCGCTGTAGGTTTGGACGAGTTTGGGTCTGTGGACTTCAGTGG 3166
3001 CAACTCGGACCCCGGCATCGCTGTAGGTTTGGACGAGTTTGGGTCTGTGGACTTCAGTGG 3060
3167 CACATTTACGTTAAACACTGACCGGAGCAGACTATGCCGCTTCTGTTGGTTACCA 3226
3061 CACATTTACGTTAAACACTGACCGGAGCAGACTATGCCGCTTCTGTTGGTTACCA 3120
3227 GTCAAGCAGCCGCTTCTATGTGGTGTGATGTGGAAGCAGGTGACGAGACCTACTTGGGAGGA 3286
3121 GTCAAGCAGCCGCTTCTATGTGGTGTGATGTGGAAGCAGGTGACGAGACCTACTTGGGAGGA 3180
3287 CAGGCCACCGGGGCTATGGCTACTCCGGGCTGTCCCTCAAGTGGTGAATCCACCAC 3346
3181 CAGGCCACCGGGGCTATGGCTACTCCGGGCTGTCCCTCAAGTGGTGAATCCACCAC 3240
3347 GGGGACGGGCGAGCACTTGGAGAACCGCTGTGGCACACGGGGAACCGCGGGGACGCT 3406
3241 GGGGACGGGCGAGCACTTGGAGAACCGCTGTGGCACACGGGGAACCGCGGGGACGCT 3300
3407 GGGAACTTTATGGCACGACCCCGAGGAACTTTGGCTGGGAAGGACTACACGGGCTTATAGTGT 3466
3301 GGGAACTTTATGGCACGACCCCGAGGAACTTTGGCTGGGAAGGACTACACGGGCTTATAGTGT 3360

2963	2Y	TGATGATGTTGCTCGAATAAATGCGCATCAGTGAGACAGACTTCAGGAACCTTCAGAT	3022	4Y	AATTAAGCATGAAAAATATTGCTGAACACTCTTTTGGTGGCTTAAAGTTGTCACTATTCTTG	4102	
1054	2b	TGATGATGTTGCTCGTGAATAAATGCGCATCAGTGAGACAGACTTCAGGAACCTTCAGAT	1113	2b	AATTAAGCATGAAAAATATTGCTGAACACTCTTTTGGTGGCTTAAAGTTGTCACTATTCTTG	2193	
3023	2Y	GGTCCCCCTCGATCCCAAGGACCAACCCAAATGATGATCCCAACCTTCAGGATCA	3082	2Y	AATTAAGAGTTGCTCTCAATAGACACACAAATCCCGTTAAATATAAACAAGGTCA	4162	
1114	2b	GGTCCCCCTCGATCCCAAGGACCAACCCAAATGATGATCCCAACCTTCAGGATCA	1173	2b	AATTAAGAGTTGCTCTCAATAGACACACAAATCCCGTTAAATATAAACAAGGTCA	2253	
3083	2Y	AGGCAAGGAGCTGGTTGACACAGCACTCGGACCCCGGATCGCTGTAGGTTTGACGA	3142	2Y	ATTCAAAATTTGCAAGTAATGTTTGTAGTAGGAGACATAGAGACACAGGATAGCAAT	4222	
1174	2b	AGGCAAGGAGCTGGTTGACACAGCACTCGGACCCCGGATCGCTGTAGGTTTGACGA	1233	2b	ATTCAAAATTTGCAAGTAATGTTTGTAGTAGGAGACATAGAGACACAGGATAGCAAT	2313	
3143	2Y	GTGTTGGGTCTGTGACCTTCACTGAGCACTTCTAGTAAACACTGACCGGACGACACTA	3202	2Y	GACATAAGCTACCGATTAACTTAATCGGAACATGTAACCAAGTTACAAAATAAACAAGAACT	4282	
1234	2b	GTGTTGGGTCTGTGACCTTCACTGAGCACTTCTAGTAAACACTGACCGGACGACACTA	1293	2b	GACATAAGCTACCGATTAACTTAATCGGAACATGTAACCAAGTTACAAAATAAACAAGAACT	2373	
3203	2Y	TGCGGGCTTCGTCTTTGGTTACAGTCAAGCAGCGCTTCTATGTGGTATGTGGAAGCA	3262	2Y	CTCCTCTGTCTCACTACATGAAGCCCTCATGTGCAGTAGAGATGAGTTTCATCAAGAA	4342	
1294	2b	TGCGGGCTTCGTCTTTGGTTACAGTCAAGCAGCGCTTCTATGTGGTATGTGGAAGCA	1353	2b	CTCCTCTGTCTCACTACATGAAGCCCTCATGTGCAGTAGAGATGAGTTTCATCAAGAA	2433	
3263	2Y	GGTGACGACACTTACTGGGAGGACAGCCACCGCGGCTATGGCTACTCCGGCGTGC	3322	2Y	TAAGTAAAGGTTAGCAGAGCAAAAGTGGGTGACGCGTTCCAGATGTGAATTCGCAAACTCATT	4402	
1354	2b	GGTGACGACACTTACTGGGAGGACAGCCACCGCGGCTATGGCTACTCCGGCGTGC	1413	2b	TAAGTAAAGGTTAGCAGAGCAAAAGTGGGTGACGCGTTCCAGATGTGAATTCGCAAACTCATT	2493	
3323	2Y	CCTCAAGGTGGTGAATCCACACCGGGACCGGCGAGCACTGAGGAAACGCGTGTGGCA	3382	2Y	GTGCGGGAGGCTCTGCTGCTGAGCTTCTTCCCGAGCTTTGCTGCTGAGAGAACCCAGAG	4522	
1414	2b	CCTCAAGGTGGTGAATCCACACCGGGACCGGCGAGCACTGAGGAAACGCGTGTGGCA	1473	2b	GTGCGGGAGGCTCTGCTGCTGAGCTTCTTCCCGAGCTTTGCTGCTGAGAGAACCCAGAG	2613	
3383	2Y	CAGGGGAACACCGCGGGGAGGTGCGAACCTTATGCGACGACCCAGGAACATTGGCTG	3442	2Y	CAGCGCACGCGCGGAAAGCGGCATCTAACGCGTATCTAGGCTTTGGTAACTGCGGAC	4582	
1474	2b	CAGGGGAACACCGCGGGGAGGTGCGAACCTTATGCGACGACCCAGGAACATTGGCTG	1533	2b	CAGCGCACGCGCGGAAAGCGGCATCTAACGCGTATCTAGGCTTTGGTAACTGCGGAC	2673	
3443	2Y	GAAGGACTACACGGCTATAGGTGGACCTGACTACAGGCCCAAGACTGGCTGATCAG	3502	2Y	GAAGTGTCTTTTACCTGATTGATGATACATTTCAATTAAGGTTCCAGTTTATAATATTITG	4642	
1534	2b	GAAGGACTACACGGCTATAGGTGGACCTGACTACAGGCCCAAGACTGGCTGATCAG	1593	2b	GAAGTGTCTTTTACCTGATTGATGATACATTTCAATTAAGGTTCCAGTTTATAATATTITG	2733	
3503	2Y	AGCTTAGTCAAGGAAACAGGTCATGGCAGACTCAGGACCTATCTATGACCAAC	3562	2Y	TTAATATTTTATAGTGACTAGAAATGCAATCTCCTATTTACCACTTAATTTAAATA	4702	
1594	2b	AGCTTAGTCAAGGAAACAGGTCATGGCAGACTCAGGACCTATCTATGACCAAC	1653	2b	TTAATATTTTATAGTGACTAGAAATGCAATCTCCTATTTACCACTTAATTTAAATA	2793	
3563	2Y	CTACGCTGGGGGGCGGTGCTTATTTGCTCTCTCAAGAAATGGTCTATTTCAGA	3622	2Y	TGCTTAGTAAACACATATGTAGTATAATTTCTAGAAACAAACATCTAATAAGTATAATC	4762	
1654	2b	CTACGCTGGGGGGCGGTGCTTATTTGCTCTCTCAAGAAATGGTCTATTTCAGA	1713	2b	TGCTTAGTAAACACATATGTAGTATAATTTCTAGAAACAAACATCTAATAAGTATAATC	2853	
3623	2Y	CCTCAAGTACGAATGACAGATATTTAAACAAGTTGCTGCAATTTCCGCAATGCCCTG	3682	2Y	CTGTGAAAATATAGGCTTGATAATATTAAGTTGTCAGATGAAGCATGCTAGAAGCTGT	4822	
1714	2b	CCTCAAGTACGAATGACAGATATTTAAACAAGTTGCTGCAATTTCCGCAATGCCCTG	1773	2b	CTGTGAAAATATAGGCTTGATAATATTAAGTTGTCAGATGAAGCATGCTAGAAGCTGT	2913	
3683	2Y	TGCATGCCATGGTCCCTAGACACCTCAGTTCAATGTGGTCTTGTGGCTTCTCTCTAG	3742	2Y	RACGAATACATAGAGATATAGGAGTTTATCATGGAACCTTAAATATATATAATGTTGC	4882	
1774	2b	TGCATGCCATGGTCCCTAGACACCTCAGTTCAATGTGGTCTTGTGGCTTCTCTCTAG	1833	2b	RACGAATACATAGAGATATAGGAGTTTATCATGGAACCTTAAATATATATAATGTTGC	2972	
3743	2Y	CAGCACCTCTGTCCTTGACCTTAACTCTGATGTTCTTCACTCTGCGCAACCCG	3802	2Y	CAGCGATTATAGTTTCAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	4942	
1834	2b	CAGCACCTCTGTCCTTGACCTTAACTCTGATGTTCTTCACTCTGCGCAACCCG	1893	2b	CAGCGATTATAGTTTCAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	3032	
3803	2Y	AAACCCAAAGTCCCTCAGAGATAAATCAATGGAACGAGAGATGAACATCTAACCCCA	3862	2Y	ATTCAAAACGCTGAAAACAAATCAGCAATTTAGTCTGCGGAGCACCCCAATAACAGTCA	5001	
1894	2b	AAACCCAAAGTCCCTCAGAGATAAATCAATGGAACGAGAGATGAACATCTAACCCCA	1953	2b	ATTCAAAACGCTGAAAACAAATCAGCAATTTAGTCTGCGGAGCACCCCAATAACAGTCA	3092	
3863	2Y	CTAGAGAAACCAAGTTGGTGATATAGACTTTATGTGAGTGAATAATGGGATGCC	3922	2Y	TGTGTAATATGCAAGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	5061	
1954	2b	CTAGAGAAACCAAGTTGGTGATATAGACTTTATGTGAGTGAATAATGGGATGCC	2013	2b	TGTGTAATATGCAAGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	3152	
3923	2Y	ATTACATTGCTTTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	3982	2Y	TGCTTTAAGTTGTCATGATCTTTCTGCAGGAATAGTCACTCATCCCACTCCACATAGGG	5121	
2014	2b	ATTACATTGCTTTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	2073	2b	TGCTTTAAGTTGTCATGATCTTTCTGCAGGAATAGTCACTCATCCCACTCCACATAGGG	3212	
3983	2Y	CTTATTGTATTATGTGATATGAGTTGAAGGAATACCTGTGCATTAAGCCATTATGATA	4042	2Y	GTTTAGTAAAGAAAGTCTGTCTGTGATGATGATAGGGGGCAAAATCTTTTCCCTTTT	5181	
2074	2b	CTTATTGTATTATGTGATATGAGTTGAAGGAATACCTGTGCATTAAGCCATTATGATA	2133	2b			

Db	3213	GTATTAGTAAGAGAGTCTGCTCTCTGATGATAGGGGCAAAATCTTTTCCCTTT	3272
Qy	5182	CTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACAATCCATAACTTTAGTCTTAAT	5241
Db	3273	CTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACAATCCATAACTTTAGTCTTAAT	3332
Qy	5242	GTACACATTGCATTTTGCATAAAATTAATTTTGTGTTTCTTTGAGTTGATCGTTGTGT	5301
Db	3333	GTACACATTGCATTTTGCATAAAATTAATTTTGTGTTTCTTTGAGTTGATCGTTGTGT	3392
Qy	5302	TGTTGTTTGTGTCACITTTTACTTTTTTTCGTTGTGAGCTGTATTCCCGAGACCAACGA	5361
Db	3393	TGTTGTTTGTGTCACITTTTACTTTTTTTCGTTGTGAGCTGTATTCCCGAGACCAACGA	3452
Qy	5362	AGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAACAGC	5402
Db	3453	AGCGTTGGGATACTTCATTAAATGTAGCGACTGTCAACAGC	3493

Search completed: March 10, 2004, 10:59:44
Job time : 1407.29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

M nucleic - nucleic search, using sw model

un on: March 10, 2004, 09:19:42 ; Search time 260.112 Seconds
(without alignments)
12152.440 Million cell updates/sec

file: US-10-084-817-25

effect score: 5696
sequence: 1 gactacgtgcactgcagg.....ggtttctataaaaaa 5696

scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0 ,

searched: 682709 seqs, 277475446 residues

total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/6C COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	1550.4	27.2	7231	4	US-09-919-172-64
2	601.6	10.6	2439	4	US-09-023-655-1455
3	590.8	10.4	619	4	US-09-401-064-327
4	559.4	9.8	3074	5	PCT-US93-11725-3
5	523.2	9.2	2820	5	PCT-US93-11725-1
6	428.4	7.5	435	4	US-09-702-705-592
7	428.4	7.5	435	4	US-09-736-457-592
8	428.4	7.5	435	4	US-09-614-124B-592
9	428.4	7.5	435	4	US-09-671-325-592
10	428.4	7.5	435	4	US-09-589-184-592
11	406.2	7.1	411	4	US-09-389-681-223
12	406.2	7.1	411	4	US-09-620-405B-223
13	406.2	7.1	411	4	US-09-339-338-223
14	406.2	7.1	411	4	US-09-633-826B-223
15	406.2	7.1	411	4	US-09-604-287A-223
16	406.2	7.1	411	4	US-09-834-759-223
17	330.6	5.8	438	4	US-09-833-381-1864
18	254.2	4.5	1326	3	US-08-594-031-143
19	251.2	4.4	657	3	US-08-985-526-2
20	162.8	2.9	270	1	US-09-985-799-43
21	162.8	2.9	270	1	US-09-985-799-136
22	162.8	2.9	270	1	US-09-985-799-143
23	162.8	2.9	270	1	US-08-594-031-143
24	162.8	2.9	270	1	US-08-594-031-136
25	162.8	2.9	270	1	US-08-594-031-143
26	104.2	1.8	390	3	US-09-197-649-7
27	100.6	1.8	312	4	US-09-702-705-952

c 28	100.6	1.8	312	4	US-09-736-457-952	Sequence 952, App
c 29	100.6	1.8	312	4	US-09-614-124B-952	Sequence 952, App
c 30	100.6	1.8	312	4	US-09-671-325-952	Sequence 952, App
c 31	88.6	1.6	1926	4	US-09-249-585A-4	Sequence 4, Appli
c 32	88.6	1.6	1931	2	US-09-130-114-2	Sequence 2, Appli
c 33	77	1.4	338	4	US-09-833-381-361	Sequence 361, App
c 34	73.8	1.3	867	4	US-09-216-393B-340	Sequence 340, App
c 35	73.8	1.3	867	4	US-09-216-393B-342	Sequence 342, App
c 36	73.8	1.3	1397	4	US-09-216-393B-343	Sequence 343, App
c 37	73.8	1.3	1397	4	US-09-216-393B-345	Sequence 345, App
c 38	69.6	1.2	275	4	US-09-833-381-359	Sequence 359, App
c 39	64.2	1.1	5163	3	US-08-700-651-1	Sequence 1, Appli
c 40	64.2	1.1	5163	3	US-08-928-361B-4	Sequence 4, Appli
c 41	64.2	1.1	5163	4	US-09-588-995A-4	Sequence 4, Appli
c 42	64.2	1.1	5318	3	US-08-700-651-2	Sequence 2, Appli
c 43	64.2	1.1	5318	3	US-08-928-361B-3	Sequence 3, Appli
c 44	64.2	1.1	5318	4	US-09-588-995A-3	Sequence 3, Appli
c 45	61.2	1.1	5511	3	US-08-928-361B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-919-172-64
; Sequence 64, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 64
; LENGTH: 7231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1399366.20
; NAME/KEY: unsure
; LOCATION: 5601, 5609, 7107
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-64

Query Match	27.2%	Score 1550.4;	DB 4;	Length 7231;
Best Local Similarity	65.9%	Pred. No. 0;		
Matches 2326;	Conservative	0;	Mismatches 1171;	Indels 33;
Gaps	4;			
QY	144	CTGTCCTCTGGCTCTGTGGGTGTGGCCAGCAGCAAGCTGTGTACCCAGGACAAAGAC	203	
DB	197	CTGTCCTCTGTGATGCTGTGTGGCCAGCAGCAAGCTGTGTACCCAGGACAAAGCTGTGTACCCAGGACAAAGAC	253	
QY	204	ACGACCTTCGACCTTTTCAGTATCAGCAACATCAACCGCAAGACCATTTGGCGCCAAAGCAG	263	
DB	254	ACGTCGTTTGACATCTTTGAACTCACCGGGCCGCCCGCAGGGGTCTGGGGCCGACTG	313	
QY	264	TTCCGGGGCCCGACCCCGGGGTGTGGCTGTACCGCTTGTGGCTTGTGACTATACATCCCA	323	
DB	314	GTGAAGGCCCGGACCTTCCAGCCAGCTTCCGATCGAGGATGCCAACCTGATCCCC	373	
QY	324	CCGCTGAACGACAGATGACCTTCAGCAAGATCACCAAGATCATCGGCGCAGAGAGGGGTTTC	383	
DB	374	CTGTGCTGTATGACAAAGTTCCAGACTCTGTGGATGCTGTGGCGCAGAAAGGGTTTC	433	
QY	384	TTCTTCACGGCCCGACCTCAAGCAGGACGCGAAGTCCAGGGGACGCTGTGGTCTCTGGAG	443	
DB	434	CTCCTCTGTGATCCCTGTAGCGCAGATGAAGAAGACCCCGGGGCGAGCTGTGGCCCTGGAG	493	

2y 444 GGCCTGGTCTCTCCAGAGAGCGATCGATCGTCTCCAAAGCGCCCGCGGACAGCTG 503
Db 494 CGAAAGACCACTCTGGCCAGTCTTTCAGCGTGTGTCCATGCGAAGCGGCGACCCCTG 553
2y 504 GATCTCACCTACTGGAATGAGCGGCACCCGCGATGTGTCTCCCTGGAGGACGTCGCGCTG 563
Db 554 GACCTCAGCTGACCGTCCAGGAAGACAGACGCTGTGTCTGTGAAGAAGCTCTCCTG 613
2y 564 GCTGACTCGAGTGGAGAAAGCTCACCGTGCAGGTGCTGGCGAGACCTACAGCTTGCAC 623
Db 614 GCAACCGCGCAGTGGAGAGATCACCTGTGTGTGAGGAAGACAGGCGCCAGCTGTAC 673
2y 624 GTGGCTGCGACCTCATAGACAGCTTCCGCTCTGACGAGCCCTTACGAGACCTGACG 683
Db 674 ATCGACTGTGAAGATGGAGATGCTGAGTGGACGTCCCATCCCAAGCGCTTTCACC 733
2y 684 GCGAAAGAGCCGATGTAGTGGCCAAAGGCTC-----TGGCAGAGAGTCACTTC 737
Db 734 AGAGACCTGGCCAGCATCGCCAGACTCCGCATCGCAAAGGGGGCGGTCAATGACAAATTC 793
2y 738 AGGGTTTGTCTCAGAACGCTCCACTAGTGTGTGAAACTCTGTGGAAGATATTTCTAAGC 797
Db 794 CAGGGGTGCTGAGATGTGAGTGTCTTGGAAACACACAGAGACATCTCTCAGG 853
2y 798 AAGAAGGTTGCCAGAGGCGCAGGAGCTGAGATCAACGCCATCAGTGAAGACACAGAG 857
Db 854 AACAAAGGCTG-----TCCAGCTTACCAGTGTCTCTCACCCTTGACAAACAGCTG 907
2y 858 ACGTGGCGCTGGTTCGCGATGTCCACACGAGTACGTGGCGCCCGACCTCAGAGAGGAGG 917
Db 908 GTGAATGGTTCAGCCCTGCCATCGCACTAACCTAATGATGGCCACAAGACAAAGGACTTG 967
2y 918 CCCAGAGTGTGGAACGCTGTGCGAGAGCTGGGAAACATGTGTCCAGGAGCTCTCGGG 977
Db 968 CAAGCCATCTCGGCATCTCTGTGATGAGTGTCCAGCATGTGTCTCGAATCAGGGGC 1027
2y 978 CTCACAGTCTGTGAAACGCTCAGCGAGAACCTCAAGAGAGTGTGCAATGATAACCAAG 1037
Db 1028 CTGGCCACCATGTGACACGCTCGAGGACAGCATCGCAAGTGAATGAGAGAGACAA 1087
2y 1038 TTTCTCTGGAGCTCATTTGTGGCCCTCTTAAGACAAAGAACATGTGAGTGTCTGCGCAG 1097
Db 1088 GAGTTGGCAATGAGTGTGAGCGCGCTC-----CCCTATGCTATCAC 1129
2y 1098 GATGCCCGTCTTTGGGAAATGAAACGTGGTGGTGGACAGCTGCACCAAGTGTACC 1157
Db 1130 AACGGAGTTCAGTACAGAAATAACGAGAAATGAGTGTGATAGCTGCATGAGTGTAC 1189
2y 1158 TGCAAGAAATTTAAACCATTTGCCACCAATCACCTGCCCGCTGCAACCTCGGCCAGT 1217
Db 1190 TGTGAGAACTCAGTTACCATCTGCAAAAAGGTGTCTGCCCATCATGCGCTGTCCAA 1249
2y 1218 CATCTCTTTGGAAAGCGAATGTGCGCTTCTCCCTCCACTCGGTGGAGGTGAGGAG 1277
Db 1250 GCCACAGTCTCTGATGGAGAAATGTGTCTCGCTGTGGCCACGCGACTGTGCGGAGCAT 1309
2y 1278 GGCTGCTCTCGTGGGAGAGTGGACCCAGTGTCTCCGTGACGTGTGGCTGTGGAGCCAG 1337
Db 1310 GGCTGCTCTCATGGTCCGAGTGGACCTCTGTCTACGAGCTGTGGCAATGGAATTCAG 1369
2y 1338 CAGAGAGCCGGTCTGTGACGTGCACAGCAACACCTGCTTTGGGGCCCTCCATCCAGACA 1397
Db 1370 CAGCGCGCGCTCTCTGCGATACGCTCAACACCGCATGTGAGGGCTCTCTCGGTCCAGACA 1429
2y 1398 CGGGTTCAGTCTGAGCAAGTGTGACACCGCATCCGGCAGGACGCGGTGTGAGGCCAC 1457
Db 1430 CGGACTGCCACATTCAGAGTGTGACAGAGATTTAAACAGGATGTGTGCTGGAGCCAC 1489
2y 1458 TGGTCACTTGGTCTTCAATGTCTGTGACCTGTGGAGTGTGGCAATATCACCGCATCCGT 1517
Db 1490 TGGTCCCGTGTGATCTTGTCTGTGACATGTGTGTGATGTGTGATCAACAGGATCCGG 1549

Qy 1518 CTCTCAACTCCCAAGTCCCAAGTGGGGGCAAGAAATTCGAAAGGAGTGGCGCGGAG 1577
Db 1550 CTCTGCAACTCTCCAGCCCCCAGATGAAACGGGAAAACCTGTGGAAGCGAAGCGCGGAG 1609
2y 1578 ACCAAAGCCTGCGAGGGCGCCCATGCCCATAATGATGCGCGCTGAGACCCCTGTGCTCCG 1637
Db 1610 ACCAAAGCCTGCAAGAAAGACGCTGCCCATCAATGAGGCTGGGTCTCTTGTGTACCA 1669
2y 1638 TGGTGGGCTCGCACTGTCTCAGCTGTGCGGTGGGATCGGGAGCGACACCGGGCTCTGCAAC 1697
Db 1670 TGGGACATCTGTCTGTCACTGTGTGGAGAGGGTACAGAAACGTAGTCTCTCTGCAAC 1729
2y 1698 AGCCCTGAGCTCAGTACGAGGGAAGCCCTGCGTGGGGATGTGCAAGAGCGTCAAGT 1757
Db 1730 AACCCACACACCCAGTTTGGAGGCAAGGACTGCGTGTGTGATGTAAACAGAAACAGATC 1789
2y 1758 TGCAACAGAGAGAGTGCCTGCTGATGCGTGTATTCACACCCCTGCTTCCCGGAGCC 1817
Db 1790 TGCAACAGAGAGTGTCTCAATGTGATGATGCTGTCCATCTCTGCTTTCGCGCGGTG 1849
2y 1818 CAGTGCAGCAGCTTCCCGATGGGTCTGTGTCATGCGGCTCTTCCCTGTGGGTTCCTG 1877
Db 1850 AAGTGTACTAGTACCTGTGATGGAGCTGGAATGTGTGTCTTCTCCCTGTGTACAGT 1909
2y 1878 GCAATGACACCCACTGTGAGGACCTGACGAGTGTGCCCTGTGCTCCCGACATCTGCTTC 1937
Db 1910 GGAATGCACTCCAGTGCACAGATGTGTGATGATGCAAGAAAGTGCCTGTGCTGCTTC 1969
2y 1938 TCCACCAAGAGTGTGCTCGCTGTCAACTCAGCCTGTGCTTCCACTGCTGCCCTGTC 1997
Db 1970 AACCACAATGAGAGACACCGGTGTGAGAAACACGGAACCCGCTACAACTGCTGCTGCTC 2029
2y 1998 CGGCCCCATACAGAGGAACACGCGCTCGGGTTCGCTTGGAGCAGCGCAAGCGAA 2057
Db 2030 CCCCACGCTTACCGGCTCAGCGCTTCAGCGCTTCGGCAGGGTGTGCAACATGCCACGCGCAAC 2089
2y 2058 AAGCAAGTGTGTGAGCCCGGAAAACCCATGCAAGGACAGACACACAACTGCCACAAGCAC 2117
Db 2090 AACAGGTGTGCAAGCCCGTAAACCCCTGCAAGTGGACCCACGCTGCAACAAGAAC 2149
2y 2118 GCGGAGTGTACTCTGGCCACTTACGACACCCCATGTACAGTGGAGTGGAGTGCAGACA 2177
Db 2150 GCCAAGTGCATCTCTGGCCACTATAGCAGACCCCATGTACCGCTGCGAGTGCAGAGCT 2209
2y 2178 GGCTACGGGGGAGCGGCTCATCTGCGGGAGGACTCGGACCTTGGAGCGGTGGCCCAAC 2237
Db 2210 GGCTACGCTGGCAATGGCATCATCTGCGGGAGGACACAGACCTGGATGGTGGCCCAAT 2269
2y 2238 CTCATCTGCTGTGCGCCACCAACGCCACCTACACTGCATCAGAGATACTGCCCCAT 2297
Db 2270 GAGAACCTGTGTGGGTGGCCAAATCGGACTTACCACTGCAAAAAGGATAATTTGCCCAAC 2329
2y 2298 CTGCCAAATTTCTGGCAGGAAAGCTTTCAGAGGACGGGATTTGGGATGCTGTGATGAT 2357
Db 2330 CTTCCCACTCAGGCGAGGAGACTATGACAGGATGGAATTTGGTGTGCTGTGATGAT 2389
2y 2358 GACGATGACATGACGGTGTGACCGATGAGAAAGGACAACTGCGAGCTCTCTTCAATCCC 2417
Db 2390 GACGATGACATGATAAAATTCAGATGACAGGGACAACTGTCTCATTTACATACACCA 2449
2y 2418 CGCCAGGCTGACTATGACAGGATGAGGTGTGGGACCGCTGTGACAACTGCCCTTACGCTG 2477
Db 2450 GCTCAGTATGACTATGACAGAGATGATGTGGAGACCGCTGTGACAACTGTCTCTACAC 2509
2y 2478 CAACAACCTTCCAGATCGACACAGACAAACAAATGAGAGGGTGCAGCTGTCTCGTGGAC 2537
Db 2510 CACAACCCAGATCAGGACAGACACAGACAAACAAATGGGAAAGGAGACGCTGTGTCTCAGAC 2569
2y 2538 ATTGATGGGACGATGTCTCAATGAACGAGACAAATGCTCCCTAGCTTACAACTGAC 2597
Db 2570 ATTGATGGAGCGGTATCTCAATGAACGGGACAACTGCTCCAGTACTCTACAACTGTGAC 2629
2y 2598 CAGAGGACACCGATGGTGAACGGTGTGGGGGATCACTGTGACAACTGCCCTGTGTGAC 2657

```

b 2630 CAGAGAGACTGATATGATGGGTGGAGATCAGTGTGACAAATGGCCCTTGAACAC 2699
Y 2658 AACCTGACAGACCGAAGTGGACAAATGACTTGTGGGACCAAGTGTGACAAACGAG 2717
b 2690 AATCCGGATCAGTGGACTCTGACTCAGACCGCATTTGGAGATACCTGTGCAACAAATCAG 2749
Y 2718 GACATAGATGACAGCGCCACAGAACCAACAGGACAACTGCGCCCTACATCTCCAAAGCC 2777
b 2750 GATATGATGAAGTGGCCACAGAACATCTGGACAACTGCTCCATGTGCCCATGCC 2809
Y 2778 AACAGGCTGACATGACAGACGCGCCAGGCGACGCTGTGACCCCTGATGATGACAAAC 2837
b 2810 AACAGGCTGACATGACAAAGATGCAAGGAGATGCTGTGACCAAGATGATGACAAAC 2869
Y 2838 GATGGCGTCCCGATGACAGGAGCAACTGCGCGCTGTGTTCAACCCAGACAGGAGGAC 2897
b 2870 GATGGCATCTCTGATGACAGGACAACTGACAGCTGTGCCAATCCGACAGAGAGAC 2929
Y 2898 TTGGACGGTGTGAGCGGGTGATATTTGTAAGATGATTTTGAACAATGACAAATCCCA 2957
b 2930 TCTGACGGGATGGTGGAGTGTGCTGCTGCAAAAGATGATTTTGACCATGACAGTGTGCCA 2989
Y 2958 GATATGATGATGTGCTGCTGAAACAAATGCAATGCAATGACAGACAGCTTCAGGAATTC 3017
b 2990 GACATGATGATCTGCTGAGATGTGACATGATGACAGGACGACTTCGCGGATTC 3049
Y 3018 CAGATGCTCCCTTGGATCCCAAGGAGCACCCAAATGTATCCCAACTGGGTCTATTCGC 3077
b 3050 CAGATGATCTCTGGACCCCAAGGACATCCCAAAATGACCCCTAACTGGTGTACGC 3109
Y 3078 CATCAAGGCAAGAGTGTGATGACAGCACTCGGACCCCGGATCGCTGTAGGTTT 3137
b 3110 CATCAGGTAAGAACTGCTGAGACTGTCACTGTGATCTCTGAGACTCGCTGTAGGTTAT 3169
Y 3138 GACGAGTGTGGTCTGTGACTTCACTGTCACATTTCTAGTAAACACTGACCGGACGAC 3197
b 3170 GATGATTTAATGCTGTGACTTCAGTGGACACTTCTTCTATCAACACCGAAGGACGAT 3229
Y 3198 GACTATCGCGCTTGTCTTTGTTACAGTCAAGAGCGCTTCTATGTGGTGTATGTTGG 3257
b 3230 GACTATGCTGGATTTGTCTTTGGCTACCACTGACAGCGCGCTTTTATGTTGTGTTGG 3289
Y 3258 AAGCAGTCAAGCAGACTTCTGAGGAGGACCGACCGCGGCTTATGCTACTCGGC 3317
b 3290 AAGCAGTCAAGCAGTCTTCTGAGACACCAACCCACGAGGCTCAGGATCTCGGC 3349
Y 3318 GTGTCCCTCAAGTGTGAACTCCACCGGAGCGGCGAGCACTCAGGAACCGCTG 3377
b 3350 CTTTCTGTGAAAGTTGTAACCTCCACACAGGCGCTGCGAGCACTCGGAAACGCGCTG 3409
Y 3378 TGCCACACGGGGAACACCGCGGCGAGGTGCAACTTATGSCACGACCCAGGAACATT 3437
b 3410 TGSCACACAGGAACACCCCTGCGCAGGTGCGACCCCTGTGTCATGACCTCTGTACATA 3469
Y 3438 GGTGGAAGGACTACACGCGCTATAGTGGCAGCTGACTCAGAGCCCAAGCTGCTAC 3497
b 3470 GGTGGAAGGATTTCAACCGCTACAGATGGCTCTCAGCCACAGGCCAAGACGCGTTTC 3529
Y 3498 ATCAGAGTCTTAGTGAAGGAACAGGTGATGCGAGACTCAGGACCTCTATGAC 3557
b 3530 ATTAGAGTGGTATGATGAAGGAAGAAATCATGGCTGACTCAGGACCCATCTATGAT 3589
Y 3558 CAACCTAGCTGGCGGCGGTGGTCTATTGTTCTCTCAAGAAATGGTCTATTTC 3617
b 3590 AAAACCTATGCTGGTGTAGACTAGGTTGTTGTTCTCTCTCAAGAAATGGTGTTC 3649
Y 3618 TCAGACTCAAGTACGAATGACAGATATTTAAACAGATTTGCTGCAAT 3667
b 3650 TCTGACCTGAATACGAATGTAGAGATCCCTAATCATCAAAATTTGTTGAT 3699

```

RESULT 2

```

US-09-023-655-1455
; Sequence 1455, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1455:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9602449
US-09-023-655-1455

Query Match 10.6%; Score 601.6; DB 4; Length 2439;
Best Local Similarity 63.1%; Pred. No. 3.3e-134;
Matches 947; Conservative 0; Mismatches 544; Indels 9; Gaps 1;

QY 2146 GCGACCCCATGTACAGTGCAGTGCAGACAGCTACGCGGCGAGCGGCTCATCTGCG 2205
Db 765 GCGATGGCTCGCGGTGTGCTGTGCTGCTGGCGCGGCAACGGATCTCTGTG 824
QY 2206 GGGAGGACTCGGACCTGGACGGCTGCGCCCAACCTCAATCTGTCTCGCCCAACGCA 2265
Db 825 GTCGACACTGACCTAGACGGCTTCCGAGACGAGAAGTGTGCTGCTGCGGAGCGG--- 880
QY 2266 CTTACCTGCTCATCAGGATACTGCCCCCATCTGCAAAATCTTGGGCGAGAGACTTG 2325
Db 881 -----CAGTCCCTAAGGACAACTGGTGACTGTGCCCACTCAGGCGAGGAGTGTGG 935
QY 2326 ACAAGACGGGATTTGGCGATGCTGTGATGATGATGATGATGATGATGATGATGATGATG 2385
Db 936 ACCGCGATGTCATCGGAGACGCTGCGATCCGATCCGATCCGAGCGGCGGTTCCCAATG 995
QY 2386 AGAGGACACTGCGAGCTCTCTTCAATCCCGCGGCTGACTGATGATGATGATGATGATG 2445
Db 996 AAAAGGACAACTGCGCGCTGTGTCGGAACCCAGACCGAGCGCAACCGGACGAGCAAGT 1055
QY 2446 TTGGGACCGCTGTGACAACTGTCCTTACGTGCAACAACTGTCGCCAGATGTCACACAGCA 2505

```

1056 GGGCGATGCGTGGCACTGCGGTCCAGAGAACGACGACCAAGAGGACAGACC 1115
 2506 ACAATGAGAGGTGACGCTGCTCGTGGACATTTGATGGGAGCAGATGCTTCAATGAAC 2565
 1116 AGACGCGCGGGCGATGCGTGGACGACATCATCGCGGACCGGATCCGCAACCAAG 1175
 2566 GAGACAATTGCTCCTAGCTTACAACTGACAGAGGACACGAGTGGTGGCGGTGG 2625
 1176 CCGACAACCTGCTAGGTACCCAACTCAGACAGAGGACGATGATGCGATGATAG 1235
 2626 GGGATCACTGTGCACTGCGCCCTGGTGCAAACTGACGACGACCGAGTGGCAATG 2685
 1236 GGGATGCTGTGCACTGCTCCCGAGAGGACACCGCGATCAGGGGATGTTGGACAG 1295
 2686 ACCTTGTGGGACGAGTGTGACAACTGAGGACATAGATGACGACGCGACCAAGAAC 2745
 1296 ACCTTGTGGAGATGCTTGTGACGAGCATCAAGCCAGGATGAGACGACATCAGGACT 1355
 2746 ACCAGGACAACTGCCCTACATCTCCAAAGCCAACTGACGATGACGAGAGCGCC 2805
 1356 CTGGGACAACTGCTCCAGCGTGCCTAACAGTGCCTCCAGGAGGACTCAGACCAAGTGGCC 1415
 2806 AGGCGAGCGCTGTGACCTGATGATGACAACTGCGTCCCGGATGACGAGCAACT 2865
 1416 AGGTGATGCTGCGAGCAGCAGCAGCATGACGAGTCCCTGACATCGGACACT 1475
 2866 GCGGCTTGTGTTCAACCCAGACGAGGACTTGACGCGTGTGACGCGGTGATATT 2925
 1476 GCGGCTTGTGTTCAACCCAGACGAGGACTTGACGCGTGTGACGCGGTGATATT 2925
 2926 GTAAGATGATTTGACAACTGACAACTCCAGATTTGATGATGATGCTCTGAAACA 2985
 1536 GCCAGGACGACTTGTGACGAGCAAGGTGTGACAGATCGACGCTGTCCGAGACG 1595
 2986 ATGCCATCAGTACAGACAGACTTCAGGAACCTCCAGATGCTCCCTTGGATCCCAAGGA 3045
 1596 CTGAAGTACGCTCAGGCTTACAGGCTTCCAGACAGTCTGCTGGACCGGAGGCTG 1655
 3046 CCACCAAAATGATCCAACTGGGTCTATCGCATCAAGCAAGGAGGCTGTTTACACAG 3105
 1656 ACGCGAGATGACCCCACTGGGTGTGCTCAACAGGGAAGGAGATCGTGACACAA 1715
 3106 CCAACTCGGACCGCGCATCGCTGATGTTGACGAGTTTGGGTCTGTGGACTTCAGTG 3165
 1716 TGAACAGGACCGAGCTGCTGCTGGTTTACACTGCTTCAATGGCGTGGACTTCGAGG 1775
 3166 GCACATTTACGTAACACTGA CCGGAGCAGCAGCTATGCGGCTTGGCTTTGGTTACC 3225
 1776 GCACGTTTCCATGTGAACACGCTCACGGATGACGACTATGCGGCTTCACTTTGGCTACC 1835
 3226 AGTCAAGCAGCGCTTCTATGCTGATGTTGGAAGCAGGTGACGACACTCTGGGAGG 3285
 1836 AGGACAGCTCCAGCTTCTACGCTGATGTTGGAAGCAGGTGGAACAACTATGGCAGG 1895
 3286 ACCAGCCACCGCGGCTTATGCTTATCCTCGGCTGCTCCCTCAAGGTTGTAATCCACCA 3345
 1896 CGAACCCCTTCCGCTGCTGCTGCGGCTGCTGCTCAACTCAAGGCTGTGAGCTTCCA 1955
 3346 CCGGAGCGGCGAGCAGCTGAGGAGCAGCTGCTGCGACACGCGGACACCGCGGCGAGG 3405
 1956 CAGGCGCGGGAACAGCTGCGGAACGCTCTGTGGCAATACAGGAGACAGATGCCAGG 2015
 3406 TCGAACTTTATGCAACGACCCCAAGCAATTTGCTGGAAAGGACTACACGCGCTATAGGT 3465
 2016 TCGGCTGCTGTGAAGGACCGCGGAACGTTGGGTTTGAAGGACAGAGTCTATCGTT 2075
 3466 GGCACCTGACTCAGAGCCCAAGACTGGCTACATCAGCTTGTAGTGCAAGGAAAC 3525
 2076 GTTCTCTGACACCGGCGCCCAAGTGGCTTACATCAGGTCGCTTATGAGGCGCTG 2135
 3526 AGGTCAATGGAGACTCAGGACCTATCTATGACCAAACTTACGCTGGCGGCGCTGGTC 3585

2136 AGCTGTGGCGGACAGCAACGCTGCTTGTGACACAAACCATGCGGGTGGCGCTGGGG 2195
 3586 TATTGTCTTCTCTCAAGAAATGCTCTATTCTCAGACCTCAAGTACGAATGCAGAGATA 3645
 2196 TCTTCTGCTTCTCCAGGAGAACATCATCTGGGCAACCTTGGCTTACCGTGCATGACA 2255

RESULT 3
 US-09-401-064-327/c
 ; Sequence 327, Application US/09401064
 ; Patent No. 6623323
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeline Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tongtong
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.471C2
 ; CURRENT APPLICATION NUMBER: US/09/401.064
 ; CURRENT FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 371
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 327
 ; LENGTH: 619
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(619)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-401-064-327

Query Match 10.4%; Score 590.8; DB 4; Length 619;
 Best Local Similarity 98.2%; Pred. No. 5.6e-132;
 Matches 606; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 4082 TTAAGTGTGCTACATCTTCTGAATTAGATTGCTCTCAATGACACACAAATCCC-GCTA 4140
 DB 617 TAAAGTTGTGCTACATCTTCTGAATTAGATTGCTCTCAATGACACACAAATCCC-GCTA 558
 QY 4141 AATAAATTTATAAACAAGGTCATTTCAAAATTTAGTAAATTTAGTAAAGAGATTA 4200
 DB 557 AATAAATTTATAAACAAGGTCATTTCAAAATTTAGTAAATTTAGTAAAGAGATTA 498
 QY 4201 GAAGCAACAGCGATGACAAATGACATGACGATTAATGACGATTAATGACGATTAATAA 4260
 DB 497 GAAGNCTWCAGGATGACAAATGACATGACGATTAATGACGATTAATGACGATTAATAA 438
 QY 4261 CAGTTTACAAAATAAACAAGGTCATTTCAAAATTTAGTAAATTTAGTAAAGAGATTA 4320
 DB 437 CAGTTTACAAAATAAACAAGGTCATTTCAAAATTTAGTAAATTTAGTAAAGAGATTA 378
 QY 4321 GAGATGCAATTTATCAAAAGAACAAATCTTTCGAAATGCGTGTGATGCGGTTCCAGAT 4380
 DB 377 GAGATGCAATTTATCAAAAGAACAAATCTTTCGAAATGCGTGTGATGCGGTTCCAGAT 318
 QY 4381 GTGGATTTGGCAAAACCTTCATTTAAGTAAAGGTTAGCAGAGCAAAAGTTCGCTTTAG 4440
 DB 317 GTGGATTTGGCAAAACCTTCATTTAAGTAAAGGTTAGTAAAGGTTAGTAAAGGTTAG 258
 QY 4441 CTGCTGCTTGTGCGCTGTGCTGCGGAGGCTCTGCTGAGCTTCCCTTCCCGAGTT 4500
 DB 257 CTGCTGCTTGTGCGCTGTGCTGCGGAGGCTCTGCTGAGCTTCCCTTCCCGAGTT 198
 QY 4501 TGCTGCTGAGAGGAGCAGAGCAGCAGCGCGGAAAGGCGCATCTAAAGCGCTAT 4560
 DB 197 TGCTGCTGAGAGGAGCAGAGCAGCAGCGCGGAAAGGCGCATCTAAAGCGCTAT 138
 QY 4561 CTAGCTTGTGTAATGCGGACAAAGTTCCTTTTACCTGATTTGATGATACATTTCAITAA 4620


```

b 137 NTAGCTTTGGTAACTGCGGACAGTCTTTTACCTGATTGATGATACATTTCATTAA 78
y 4621 GGTTCAGTTATTAATATTTGTTAAATTTTATTAAGTACATATAGATGCACTCCATT 4680
b 77 GGTTCAGTTATTAATATTTGTTAAATTTTATTAAGTACATATAGATGCACTCCATT 18
y 4681 TACCAGTAACTTATTTT 4697
b 17 TACCAGTAACTTATTTT 1

```

```

RESULT 4
CT-US93-11725-3
Sequence 3, Application PC/TUS9311725
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN THROMBOSPONDIN-4
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield, & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch
COMPUTER: IBM-compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11725
FILING DATE: filed herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/985,296
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: GATES, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7005WO
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: no
CT-US93-11725-3

```

```

Query Match          9.8%; Score 559.4; DB 5; Length 3074;
Best Local Similarity 62.1%; Pred. No. 5.2e-124;
Matches 928; Conservative 0; Mismatches 546; Indels 21; Gaps 2;

y 2163 TGGAGTGGCCAGACAGGCTACCGGGCGACGGGCTCATCTGGGGAGAGACTCGGACCTG 2222
b 1369 TGTGTGTGGAGTGGTGGGCTGGAGATGGCTATCTGTGAAAGGATGTGGACATC 1428
y 2223 GACGGCTGGCCAACTCAATCTGGTCTGGCCACCAACGCCACCTACCACTGCATCAAG 2282
b 1429 GACAGTTACCCGACGAAGAACTGCCATCTTGCCA-----GGAACTGTAAAG 1479
y 2283 GATACTGCCCCCATCTGCCAAATTTGGGCGAGGAGACTTTGACAAAGACGGGATTGGC 2342
b 1480 GACAACTGCAATATGTGCCAAATTTCTGCCAAGAGATGCCAGACAGAGATGGCATGGC 1539
y 2343 GATGCTGTGATGATGACATGACATGACATGACGATGACGATGACGATGACGATGACGAT 2402
b 1540 GACGCTGTGACAGGATGCTGACGAGATGGATCTCTGAATGAGCAGGATAACTGTGTC 1599
y 2403 CTCCTCTCAATCCCGCAGGCTGACTATGACAAAGGATGAGGTTGGGACCGCTGTGAC 2462

```

```

1600 CTGATTCTATAATGTGACCAAGAAAGAGATATCTTTGGGATGCTCTGTGAT 1659
2463 AACTGCGCTTACGTGACACACCTGCTCCAGATCGACACAGACAAATCGAGAGGTGAC 2522
1660 AACTGCTGTAGTGTCTTAAATACGACCAAGAACACCGATGGGATGGAAGAGAT 1719
2523 GCTGTGCTGGTGGACATTTGATGGGACGATGCTTCAATGAACGAGACAAATTTGTCCTAC 2582
1720 GCCTGTGATGATGACATGGATGGAGATGGAATAAAAAACATTTCTGACAACTGCCCAAA 1779
2583 GTCTACAACTGACACGAGGAGACCGGATGTGACGGTGTGGGGATCACTGTGACAA 2642
1780 TTTCCCAATCGTGAACCAACCGGACAGGATGGTGTGGGGATGCTCTGTGACAT 1839
2643 TGCCCTCTGTGCAAAACCTGTACAGACCGCTGACCAATGATGATGATGATGATGATGAT 2702
1840 TGTCTCTGTGTCAGCAACCTTAACAGTCTGTGATGATGATGATGATGATGATGATGAT 1899
2703 TGTGACAAACGAGGACATAGATGACGAGCGCCACCAAGAACCAACGAGACAACTGCC 2762
1900 TGTGACCAACCAATCAGGACAGTGTGATGGATGGGACCAAGACAGACAGACAACTGCC 1959
2763 TACATCTCCAAACCGCAACCGAGCTGACCATGACAGAGACGGCCAGGCGACGCTGTGAC 2822
1960 ACCGTCAATTAACAGTGTGCTGACACCGGATGGAATTTGTTGACGATGATGAT 2019
2823 CTGTGATGACAAACGATGCTGCCGA-----TGACAGGACAACTGCC 2870
2020 GATGATGATGACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2079
2871 CTGTGTCTCAACCCAGACAGGAGGACTTGGACGGTGTGAGCGGCTGATATTTGTAA 2930
2080 CTGTGCTCCCAACCCAGGAGGATGACACAGGACGGAGTGGAGACATCTGTGAT 2139
2931 GATGATTTTGAACATGACAACTCCAGATATTTGATGATGATGATGATGATGATGATGATGAT 2990
2140 TCTGACTTTGACAGGACCGAGTCTGATCGATCGATCGATCGATCGATCGATCGATCGAT 2199
2991 ATCAGTGGAGACAGACTTCCAGAACTTCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3050
2200 GTACCTGACCGACTTCCAGGCTTACAGACCGTGGGCTGATCTTGAAGGGATGCC 3259
3051 CAAATTGATCCCACTGGGTCTATTCGCCATCAAGGCAAGAGCTGGTTGAGACGCAAC 3110
2260 CAGATCGATCCCACTGGGTCTTCTGAAACAGGCGATGGAGATTGTACAGACCATGAAC 2319
3111 TCGGACCCCGGCTCGCTGTAGGTTTGTGAGCTTTGGGCTCTGTGACTTCACTGTGACCA 3170
2320 AGTATCTCTGGCTGGCAGTGGGTTACAGCTTTTATGGAGTTGACTTCCGAGGAC 2379
3171 TTCTACGTAAACACTGACCGGACGACGACTATGCGGGCTTCTCTTTGGTTACAGTCA 3230
2380 TTCCATGTGAATACCCAGACAGATGATGACTATGACGGCTTTATCTTTGGCTACCAAGAT 2439
3231 AGCAGCGCTTCTATGTGTGATGTGAGAGCAGTGTGACGACGACTTCTGAGGAGGAC 3290
2440 AGCTCCAGCTTCTACGTTGCTGTGAGAGCAGACGAGCAGACATATTGGCAAGCAAC 2499
3291 CCACAGCGGCTTATGCTACTCCGGCTGTCTCCCTCAAGGTGCTGAACTCCACCAACGGGG 3350
2500 CCATTCCGACAGTTGACAACTGCAATTCAGTCAAGGCTGTGAAGTCTAAGACAGGT 2559
3351 ACGGCGAGACCTGAGGAAACCGCTGTGACACCGGGAACACGCGGGGAGGTGCGA 3410
2560 CAGGGGAGATCTCCGGAACTCCCTGTGGCAACGCGGGGACACCACTGACAGGTGAC 2619
3411 ACCTTATGGACACACCCAGGAACTTGGCTGGAAGACTATACAGGCTTATAGGTGGCAC 3470
2620 CTGCTGTGGAGGACTCCAGGATGTGGGCTGGAAGACAAAGGTGCTTACCGCTGTTTC 2679
3471 CTGACTCAGAGGCGCAAGACTGGCTACATCAGAGTCTTAGTGTGATGAAGAAACAGGTC 3530
2680 CTACAGCAGACGGGCGGCTGAGTGGGCTACATCAGGCTACAGTTTATGAAGGCTCTGAGTTG 2739

```

2y 3531 ATGCGAGCTCAGGACCTATCTATGACCAAACTACGCTGGGGGGCTGGTCTATT 3590
2b 2740 GTGGCTGACTCTGGCTCACCATTAGACACCAATCGGTGGAGCCGACTTGGCTTTC 2799
2y 3591 GTCTTCTCTCAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATGCGAGATA 3645
2b 2800 TGCTTCTCTCAAGAAACATCATCTGCTCCAACTCAAGTATCGCTGCAATGACA 2854

RESULT 5

PCT-US93-11725-1
Sequence 1, Application PC/TUS9311725
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN THROMBOSPONDIN-4
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield, & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch
COMPUTER: IBM-compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11725
FILING DATE: filed herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/985,296
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: GATES, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7005W0
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Xenopus laevis
DEVELOPMENTAL STAGE: Stage 45 (germ line)
PCT-US93-11725-1

Query Match 9.2%; Score 523.2; DB 5; Length 2820;
Best Local Similarity 61.8%; Pred. No. 2.4e-115;
Matches 856; Conservative 0; Mismatches 518; Indels 12; Gaps 1;
Qy 2272 ACTGATCAAGGATAAATGCCCCCATCTGCCAAATCTGGCGAGGAAGAATTGCAAGG 2331
Db 1235 ACTGCAAAAGGACAACTGTGTATATGTTCTTAACCTCGGGTCAAGAAGACACTGATAAG 1294
Qy 2332 ACGGATTTGGCGATCGCTGTGATGATGACGATCAATGACGGTGTGACCGATGAGAGG 2391
Db 1295 ATACATTGGAGATGCTTGTGATGAAGTGGGATGGAGATGATCTTAATGAGCAGG 1354
Qy 2392 ACAACTGCCAGCTCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGG 2451
Db 1355 ACNACTGTGTGGCTGCCAACATCGATCAGAAAAACAGTGACCAAGATATATTGGGG 1414
Qy 2452 ACCGCTGTGACAACTGCCCTTACGTGACACACCTGCCAGATCGACACAGACAACATG 2511
Db 1415 ACGCTGTGACAACTGCCCTTAACTCAACATGACCAAGGACACAGACAATGACG 1474
Qy 2512 GAGAGGGTGACGCTCTCCGTGGGACATTTGATGGGGACGATGCTTCAATGAACAGACA 2571

Db 1475 GGAAAGGAGATGCTTGTGACGATGACATGGATGGATGGCATCAAGAAATATCTTGGATA 1534
Qy 2572 ATTTCTCCTACGCTCTACCACTGACGAGGAGGACCGGATGTGTGCGGTGGGATC 2631
Db 1535 ACTCCAGAGAGTTCCCAATGTGGACCGAAGAAAGATGGAGATGGATGGTGGTATA 1594
Qy 2632 ACTGTGACAACTGCCCTTGTGTGCACAACTGTGACCAAGCCGACGCTGGGACAATGACCTTG 2691
Db 1595 TATGTGACAGCTGTCTGTGACATCAATAATCCAAACCACTGACAGCAATGACAATGACCTTG 1654
Qy 2692 TTGGGGACCACTGTGACAAAGGAGGACATAGATGACGCGGACCGCCACAGCAAGCAACAGG 2751
Db 1655 TTGGAGATTCCTGTGATACCAACAGACAGCGGATGTGTGATGTCACCAAGACAGCAG 1714
Qy 2752 ACAACTGCCCTACATCTCCAAACCGCAACGAGCTGACCAATGACAGAGCGCGGAGCG 2811
Db 1715 ACAACTGCCCCACAGTGATAAACAGCAACCACTGACAGACAGCAAGGACGGCATCGAG 1774
Qy 2812 ACGCTGTGACCTGTGATGACAAAGGATGGCTGCCCGAT-----GACAGGG 2859
Db 1775 ATGAATGTGACGATGATGATTAACGATGGAAATCCCGGATACGTTCCTCCCGGACCTG 1834
Qy 2860 ACAACTGCCGCTTGTGTTCAAACCCAGACAGGAGGACTTTGGACGGTGTGAGCGGGTG 2919
Db 1835 ATAACTGTAACTGTTCCCAACCCAGCGGAGGAGGATGACAAATGATGGAGTGGAG 1894
Qy 2920 ATATTGTAAAGATGATTTTGAATGACAAATGACAACTCCAGATATTTGATGATGTGTCTTG 2979
Db 1895 ACGTCTGTGAGGCGGATTTTGAACAGGACAGCGGTCATTGACCGGAATGAGCTTTGCCCTG 1954
Qy 2980 AAAACAATGCCATCAGTGAGACAGACTTCCAGAACTTCCAGATGGTCCCTTGGATCCCA 3039
Db 1955 AAATGCGAGATCACCTGACAGATTTTCAGAGCTTATCAACTGTAGTTCTGGATCCCG 2014
Qy 3040 AAGGACCAACCAAAATGATCCCACTGGGTGATTCGCCATCAAGGCAAGAGCTGGTTC 3099
Db 2015 AAGGAGATGCCCAAAATGATCAAACTGGATTTGTTTGAACAGGGAATGGAGATTTGTC 2074
Qy 3100 AGACAGCCAACTCGGACCCCGCATCGCTGTAGGTTTTCAGAGTTTGGGTCTCTGGACT 3159
Db 2075 AGACGATGAACAGTGACCTGGACTGGCAGTTGTATACAGAGCATTTAATGGAGTGTATT 2134
Qy 3160 TCAGTGGCACATTTACGTAAACACTGACCGGGACGACGATGATGCGCGCTTCTCTTTG 3219
Db 2135 TCGAGGGCACATTTCCACGTGAACCACTGACGAGTATGATTTACGCTGGTTTCACTCTTG 2194
Qy 3220 GTTACCACTCAAGCAGCGCTTCTATGTGGTGTGTTGGAAGCAGGTGACGACGACTACT 3279
Db 2195 GTTATCAGACAGTTCAAGCTTTTATGTGGTGTGTTGGAAGCAGACTGAGCAGACTTACT 2254
Qy 3280 GGGAGGACCCCAACGCGGCTTATGGCTACTCCGGGCTTCCCTCAAGTGTGTGAAT 3339
Db 2255 GGCAGGCAACCCCTTTCAGAGCAGTTGACAGAGCTGGAATCCAACTGAAGCTGTGAAT 2314
Qy 3340 CCACACCGGAGACCGGCGAGCAGCTGAGGACGCGCTGTGGCACACCGGGGAACACGCGG 3399
Db 2315 CCAAGTCAGGACCGGGGAAACATCTGAGAACTGCTGTGGCACACAGGACACCAATG 2374
Qy 3400 GGCAGGTGCGAACTTTATGGCACGACCCAGCAACATTTGGCTGGAAGGACTTACACGGCT 3459
Db 2375 ATCAAGTGGAGGTGCTCTGGAAGAGACCCAGCAATGTGCGCTGGAAGACAAAGTCTCCT 2434
Qy 3460 ATAGTGGACCTGACTCAGAGGCCAGACTGGCTACATCAGAGTCTTAGTGATGAAG 3519
Db 2435 ACCGCTGGTCTTTACAGACAGCGGCAAGTCGGCTACATCAGAGCCAGATTTTATGAAG 2494
Qy 3520 GAAACAGAGTCATGGCAGACTCAGGACCTATCTATGACCAAACTTACGCTGGCGGGCGG 3579
Db 2495 GCAACGAGCTGTGGCTGACTCTGGAGTCACTGTGGACACCACTGCGAGGAGGAGAC 2554
Qy 3580 TGGGTCTATTGTCTTCTCTCAAGAAATGGTCTATTCTCAGACCTCAAGTACGATGCA 3639

b 2555 TGGGAGTATTCGTCTTTTCACAGGAAACATAAATTTGGTCCAATCTGAATACCGGTGTA 2614
 y 3640 GAGATA 3645
 c 2615 ATGATA 2620

RESULT 6

S-09-702-705-592/c

Sequence 592, Application US/09702705

Patent No. 6504010

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Lodes, Michael A.

APPLICANT: Fanger, Gary

APPLICANT: Vedvick, Tom

APPLICANT: Carter, Darrick

APPLICANT: Retter, Marc

APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.478C14

CURRENT APPLICATION NUMBER: US/09/702,705

CURRENT FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 1833

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 592

LENGTH: 435

TYPE: DNA

ORGANISM: Homo sapien

NAME/KEY: misc_feature

LOCATION: (1)...(435)

OTHER INFORMATION: n = A,T,C or G

S-09-702-705-592

Query Match 7.5%; Score 428.4; DB 4; Length 435;

Best Local Similarity 98.6%; Pred. No. 4.4e-93;

Matches 429; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

y 4123 GACACAAATCCCGTAAATTAATAAACAAGGTCAAATTCAAATTTGAAGTAATGT 4182

b 435 GACACNCAATCCCGTAAATTAATAAACAAGGTCAAATTTGAAGTAATGT 376

y 4183 TTTAGTAGGAGAGATTAGAGACACAGGCATAGCAATGACATAAGCTACCGATTAC 4242

b 375 TTTAGTAGGAGAGATTAGAGACACAGGCATAGCAATGACATAAGCTACCGATTAC 316

y 4243 TAATCGGAACATGTAAACAGATTACAAAATAAAGCAACTCTCTCTTGTCTTCAATGA 4302

b 315 TAATCGGAACATGTAAACAGATTACAAAATAAAGCAACTCTCTCTTGTCTTCAATGA 256

y 4303 AAGCCCTCATGTCCAGATGCGATTGGCAAAACCTTCATTAAGTAAAGGTTAGCAGAG 4362

b 255 AAGCCNTCATGTCCAGATGCGATTGGCAAAACCTTCATTAAGTAAAGGTTAGCAGAG 196

y 4363 TGTGATCGGTTCCAGATGCGATTGGCAAAACCTTCATTAAGTAAAGGTTAGCAGAG 4422

b 195 TGTGATCGGTTCCAGATGCGATTGGCAAAACCTTCATTAAGTAAAGGTTAGCAGAG 136

y 4423 CAAAGTGCAGTGTAGTGTGTCGCGCTGTGTCGCGCTGTGTCGCGCTGTGTCGCGCTG 4482

b 135 CAAAGTGCAGTGTAGTGTGTCGCGCTGTGTCGCGCTGTGTCGCGCTGTGTCGCGCTG 76

y 4483 AGTTCTCTTCCCGAGTTTGTGCTGAGAGGAACACAGAGCAGACGACGACGACGACGACG 4542

b 75 AGTTCTCTTCCCGAGTTTGTGCTGAGAGGAACACAGAGCAGACGACGACGACGACGACG 16

y 4543 GCGCATCTAACGCG 4557

b 15 GCGCATCTAACGCG 1

RESULT 8

US-09-614-124B-592/c

RESULT 7

US-09-736-457-592/c

Sequence 592, Application US/09736457

Patent No. 6509448

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Lodes, Michael A.

APPLICANT: Fanger, Gary

APPLICANT: Vedvick, Tom

APPLICANT: Carter, Darrick

APPLICANT: Retter, Marc

APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun

APPLICANT: Wang, Aijun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.478C15

CURRENT APPLICATION NUMBER: US/09/736,457

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 1864

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 592

LENGTH: 435

TYPE: DNA

ORGANISM: Homo sapien

NAME/KEY: misc_feature

LOCATION: (1)...(435)

OTHER INFORMATION: n = A,T,C or G

US-09-736-457-592

Query Match 7.5%; Score 428.4; DB 4; Length 435;

Best Local Similarity 98.6%; Pred. No. 4.4e-93;

Matches 429; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4123 GACACAAATCCCGTAAATTAATAAACAAGGTCAAATTCAAATTTGAAGTAATGT 4182

Db 435 GACACNCAATCCCGTAAATTAATAAACAAGGTCAAATTTGAAGTAATGT 376

Qy 4183 TTTAGTAGGAGAGATTAGAGACACAGGCATAGCAATGACATAAGCTACCGATTAC 4242

Db 375 TTTAGTAGGAGAGATTAGAGACACAGGCATAGCAATGACATAAGCTACCGATTAC 316

Qy 4243 TAATCGGAACATGTAAACAGATTACAAAATAAAGCAACTCTCTCTTGTCTTCAATGA 4302

Db 315 TAATCGGAACATGTAAACAGATTACAAAATAAAGCAACTCTCTCTTGTCTTCAATGA 256

Qy 4303 AAGCCCTCATGTCCAGATGCGATTGGCAAAACCTTCATTAAGTAAAGGTTAGCAGAG 4362

Db 255 AAGCCNTCATGTCCAGATGCGATTGGCAAAACCTTCATTAAGTAAAGGTTAGCAGAG 196

Qy 4363 TGTGATCGGTTCCAGATGCGATTGGCAAAACCTTCATTAAGTAAAGGTTAGCAGAG 4422

Db 195 TGTGATCGGTTCCAGATGCGATTGGCAAAACCTTCATTAAGTAAAGGTTAGCAGAG 136

Qy 4423 CAAAGTGCAGTGTAGTGTGTCGCGCTGTGTCGCGCTGTGTCGCGCTGTGTCGCGCTG 4482

Db 135 CAAAGTGCAGTGTAGTGTGTCGCGCTGTGTCGCGCTGTGTCGCGCTGTGTCGCGCTG 76

Qy 4483 AGTTCTCTTCCCGAGTTTGTGCTGAGAGGAACACAGAGCAGACGACGACGACGACGACG 4542

Db 75 AGTTCTCTTCCCGAGTTTGTGCTGAGAGGAACACAGAGCAGACGACGACGACGACGACG 16

Qy 4543 GCGCATCTAACGCG 4557

Db 15 GCGCATCTAACGCG 1

Query Match 7.5%; Score 428.4; DB 4; Length 435;
Best Local Similarity 98.6%; Pred. No. 4.4e-93;
Matches 429; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

	D	b	435	GACACNCAATCCCGTTAAATTATATAAACAAGGTCAAATTNAATTTGAAGTAAATGT	376
	Q	y	4193	TTTTAGTAGGAGAGATTAGAAGACAAACAGGCATAGCAAATGACATAGCTACCAGTTAAC	4242
	D	b	375	TTTTAGTAGGAGAGATTAGAAGACAAACAGGCATAGCAAATGACATAGCTNCCGATTAA	316
	Q	y	4243	TAAATCGGAACATGTAAAAACAGTTTACAAAATAAAACGAACCTCCTCTTGCTGCTCAAAATGA	4302
	D	b	315	TAAATCGGNAACATGTAARAACAGTTTACAAAATAAACAAGACTCTCCTCTTGCTCAAAATGA	256
	Q	y	4303	AAGCCCTCATGTGCAGTAGAGATGCGAGTTTCATCAAGAAGAACAAACATCCTTGCAAAATGGG	4366
	D	b	255	AAGCNTCATGTGCAGTAGAGATGCGAGTTTCATCAAGAAGAACAAACATCCTTGCAAAATGGG	196
	Q	y	4363	TGTGATCGGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCACAG	4422
	D	b	195	TGTGATCGGGTTCCAGATGTGGATTTGGCAAAACCTCATTTAAGTAAAAGGTTAGCACAG	136
	Q	y	4423	CAAAGTCGGTGTCTTTAGCTGCTGTGTGTCGCCGCTGTGTGTCGGAGGCTTCCTGCCCTG	4482
	D	b	135	CAAAGTCGGTGTCTTTAGCTGCTGTGTGTCGCCGCTGTGTGTCGGAGGCTTCCTGCCCTG	76
	Q	y	4483	AGCTTCCCTCCCAGCTTTCCTGCTTGAGAGGAACCAAGACAGACAGCACAGGCCCGGAAAA	4542
	D	b	75	AGCTTCCCTCCCAGCTTTCCTGCTTGAGAGGAACCAAGACAGACAGCACAGGCCCGGAAAA	16
	Q	y	4543	GGCGCATCTAACGG	4557
	D	b	15	GGCGCATCTAACGG	1

RESULT 10
 3-09-589-184-592/c
 Sequence 592, Application US/09589184
 Patent No. 6686447
 GENERAL INFORMATION:
 APPLICANT: Wang, Tongtong
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Lodes, Michael A.
 APPLICANT: Fanger, Gary
 APPLICANT: Vedvick, Tom
 APPLICANT: Carter, Darrick
 APPLICANT: Retter, Marc
 APPLICANT: Mannion, Jane

APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane


```
121 AGTACCGATTAACTATCGAATCATGTAACAGTTACAAAATTAACGAACTCTCTC 180
4289 TTGCTCTACAAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 4348
181 TTGCTCTACAAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 240
4349 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 4408
241 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 300
4409 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 4468
301 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 360
4469 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 4519
361 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 411

RESULT 13
US-09-339-338-223
; Sequence 223, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 223
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-223

Query Match 7.1%; Score 406.2; DB 4; Length 411;
Best Local Similarity 99.3%; Pred. No. 9e-88; Indels 0; Gaps 0;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4109 AGTTGCTCTACAATGACACACAAATCCGCTAAATAAATTAATAAAGGTCATTTCAA 4168
Db 1 AGTTGCTCTACAATGACACACAAATCCGCTAAATAAATTAATAAAGGTCATTTCAA 60
QY 4169 ATTTGAAGTAAATGTTTAGTAAGGAGAGATTAGAGCAACAGCATAGCAATGACATA 4228
Db 61 ATTTGAAGTAAATGTTTAGTAAGGAGAGATTAGAGCAACAGCATAGCAATGACATA 120
QY 4229 AGCTACCGATTAACTATCGGAACATGTAAACAGTTTACAAAAATAAACGAACTCTCTC 4288
Db 121 AGCTACCGATTAACTATCGGAACATGTAAACAGTTTACAAAAATAAACGAACTCTCTC 180
QY 4289 TTGCTCTACAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 4348
Db 181 TTGCTCTACAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 240
QY 4349 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 4408
Db 241 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 300
QY 4409 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 4468
Db 301 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 360
QY 4469 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 4519
Db 361 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 411

RESULT 14
US-09-433-826B-223
; Sequence 223, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 223
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-223

Query Match 7.1%; Score 406.2; DB 4; Length 411;
Best Local Similarity 99.3%; Pred. No. 9e-88; Indels 0; Gaps 0;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4109 AGTTGCTCTACAATGACACACAAATCCGCTAAATAAATTAATAAAGGTCATTTCAA 4168
Db 1 AGTTGCTCTACAATGACACACAAATCCGCTAAATAAATTAATAAAGGTCATTTCAA 60
QY 4169 ATTTGAAGTAAATGTTTAGTAAGGAGAGATTAGAGCAACAGCATAGCAATGACATA 4228
Db 61 ATTTGAAGTAAATGTTTAGTAAGGAGAGATTAGAGCAACAGCATAGCAATGACATA 120
QY 4229 AGCTACCGATTAACTATCGGAACATGTAAACAGTTTACAAAAATAAACGAACTCTCTC 4288
Db 121 AGCTACCGATTAACTATCGGAACATGTAAACAGTTTACAAAAATAAACGAACTCTCTC 180
QY 4289 TTGCTCTACAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 4348
Db 181 TTGCTCTACAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 240
QY 4349 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 4408
Db 241 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 300
QY 4409 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 4468
Db 301 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 360
QY 4469 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 4519
Db 361 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 411

RESULT 15
US-09-604-287A-223
; Sequence 223, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Repler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
```

```
121 AGTACCGATTAACTATCGAATCATGTAACAGTTACAAAATTAACGAACTCTCTC 180
4289 TTGCTCTACAAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 4348
181 TTGCTCTACAAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 240
4349 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 4408
241 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 300
4409 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 4468
301 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 360
4469 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 4519
361 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 411

RESULT 13
US-09-339-338-223
; Sequence 223, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 223
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-223

Query Match 7.1%; Score 406.2; DB 4; Length 411;
Best Local Similarity 99.3%; Pred. No. 9e-88; Indels 0; Gaps 0;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4109 AGTTGCTCTACAATGACACACAAATCCGCTAAATAAATTAATAAAGGTCATTTCAA 4168
Db 1 AGTTGCTCTACAATGACACACAAATCCGCTAAATAAATTAATAAAGGTCATTTCAA 60
QY 4169 ATTTGAAGTAAATGTTTAGTAAGGAGAGATTAGAGCAACAGCATAGCAATGACATA 4228
Db 61 ATTTGAAGTAAATGTTTAGTAAGGAGAGATTAGAGCAACAGCATAGCAATGACATA 120
QY 4229 AGCTACCGATTAACTATCGGAACATGTAAACAGTTTACAAAAATAAACGAACTCTCTC 4288
Db 121 AGCTACCGATTAACTATCGGAACATGTAAACAGTTTACAAAAATAAACGAACTCTCTC 180
QY 4289 TTGCTCTACAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 4348
Db 181 TTGCTCTACAATGAAGCCCTCATGTGCAGTACAGATGAGTTTCATCAAGAAACAA 240
QY 4349 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 4408
Db 241 TCCTTGCAAAATGGGTGTGATGCGGTTCCAGATGATGATTTGGCAAAACCTCATTTA 300
QY 4409 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 4468
Db 301 AAGGTTAGCAGAGCAAAAGTGGGTGCTTTAGCTGCTGTGCGCGCTGTGCTGCGG 360
QY 4469 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 4519
Db 361 GAGGCTCCTGCTGAGTCTCTTCCCGCAGCTTTGCTGCTGCTGAGAGGAACCA 411
```

CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 223
LENGTH: 411
TYPE: DNA
ORGANISM: Homo sapiens
S-09-604-287A-223

Query Match 7.1%; Score 406.2; DB 4; Length 411;
Best Local Similarity 99.3%; Pred. No. 9e-88;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

y	4109	AGTTGCTCTACAAATGACACAAATCCCGCTAAATAAATTATAAACAAGGTCATTCAA	4168
b	1	AGTTGCTCTACAAATGACACAAATCCCGCTAAATAAATTATAAACAAGGTCATTCAA	60
y	4169	ATTGTAAGTAATGTTTTAGTAAGGAGAGATTAGAAGACAAACAGGCATAGCAAAATGACATA	4228
b	61	ATTGTAAGTAATGTTTTAGTAAGGAGAGATTAGAAGACAAACAGGCATAGCAAAATGACATA	120
y	4229	AGCTACCGATTAACTAATCGGAACATGTAAACAGTTACAAAAATAAAGGAACTCTCTC	4288
b	121	AGCTACCGATTAACTAATCGGAACATGTAAACAGTTACAAAAATAAAGGAACTCTCTC	180
y	4289	TTGTCTTACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTTCATCAAAAGAACAAACA	4348
b	181	TTGTCTTACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTTCATCAAAAGAACAAACA	240
y	4349	TCCTTGCAAAATGGTGTGATGCGGTTCCAGATGTGGATTGGCAAAACCTCATTTAAGTA	4408
b	241	TCCTTGCAAAATGGTGTGATGCGGTTCCAGATGTGGATTGGCAAAACCTCATTTAAGTA	300
y	4409	AAAGGTTAGCAGAGCAAGTGGGTGCTTTAGCTGCTGCTGCGGTGGTGGTGGTGGG	4468
b	301	AAAGGTTAGCAGAGCAAGTGGGTGCTTTAGCTGCTGCTGCGGTGGTGGTGGTGGG	360
y	4469	GAGGCTCCTGCGCTGAGCTTCCTTCCCGAGCTTTGCTGCTGAGAGGAACCA	4519
b	361	GAGGCTCCTGCGCTGAGCTTCCTTCCCGAGCTTTGCTGCTGAGAGGAACCA	411

Search completed: March 11, 2004, 14:41:38
Job time : 265.112 secs

result No.	Score	Query Match	Length	DB	ID	Description
1	5696	100.0	5696	14	US-10-084-817-25	Sequence 25, Appl
2	5874	97.9	5874	9	US-09-919-770-3	Sequence 3, Appl
3	5876.6	97.9	5874	9	US-09-880-107-2160	Sequence 997, Ap
4	5876.6	97.9	5874	10	US-09-873-367C-997	Sequence 997, Appl
5	5876.6	97.9	5874	12	US-10-240-425-1280	Sequence 1280, Ap
6	5876.6	97.9	5874	14	US-10-060-038-149	Sequence 149, Appl
7	5876.6	97.9	5874	14	US-10-020-141-13	Sequence 13, Appl
8	5876.6	97.9	5874	14	US-10-017-724-1	Sequence 1, Appl
9	5876.6	97.9	5874	14	US-10-101-510-193	Sequence 193, Appl
10	5876.6	97.9	5874	14	US-10-301-822-202	Sequence 202, Appl
11	5876.6	97.9	5874	14	US-10-008-093-3	Sequence 3, Appl
12	5876.6	97.9	5874	14	US-10-269-909-77	Sequence 77, Appl
13	5876.6	97.9	5874	14	US-10-269-909-78	Sequence 78, Appl
14	5876.6	97.9	5874	14	US-10-269-909-79	Sequence 79, Appl
15	5876.6	97.9	5874	14	US-10-007-781-1	Sequence 1, Appl

121 CAGAGGACGAGTGGTCTGAGGCTGGTCTCTGCTGGCTCTGCTGGTGGTGGCCAGCAGC 180
121 CAGAGGACGAGTGGTCTGAGGCTGGTCTCTGCTGGCTCTGCTGGTGGTGGCCAGCAGC 180
181 AGCTGGTACACAGGACAAAGACACACCTTCGACCTTTTCTAGTATCAGACATCAACC 240
181 AGCTGGTACACAGGACAAAGACACACCTTCGACCTTTTCTAGTATCAGACATCAACC 240
241 GCAAGACCAATTGGCGCCAAAGCAGTTCCGGGGGCCGACCCCGGGCTTACCGCT 300
241 GCAAGACCAATTGGCGCCAAAGCAGTTCCGGGGGCCGACCCCGGGCTTACCGCT 300
301 TCGTGGCTTTGACTACATCCACCGGTGAACGAGATGACCTCAGCAAGATCAACAAGA 360
301 TCGTGGCTTTGACTACATCCACCGGTGAACGAGATGACCTCAGCAAGATCAACAAGA 360
361 TCATGGGGCAAGAGAGGGCTTCTTCTCAAGCCAGCTCAAGCAGGACGGCAAGTCCA 420
421 GGGGACCGCTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGACGTTTCAAGATCGTCT 480
421 GGGGACCGCTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGACGTTTCAAGATCGTCT 480
481 CCAACGGCCCGCGGACACGCTGGATCTCACTTCTGATTTGACGGCACCCGGCATGTGG 540
481 CCAACGGCCCGCGGACACGCTGGATCTCACTTCTGATTTGACGGCACCCGGCATGTGG 540
541 TCTCCCTGGAGGACGTGGCTGGCTGACTGCGAGTGGAGAACGTCACCGTGCAGGTGG 600
541 TCTCCCTGGAGGACGTGGCTGGCTGACTGCGAGTGGAGAACGTCACCGTGCAGGTGG 600
601 CTGGGAGACCTACAGCTTTCAGGGTTCGCTTCAAGCTTCAAGCTTCTGGAGC 660
601 CTGGGAGACCTACAGCTTTCAGGGTTCGCTTCAAGCTTCAAGCTTCTGGAGC 660
661 AGCCCTTCTACGAGACCTGAGGGTTCGCTTCAAGCTTCAAGCTTCTGGAGC 720
661 AGCCCTTCTACGAGACCTGAGGGTTCGCTTCAAGCTTCAAGCTTCTGGAGC 720
721 CCAGAGAGCTCACTTCAAGAGAGGTTTCGCTTCAAGCTTCAAGCTTCTGGAGC 780
721 CCAGAGAGCTCACTTCAAGAGAGGTTTCGCTTCAAGCTTCAAGCTTCTGGAGC 780
781 TGGAGATATTTAAGCAAGAGGTTTCGCTTCAAGCTTCAAGCTTCTGGAGC 840
781 TGGAGATATTTAAGCAAGAGGTTTCGCTTCAAGCTTCAAGCTTCTGGAGC 840
841 TCAGTGAGACACAGAGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 900
841 TCAGTGAGACACAGAGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 900
901 CCAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
901 CCAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
961 TCAGAGAGCTTCCGGGCTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1020
961 TCAGAGAGCTTCCGGGCTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1020
961 TCAGAGAGCTTCCGGGCTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1020
1021 TGTGGAATGATAACAGGTTCTTGGAGGCTTCTTGGAGGCTTCTTGGAGGCTTCTTGG 1080
1021 TGTGGAATGATAACAGGTTCTTGGAGGCTTCTTGGAGGCTTCTTGGAGGCTTCTTGG 1080
1081 TGTGAGCTTGTGAGAGTGGCGGTTCTTGGAGGCTTCTTGGAGGCTTCTTGGAGGCT 1140
1081 TGTGAGCTTGTGAGAGTGGCGGTTCTTGGAGGCTTCTTGGAGGCTTCTTGGAGGCT 1140
1141 GCTGACACAGCTGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
1141 GCTGACACAGCTGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
1201 CTGCAACCTGGCCAGCTGATCTCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260

1201 CTGCAACCTGGCCAGTCCATCTTTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
1261 CGGTGAGACGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
1261 CGGTGAGACGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
1321 GTGGCTCTGGGACCCAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
1321 GTGGCTCTGGGACCCAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
1381 GGGCTCTCATCCAGACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
1381 GGGCTCTCATCCAGACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
1441 ACGCGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
1441 ACGCGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
1501 ATATCACAACGATCCGCTCTGCAACTCCCGAGTGGCCAGATGGGGGGGCAAGAAATGCA 1560
1501 ATATCACAACGATCCGCTCTGCAACTCCCGAGTGGCCAGATGGGGGGGCAAGAAATGCA 1560
1561 AAGGAGTGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620
1561 AAGGAGTGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620
1621 GAGCGCTGGTCCCGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1680
1621 GAGCGCTGGTCCCGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1680
1681 GCACCCGGGCTGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
1681 GCACCCGGGCTGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
1741 TGCAAGAGCTGAGATGTCACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
1741 TGCAAGAGCTGAGATGTCACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
1801 CCTCTTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
1801 CCTCTTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
1861 GCGCTGGGCTTCTGGGCAATGGGACCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1920
1861 GCGCTGGGCTTCTGGGCAATGGGACCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1920
1921 TCCCGGACATCTGCTTCTCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
1921 TCCCGGACATCTGCTTCTCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
1981 TCAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2040
1981 TCAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2040
2041 AAGCAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
2041 AAGCAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
2101 ACACTGGCAACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
2101 ACACTGGCAACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
2161 AGTGGAGTGGCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
2161 AGTGGAGTGGCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
2221 TGGAGGCTGGCCCAACCTCAATCTGGTCTGGCAGGAGGAGGAGGAGGAGGAGGAGGAG 2280
2221 TGGAGGCTGGCCCAACCTCAATCTGGTCTGGCAGGAGGAGGAGGAGGAGGAGGAGGAG 2280
2281 AGGATACTGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340

b 589 CCAACGGCCCGCGACACGCTGGATCTCACCTACTGGATTGACGGCACCGCGCATGTGG 648
 y 541 TCTCCCTGAGGACACGCTGGCTGGCTGACTCCAGTGGAGAACTCACCCTGCGAGGTGG 600
 b 649 TCTCCCTGAGGACGCTGGCTGGCTGACTCCAGTGGAGAACTCACCCTGCGAGGTGG 708
 y 601 CTGGCGAGACCTACAGCTTGCACGTGGGGTGGCACTCATAGACAGCTTCGCTTGGACG 660
 b 709 CTGGCGAGACCTACAGCTTGCACGTGGGGTGGCACTCATAGACAGCTTCGCTTGGACG 768
 y 661 AGCCCTTCTACGAGACCTGCGAGGCGGAAAGAGCGGATGTAAGTGGCCAAAGGCTCTG 720
 b 769 AGCCCTTCTACGAGACCTGCGAGGCGGAAAGAGCGGATGTAAGTGGCCAAAGGCTCTG 828
 y 721 CCAGAGAGAGTCACTTCAGGGGTTCCTTCAGAAAGTCCACCTAGTTCGAAAGTCTG 780
 b 829 CCAGAGAGAGTCACTTCAGGGGTTCCTTCAGAAAGTCCACCTAGTTCGAAAGTCTG 888
 y 781 TGAAGATATTTAAGCAAGAGGTTGCCAGAGCGGAGCGGAGCTGAGATCAAGGCCA 840
 b 889 TGAAGATATTTAAGCAAGAGGTTGCCAGAGCGGAGCGGAGCTGAGATCAAGGCCA 948
 y 841 TCAGTGAAGAACACAGAGACGCTGCGCTGGGTCCGATGTCCACCGAGTACGTGGGCC 900
 b 949 TCAGTGAAGAACACAGAGACGCTGCGCTGGGTCCGATGTCCACCGAGTACGTGGGCC 1008
 y 901 CCAGCTCAGAGGAGGCGCGAGGTGTGCGACGCTCGTGGGAGAGCTGGGAACATGG 960
 b 1009 CCAGCTCAGAGGAGGCGCGAGGTGTGCGACGCTCGTGGGAGAGCTGGGAACATGG 1068
 y 961 TCAGGAGCTCTCGGGGCTCCAGCTCTCGTGAACAGCTCAGCGAGAACCTCAAGAGAG 1020
 b 1069 TCAGGAGCTCTCGGGGCTCCAGCTCTCGTGAACAGCTCAGCGAGAACCTCAAGAGAG 1128
 y 1021 TGTGCAATGATACCAAGTCTCTGGAGCTCATTTGGGCGCTCTTAAGACAGAGAAC 1080
 b 1129 TGTGCAATGATACCAAGTCTCTGGAGCTCATTTGGGCGCTCTTAAGACAGAGAAC 1188
 y 1081 TGTGCAATGATACCAAGTCTCTGGAGCTCATTTGGGCGCTCTTAAGACAGAGAAC 1140
 b 1189 TGTGCAATGATACCAAGTCTCTGGAGCTCATTTGGGCGCTCTTAAGACAGAGAAC 1248
 y 1141 GCTGCAACAGTGTACCTGCAAGAAATTTAAACCAATTTGCCACCAATACCTGCGCGC 1200
 b 1249 GCTGCAACAGTGTACCTGCAAGAAATTTAAACCAATTTGCCACCAATACCTGCGCGC 1308
 y 1201 CTGCAACCTGCGCGAGTCCATCTCTTGTGGAAGGGAATGCTGCTCTCTGCTCCACT 1260
 b 1309 CTGCAACCTGCGCGAGTCCATCTCTTGTGGAAGGGAATGCTGCTCTCTGCTCCACT 1368
 y 1261 CGGTGACCGTGAAGGAGGCTGGTCTCGTGGGCAAGTGGACCAAGTCTGCTCGGTGAG 1320
 b 1369 CGGTGACCGTGAAGGAGGCTGGTCTCGTGGGCAAGTGGACCAAGTCTGCTCGGTGAG 1428
 y 1321 GTGGCTCTGGGACCCAGAGAGGCGGCTCTGTGAGCTCAGCAGCAACACCTCTCTGG 1380
 b 1429 GTGGCTCTGGGACCCAGAGAGGCGGCTCTGTGAGCTCAGCAGCAACACCTCTCTGG 1488
 y 1381 GGCCTCTCCATCCAGACACGCGGCTTGCAGTCTGAGCAAGTGTGACACCGGCAATCCG 1440
 b 1489 GGCCTCTCCATCCAGACACGCGGCTTGCAGTCTGAGCAAGTGTGACACCGGCAATCCG 1548
 y 1441 ACGGCGCTGGAGCCACTGGTCACTGGTCTTCATGCTCTGACCTGTGGAGTGGCA 1500
 b 1549 ACGGCGCTGGAGCCACTGGTCACTGGTCTTCATGCTCTGACCTGTGGAGTGGCA 1608
 y 1501 ATATCACAGCATCCCTCTCTGCAATCCCGAGTGGCCAGATGGGGGCAAGAAATTGCA 1560
 b 1609 ATATCACAGCATCCCTCTCTGCAATCCCGAGTGGCCAGATGGGGGCAAGAAATTGCA 1668
 y 1561 AAGGAGTGGCGGAGACCAAGACCTGCGAGGCGGCCCATGCGCCATCGATGCGCGCT 1620

Db 1669 AAGGAGTGGCGGAGACCAAGACCTGCGAGGCGGCCCATCGCATGATGCGCGCT 1728
 Qy 1621 GAGAGCCCTGCTCCCGTGGTGGGCTGGCTGACTCTCACTGTGGCGGTGGATCCGGGAGC 1680
 Db 1729 GAGAGCCCTGCTCCCGTGGTGGGCTGGCTGACTCTCACTGTGGCGGTGGATCCGGGAGC 1788
 Qy 1681 GACCCCGGCTCTCAACAGCCCTGAGCCCTCAGTACGAGAGGAAGGCTGCTGGTGGGAGT 1740
 Db 1789 GACCCCGGCTCTCAACAGCCCTGAGCCCTCAGTACGAGAGGAAGGCTGCTGGTGGGAGT 1848
 Qy 1741 TGAGGAGCGCTCAGATGTGCAACAGAGGAGCTGCCCGTGGATGCTGTTATCAAC 1800
 Db 1849 TGAGGAGCGCTCAGATGTGCAACAGAGGAGCTGCCCGTGGATGCTGTTATCAAC 1908
 Qy 1801 CTTGCTTCCGGAGCGCAGTGTGAGCAGCTTCCCGATGGGCTCTGCTGATGCGGCTCT 1860
 Db 1909 CTTGCTTCCGGAGCGCAGTGTGAGCAGCTTCCCGATGGGCTCTGCTGATGCGGCTCT 1968
 Qy 1861 GCCTGTGGCTTCTTGGGCAATGGCACTGTGAGGAGCTGGAGAGTGTGCCCTGG 1920
 Db 1969 GCCTGTGGCTTCTTGGGCAATGGCACTGTGAGGAGCTGGAGAGTGTGCCCTGG 2028
 Qy 1921 TCCCGACATCTGCTTCTCCACAGCAAGTGTGCTGCTGCTGTCACACTCAGCTTGCT 1980
 Db 2029 TCCCGACATCTGCTTCTCCACAGCAAGTGTGCTGCTGCTGTCACACTCAGCTTGCT 2088
 Qy 1981 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
 Db 2089 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2148
 Qy 2041 AAGCAGCAAGACGGAAGAAAGTGTGAGCGGCGGAAACCCATCAAGGAGCAAGAC 2100
 Db 2149 AAGCAGCAAGACGGAAGAAAGTGTGAGCGGCGGAAACCCATCAAGGAGCAAGAC 2208
 Qy 2101 ACAACTGCCACAGACGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
 Db 2209 ACAACTGCCACAGACGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2268
 Qy 2161 AGTGCAGTGTCCAGACAGGCTACGCGGCGGAGCGGCTGCTGCTGCGGGGAGGACTCG 2220
 Db 2269 AGTGCAGTGTCCAGACAGGCTACGCGGCGGAGCGGCTGCTGCTGCGGGGAGGACTCG 2328
 Qy 2221 TGGACGCTGCGCCCAACCTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
 Db 2329 TGGACGCTGCGCCCAACCTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2388
 Qy 2281 AGGATAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
 Db 2389 AGGATAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2448
 Qy 2341 GCGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
 Db 2449 GCGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2508
 Qy 2401 AGCTGCTCTTCAATCCCGCGGAGCTGATGATGATGATGATGATGATGATGATGATGAT 2460
 Db 2509 AGCTGCTCTTCAATCCCGCGGAGCTGATGATGATGATGATGATGATGATGATGATGAT 2568
 Qy 2461 ACAATGCTGCTTCAATCCCGCGGAGCTGATGATGATGATGATGATGATGATGATGATGAT 2520
 Db 2569 ACAATGCTGCTTCAATCCCGCGGAGCTGATGATGATGATGATGATGATGATGATGATGAT 2628
 Qy 2521 ACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
 Db 2629 ACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2688
 Qy 2581 ACGTCTTCAACACTGACAGAGGAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
 Db 2689 ACGTCTTCAACACTGACAGAGGAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2748
 Qy 2641 ACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
 Db 2749 ACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2808

2701 AGTGTGACAAACAGGACATAGATGACGACGCGCCACAGAACACACAGGACAACTGCC 2760
 2809 AGTGTGACAAACAGGACATAGATGACGACGCGCCACAGAACACACAGGACAACTGCC 2868
 2761 CCTACATCTCCAAACGCGACAGGCTGACGATGACAGAGACGCGCGACGCGCTGTG 2820
 2869 CCTACATCTCCAAACGCGACAGGCTGACGATGACAGAGACGCGCGACGCGCTGTG 2928
 2821 ACCCTGATGATGACAAAGATGGCGTCCCCGATGACAGGACAACTCCCGGCTGTGTTC 2880
 2929 ACCCTGATGATGACAAAGATGGCGTCCCCGATGACAGGACAACTCCCGGCTGTGTTC 2988
 2881 ACCCAGACCAAGGAGACTTGGACGCTGATGGAAGGCGGCTGATATTTGTAAGATGATTTG 2940
 2989 ACCCAGACCAAGGAGACTTGGACGCTGATGGAAGGCGGCTGATATTTGTAAGATGATTTG 3048
 2941 ACAATGACAACTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
 3049 ACAATGACAACTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3108
 3001 CAGACTTCAGAACTTCCAGATGGTCCCTTGGATCCCAAGGACCAACCCAAATGATC 3060
 3109 CAGACTTCAGAACTTCCAGATGGTCCCTTGGATCCCAAGGACCAACCCAAATGATC 3168
 3061 CCAACTGGGTCACTCCGATCAAGGACAGAGCTGTTGACAGACCAACTCGGACCCCG 3120
 3169 CCAACTGGGTCACTCCGATCAAGGACAGAGCTGTTGACAGACCAACTCGGACCCCG 3228
 3121 GCATCGCTGAGGTTTACGAGCTTTGGTCTCTGACCTTCACTGACCACTTCACTGATA 3180
 3229 GCATCGCTGAGGTTTACGAGCTTTGGTCTCTGACCTTCACTGACCACTTCACTGATA 3288
 3181 ACATGACGCGGACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3240
 3289 ACATGACGCGGACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3348
 3241 TCTATGTGTGATGTAAGCAGGTGACGACGACCTACTGGGAGGACCAACCCCAAGCGGG 3300
 3349 TCTATGTGTGATGTAAGCAGGTGACGACGACCTACTGGGAGGACCAACCCCAAGCGGG 3408
 3301 CCTATGCTACTCCGCGTCTCTGACGATGATGATGATGATGATGATGATGATGATGATG 3360
 3409 CCTATGCTACTCCGCGTCTCTGACGATGATGATGATGATGATGATGATGATGATGATG 3468
 3361 ACCTGAGGAAACGCGCTCTGACGACGCGGACACGCGGCGGACGAGTCCGAACCTTATGGC 3420
 3469 ACCTGAGGAAACGCGCTCTGACGACGCGGACACGCGGCGGACGAGTCCGAACCTTATGGC 3528
 3421 ACGACCCAGGAAATTTGGCTGGAAGACTACAGGCTTATAGGTGGACCTGACTCACA 3480
 3529 ACGACCCAGGAAATTTGGCTGGAAGACTACAGGCTTATAGGTGGACCTGACTCACA 3588
 3481 GGCCCAAGACTGGCTACATCAGAGCTTTAGTGCATGAAGAAACAGGTCATGGCAGACT 3540
 3589 GGCCCAAGACTGGCTACATCAGAGCTTTAGTGCATGAAGAAACAGGTCATGGCAGACT 3648
 3541 CAGGACCTATCTATGACCAAACTACGCTGGCGGCGGCTGGGTCTATTTGTTCTTCTC 3600
 3649 CAGGACCTATCTATGACCAAACTACGCTGGCGGCGGCTGGGTCTATTTGTTCTTCTC 3708
 3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGATATTTAAACAGATTTG 3660
 3709 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGATATTTAAACAGATTTG 3768
 3661 CTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTTGG 3720
 3769 CTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTTGG 3828
 3721 TCCCTGTGGCTTCTCTCTAGCAGACCTCCCTGCTGACCTTAACTCCTCATGTTGTC 3780
 3829 TCCCTGTGGCTTCTCTCTCTAGCAGACCTCCCTGCTGACCTTAACTCCTCATGTTGTC 3888

3781 TTCACTCTCTGCCAGCAACCCCAAAACCCCAAGTCCCTCAGAGGATAAATATCAATGGAAC 3840
 3889 TTCACTCTCTGCCAGCAACCCCAAAACCCCAAGTCCCTCAGAGGATAAATATCAATGGAAC 3948
 3841 GCAGAGATGACATCTTAACCCACTAGAGGAAACAGTTTGGTGATATATGAGACTTTATG 3900
 3949 TCAGAGATGACATCTTAACCCACTAGAGGAAACAGTTTGGTGATATATGAGACTTTATG 4008
 3901 TGGAGTGAATAATTTGGGATGCCATTAATTCATTTCTTTCTTTCTTTCTTTCTTTCTTTCT 3960
 4009 TGGAGTGAATAATTTGGGATGCCATTAATTCATTTCTTTCTTTCTTTCTTTCTTTCTTTCT 4068
 3961 GTTTACATATAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4020
 4069 GTTTACATATAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4128
 4021 CTGTGCATAAGCCATTAATGATAAATTAAGCATGAAATAATTTGCTGAACTTCTTTGGTG 4080
 4129 CTGTGCATAAGCCATTAATGATAAATTAAGCATGAAATAATTTGCTGAACTTCTTTGGTG 4188
 4081 CTTAAAGTGTCTCACTATTTCTTTGAAATTAAGTGTCTCTACAAATGACACACAAATCCCGCTA 4140
 4189 CTTAAAGTGTCTCACTATTTCTTTGAAATTAAGTGTCTCTACAAATGACACACAAATCCCGCTA 4248
 4141 AATAAATTAATAACAAGGTCATTTCAATTTGAAGTAATTTTGAAGTAATTTTGAAGTAATTT 4200
 4249 AATAAATTAATAACAAGGTCATTTCAATTTGAAGTAATTTTGAAGTAATTTTGAAGTAATTT 4308
 4201 GAAGACACAGGACATGACATTAAGTACCTACCTACCTACCTACCTACCTACCTACCTACCT 4260
 4309 GAAGACACAGGACATGACATTAAGTACCTACCTACCTACCTACCTACCTACCTACCTACCT 4368
 4261 CAGTTACAAAATAAAGCAACT 4320
 4369 CAGTTACAAAATAAAGCAACT 4428
 4321 GAGATGCAATTTCAATAAGAAACAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4380
 4429 GAGATGCAATTTCAATAAGAAACAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4488
 4381 GTGATTTGGCAAAACCT 4440
 4489 GTGATTTGGCAAAACCT 4548
 4441 CTGCTGCTTGTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4500
 4549 CTGCTGCTTGTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4608
 4501 TGCTGCTGAGAGAACCCAGAGCAGACGCAAGGCGGAAAGGCGCATCTAAACGCGTAT 4560
 4609 TGCTGCTGAGAGAACCCAGAGCAGACGCAAGGCGGAAAGGCGCATCTAAACGCGTAT 4668
 4561 CTAGGCTTTGGTAACTCGGCAAGGTTGCTTTTACCTGATTTGATGATGATGATGATGATGAT 4620
 4669 CTAGGCTTTGGTAACTCGGCAAGGTTGCTTTTACCTGATTTGATGATGATGATGATGATGAT 4728
 4621 GGTTCACGTTAATAATTTTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 4680
 4729 GGTTCACGTTAATAATTTTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 4788
 4681 TACCACTAACTATTTTAAATTTATGCTAGTAAACATATGATGATGATGATGATGATGATGAT 4740
 4789 TACCACTAACTATTTTAAATTTATGCTAGTAAACATATGATGATGATGATGATGATGATGAT 4848
 4741 AACATCTAATGATATATAATCTCTGTAATAATGAGGCTTGATAATTAATTAATTAATTAATTA 4800
 4849 AACATCTAATGATATATAATCTCTGTAATAATGAGGCTTGATAATTAATTAATTAATTAATTA 4908
 4801 GATGAAGCATCTGAGAGCTGTAACAGAAATACATAGAGAAATTAATGAGAGTTTATGATGG 4860
 4909 GATGAAGCATCTGAGAGCTGTAACAGAAATACATAGAGAAATTAATGAGAGTTTATGATGG 4968
 4861 AACCTTAATATATAATGTTGCCAGGATTTTGTCTCAATATTTTGTACTGTTATCTATCTATC 4920

2y 901 CCAGCTCAGAGGAGGCGGAGGTGCGAAGCTCGTCGAGGAGCTGGGAAACATGG 960
 Db 1009 CCAGCTCGGAGAGGAGGCGGAGGTGCGAAGCTCGTCGAGGAGCTGGGAAACATGG 1068
 2y 961 TCCAGGAGCTCTCGGGGCTCGAAGCTCTGCTGTAACAGCTCAGCGAAGAACTCAAGAG 1020
 Db 1069 TCCAGGAGCTCTCGGGGCTCGAAGCTCTGCTGTAACAGCTCAGCGAAGAACTCAAGAG 1128
 2y 1021 TGTGCAATGATAAACAAGCTTCTCTGGAGAGTCAATGCTGGGCTCTCTTAAGACAAGAA 1080
 Db 1129 TGTGCAATGATAAACAAGCTTCTCTGGAGAGTCAATGCTGGGCTCTCTTAAGACAAGAA 1188
 2y 1081 TGTGAGCTTGTGCGAGGAGTGGCGGCTTCTTGGCGAAATGAAAGTGGGCTGGGACA 1140
 Db 1189 TGTGAGCTTGTGCGAGGAGTGGCGGCTTCTTGGCGAAATGAAAGTGGGCTGGGACA 1248
 2y 1141 GCTGCACACAGTGTACCTGCAAGAAATTTAAACCAATTTCGCCAACAAATCACCTGCGCG 1200
 Db 1249 GCTGCACACAGTGTACCTGCAAGAAATTTAAACCAATTTCGCCAACAAATCACCTGCGCG 1308
 2y 1201 CTGCAACTGCGGCCAGTCCATCTCTTTGTGGAAGCGAATGCTGCGCTTCTGCTCTCACT 1260
 Db 1309 CTGCAACTGCGGCCAGTCCATCTCTTTGTGGAAGCGAATGCTGCGCTTCTGCTCTCACT 1368
 2y 1261 CGGTGGAGCGGTGAGAGGCTGGTCTCCGTGGGAGAGTGGACCAAGTCTCCGTGACGT 1320
 Db 1369 CGGTGGAGCGGTGAGAGGCTGGTCTCCGTGGGAGAGTGGACCAAGTCTCCGTGACGT 1428
 2y 1321 GTGGCTCTGGGACCCAGCAGAGAGCGGCTCTGTGACGTGACAGCAACCTGCTGTGG 1380
 Db 1429 GTGGCTCTGGGACCCAGCAGAGAGCGGCTCTGTGACGTGACAGCAACCTGCTGTGG 1488
 2y 1381 GGCCCTCCATCCAGACAGGCTTGCAGTCTGAGCAAGTGTGACCCGATCCGCGAGG 1440
 Db 1489 GGCCCTCCATCCAGACAGGCTTGCAGTCTGAGCAAGTGTGACCCGATCCGCGAGG 1548
 2y 1441 ACGCGGCTGGAGCACCAGTGTGACCTTGGTCTTCAATGCTGTGAGCTGTGAGTGGCA 1500
 Db 1549 ACGCGGCTGGAGCACCAGTGTGACCTTGGTCTTCAATGCTGTGAGCTGTGAGTGGCA 1608
 2y 1501 ATATCACAGCATCGCTCTGCACTCCAGTCCCGAGTCCCGAGAGTGGGGGCAAGATTGCA 1560
 Db 1609 ATATCACAGCATCGCTCTGCACTCCCGAGTCCCGAGAGTGGGGGCAAGATTGCA 1668
 2y 1561 AAGGAGTGGCGGAGACCAAGGCTGCCAGGCGGCCCATGCCCCAATCGATGGCGCT 1620
 Db 1669 AAGGAGTGGCGGAGACCAAGGCTGCCAGGCGGCCCATGCCCCAATCGATGGCGCT 1728
 2y 1621 GGAGCCCTGTGCTCCGCTGCTGAGTCCCGAGTCCCGAGTCCCGAGTCCCGAGTCCCGAG 1680
 Db 1729 GGAGCCCTGTGCTCCGCTGCTGAGTCCCGAGTCCCGAGTCCCGAGTCCCGAGTCCCGAG 1788
 2y 1681 GCACCCGGGTCTGCAACAGCCCTGAGCTCAGTACGGAGGGAAGGCTGCGTGGGGATG 1740
 Db 1789 GCACCCGGGTCTGCAACAGCCCTGAGCTCAGTACGGAGGGAAGGCTGCGTGGGGATG 1848
 2y 1741 TGCAGGAGCTCAGATGTGCAACAGAGGAGTCCCGCTGAGTGGCTGTTATCCAACT 1800
 Db 1849 TGCAGGAGCTCAGATGTGCAACAGAGGAGTCCCGCTGAGTGGCTGTTATCCAACT 1908
 2y 1801 CCTGCTTCCCGGAGCCAGTGTGACAGCTTCCCGAGTGGGTCTGCTGATGGGCTCT 1860
 Db 1909 CCTGCTTCCCGGAGCCAGTGTGACAGCTTCCCGAGTGGGTCTGCTGATGGGCTCT 1968
 2y 1861 GCCTGTGGGCTTCTTGGGGAATGGGACCCATCTGTGAGGAGCTGGAGAGTGTGCCCTGG 1920
 Db 1969 GCCTGTGGGCTTCTTGGGGAATGGGACCCATCTGTGAGGAGCTGGAGAGTGTGCCCTGG 2028
 2y 1921 TCCCGGAGCTGTCTTCCAGCAGAGGCTGCTGCTGTGTCACACTCAGCTGGCT 1980
 Db 2029 TCCCGGAGCTGTCTTCCAGCAGAGGCTGCTGCTGTGTCACACTCAGCTGGCT 2088

Qy 1981 TCCACTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 Db 2089 TCCACTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2148
 2y 2041 AAGCAGCACAAGCAGGAAAGCAAGTGTGTGAGCCGGAAGAACCCATGCAAGGACAAAGCAC 2100
 Db 2149 AAGCAGCACAAGCAGGAAAGCAAGTGTGTGAGCCGGAAGAACCCATGCAAGGACAAAGCAC 2208
 2y 2101 ACAACTGCCACAAGCAGCAGGAGTGCATCTACCTGGGCTCACTTACGAGACCCCATGTACA 2160
 Db 2209 ACAACTGCCACAAGCAGCAGGAGTGCATCTACCTGGGCTCACTTACGAGACCCCATGTACA 2268
 2y 2161 AGTGGAGTGCAGACAGGCTACCGGCGGAGGCTCATCTGCGGGAGGAGTCTCGGAGC 2220
 Db 2269 AGTGGAGTGCAGACAGGCTACCGGCGGAGGCTCATCTGCGGGAGGAGTCTCGGAGC 2328
 2y 2221 TGGAGCGGTGCGCCAAACCTCAATCTGCTGCGCCACCAAGCGCCACCTTACCATGTGATCA 2280
 Db 2329 TGGAGCGGTGCGCCAAACCTCAATCTGCTGCGCCACCAAGCGCCACCTTACCATGTGATCA 2388
 2y 2281 AGGATACTGCGCCCATCTGCGCAATTTCTGGCAGGAGACTTTGACAAGGACCGGATG 2340
 Db 2389 AGGATACTGCGCCCATCTGCGCAATTTCTGGCAGGAGACTTTGACAAGGACCGGATG 2448
 2y 2341 GCGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
 Db 2449 GCGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2508
 2y 2401 AGCTCTCTTCAATCCCGCCAGGCTGATGATGATGATGATGATGATGATGATGATGATG 2460
 Db 2509 AGCTCTCTTCAATCCCGCCAGGCTGATGATGATGATGATGATGATGATGATGATGATG 2568
 2y 2461 ACAACTGCTCTTCAATGTCACAACTGTCACAACTGTCACAACTGTCACAACTGTCACAA 2520
 Db 2569 ACAACTGCTCTTCAATGTCACAACTGTCACAACTGTCACAACTGTCACAACTGTCACAA 2628
 2y 2521 AGCTCTCTTCAATGTCACAACTGTCACAACTGTCACAACTGTCACAACTGTCACAACT 2580
 Db 2629 AGCTCTCTTCAATGTCACAACTGTCACAACTGTCACAACTGTCACAACTGTCACAACT 2688
 2y 2581 AGCTCTCAACAACACTGACAGAGGACAGGATGATGATGATGATGATGATGATGATGATG 2640
 Db 2689 AGCTCTCAACAACACTGACAGAGGACAGGATGATGATGATGATGATGATGATGATGATG 2748
 2y 2641 AGTGGCTCTGCTGTCACAACTGTCACAACTGTCACAACTGTCACAACTGTCACAACTG 2700
 Db 2749 AGTGGCTCTGCTGTCACAACTGTCACAACTGTCACAACTGTCACAACTGTCACAACTG 2808
 2y 2701 AGTGTGACAAACAAGGAGCATAGATGATGATGATGATGATGATGATGATGATGATG 2760
 Db 2809 AGTGTGACAAACAAGGAGCATAGATGATGATGATGATGATGATGATGATGATGATG 2868
 2y 2761 CCTACATCTCCAAAGCCAAAGGCTGATGATGATGATGATGATGATGATGATGATGATG 2820
 Db 2869 CCTACATCTCCAAAGCCAAAGGCTGATGATGATGATGATGATGATGATGATGATGATG 2928
 2y 2821 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880
 Db 2929 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2988
 2y 2881 ACCCAGACAGGAGGACTTGGACGCTGATGATGATGATGATGATGATGATGATGATGATG 2940
 Db 2989 ACCCAGACAGGAGGACTTGGACGCTGATGATGATGATGATGATGATGATGATGATGATG 3048
 2y 2941 ACAATGACAAATCCAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
 Db 3049 ACAATGACAAATCCAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 3108
 2y 3001 CAGACTTCCAGGAACTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
 Db 3109 CAGACTTCCAGGAACTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3168
 2y 3061 CCAACTGGGTGATTCGCTTCAAGCAGAGGAGTGGTTCAGACAGCCCACTCGGACCCCG 3120

b	3169	CCAAC	TGGGTCA	TTGCC	ATCAAGG	CAAGAG	CTGGT	CAGACAG	CAACTGG	ACCCCG	3228			
y	3121	GCAT	CGCTAG	GTTTG	ACGAG	TTTGG	TCTGTG	ACTTTC	AGTGG	CACATTT	CGTAA	3180		
b	3229	GCAT	CGCTAG	GTTTG	ACGAG	TTTGG	TCTGTG	ACTTTC	AGTGG	CACATTT	CGTAA	3288		
y	3181	ACACT	GACCGG	ACGAC	TATCG	CGGCT	TCGTCT	TTGGT	TACAGT	CAAGCAG	CGCGT	3240		
b	3289	ACACT	GACCGG	ACGAC	TATCG	TGGCT	TCGTCT	TTGGT	TACAGT	CAAGCAG	CGCGT	3348		
y	3241	TCTAT	TGTTG	TATGT	TGGAA	GACAG	GTGAC	GACAC	CTACT	TGGAG	GACACG	CGCGG	3300	
b	3349	TCTAT	TGTTG	TATGT	TGGAA	GACAG	GTGAC	GACAC	CTACT	TGGAG	GACACG	CGCGG	3408	
y	3301	CCAT	TGGCT	ACTCC	GGCGT	GCCTC	CAAGT	TGGTGA	ACTCC	ACCGG	GACGGG	CGGAC	3360	
b	3409	CCAT	TGGCT	ACTCC	GGCGT	GCCTC	CAAGT	TGGTGA	ACTCC	ACCGG	GACGGG	CGGAC	3468	
y	3361	ACCT	GAGGA	ACCG	CTGT	TGGCA	CACG	GGGAACA	CGCC	GGGCGAG	GTGCG	AAACCTT	ATGCG	3420
b	3469	ACCT	GAGGA	ACCG	CTGT	TGGCA	CACG	GGGAACA	CGCC	GGGCGAG	GTGCG	AAACCTT	ATGCG	3528
y	3421	ACGAC	CCCAAG	GAACAT	TGGCT	TGGA	AGGAT	CTACA	CGGCT	TATAG	TGGCG	ACCTG	ACTCACA	3480
b	3529	ACGAC	CCCAAG	GAACAT	TGGCT	TGGA	AGGAT	CTACA	CGGCT	TATAG	TGGCG	ACCTG	ACTCACA	3588
y	3481	GGCC	CAAGACT	GGCTAC	ATCAG	AGTCT	TATAG	TGATGA	AGAAAC	AGGT	CATGG	CAAGCT	3540	
b	3589	GGCC	CAAGACT	GGCTAC	ATCAG	AGTCT	TATAG	TGATGA	AGAAAC	AGGT	CATGG	CAAGCT	3648	
y	3541	CAGG	ACCTAT	CTATG	ACCAAA	CCTAC	GCCTGG	GGGGCG	GTGG	TCTAT	TGTCT	CTCTC	3600	
b	3649	CAGG	ACCTAT	CTATG	ACCAAA	CCTAC	GCCTGG	GGGGCG	GTGG	TCTAT	TGTCT	CTCTC	3708	
y	3601	AAGAA	TGTTCT	ATTTCT	CAGAC	CTCA	AGTAC	GAATGC	AGAGAT	ATTTAA	ACAAG	ATTTG	3660	
b	3709	AAGAA	TGTTCT	ATTTCT	CAGAC	CTCA	AGTAC	GAATGC	AGAGAT	ATTTAA	ACAAG	ATTTG	3768	
y	3661	CTGC	ATTTCC	GGCAAT	GCCTGT	GCATG	CCATCG	TCCCTAG	ACAC	CTCAG	TTCAT	TGTGG	3720	
b	3769	CTGC	ATTTCC	GGCAAT	GCCTGT	GCATG	CCATCG	TCCCTAG	ACAC	CTCAG	TTCAT	TGTGG	3828	
y	3721	TCTTG	TGCTCT	CTCT	CTAG	CAG	CACTCT	CTGT	CCCTTG	ACTTAA	CTCTGA	CTGCTC	3780	
b	3829	TCTTG	TGCTCT	CTCT	CTAG	CAG	CACTCT	CTGT	CCCTTG	ACTTAA	CTCTGA	CTGCTC	3888	
y	3781	TTCA	CTCTCT	CCAG	CAACCC	CAAA	CCCAAG	TGCCCT	CTAG	AGATAA	TATCA	ATCGGA	3840	
b	3889	TTCA	CTCTCT	CCAG	CAACCC	CAAA	CCCAAG	TGCCCT	CTAG	AGATAA	TATCA	ATCGGA	3948	
y	3841	GCAG	ATGA	CACTTAA	CCCACT	CTAG	GAGAA	CCAGT	TTGGT	GATATAT	GAGACT	TTATG	3900	
b	3949	TCAG	ATGA	CACTTAA	CCCACT	CTAG	GAGAA	CCAGT	TTGGT	GATATAT	GAGACT	TTATG	4008	
y	3901	TGGAG	TGAAA	TTGG	CACTTAA	CCCACT	CTAG	TGCTTTT	CTGT	TTGTTTAA	AAAGA	ATGAC	3960	
b	4009	TGGAG	TGAAA	TTGG	CACTTAA	CCCACT	CTAG	TGCTTTT	CTGT	TTGTTTAA	AAAGA	ATGAC	4068	
y	3961	GTTT	CATATA	AAATGT	ATACT	ATAT	TGTTAT	TATGT	GTATAT	TGGAGT	TGA	AGGAATA	4020	
b	4069	GTTT	CATATA	AAATGT	ATACT	ATAT	TGTTAT	TATGT	GTATAT	TGGAGT	TGA	AGGAATA	4128	
y	4021	CTGT	GCTA	AGCCAT	TATG	ATAA	TTAAG	CATG	AAAAA	TATGCT	CAACT	CTTTTGGTG	4080	
b	4129	CTGT	GCTA	AGCCAT	TATG	ATAA	TTAAG	CATG	AAAAA	TATGCT	CAACT	CTTTTGGTG	4188	
y	4081	CTTTAA	AGTTG	CTCA	TATCT	TGAA	TTAG	AGTTG	CTCTA	CAATG	ACACA	MAATCCGCTA	4140	
b	4189	CTTTAA	AGTTG	CTCA	TATCT	TGAA	TTAG	AGTTG	CTCTA	CAATG	ACACA	MAATCCGCTA	4248	
y	4141	AATA	AAATATA	AAACA	AGGCT	CAAT	TTCA	AAATTT	CGAAGT	TAATG	TTTTAGT	TAAGAG	ATTA	4200

1201 CTGCAACTGCGCCAGTCCATCCTTTGTGGAAGCGAAATGCTGCCCTTCTCTGCCCTCCACT 1260
1309 CTGCAACTGCGCCAGTCCATCCTTTGTGGAAGCGAAATGCTGCCCTTCTCTGCCCTCCACT 1368
1261 CGGTGACGGTGAAGAGGCTGTCTCCGTGGCAGAGTGGACCAAGTCTCCGTGACGT 1320
1369 CGGTGACGGTGAAGAGGCTGTCTCCGTGGCAGAGTGGACCAAGTCTCCGTGACGT 1428
1321 GTGGCTCTGGGACCCAGCAGAGAGCGCGTCTCTGTGACGTCCACAGCAACACCTGCTTGG 1380
1429 GTGGCTCTGGGACCCAGCAGAGAGCGCGTCTCTGTGACGTCCACAGCAACACCTGCTTGG 1488
1381 GGGCTTCCATCCAGACACGGGCTTGAAGTCTGAGCAAGTGTGACACCGCATCCGGCAGG 1440
1489 GGGCTTCCATCCAGACACGGGCTTGAAGTCTGAGCAAGTGTGACACCGCATCCGGCAGG 1548
1441 ACGGCGGCTGGAGCCACTGTGTCACTTGTGTCTTCACTGTCTGTGACCTGTGGAGTTGGCA 1500
1549 ACGGCGGCTGGAGCCACTGTGTCACTTGTGTCTTCACTGTCTGTGACCTGTGGAGTTGGCA 1608
1501 ATATCACAGCATCCGTCTCTGCAACTCCCGAGTGCCTCCAGATGGGGGCAAGATTGCA 1560
1609 ATATCACAGCATCCGTCTCTGCAACTCCCGAGTGCCTCCAGATGGGGGCAAGATTGCA 1668
1561 AAGGGAGTGGCCGGGAGACCAAGAGCTGCGAGGGCCGCCATGCCCAATCGATGGCGCT 1620
1669 AAGGGAGTGGCCGGGAGACCAAGAGCTGCGAGGGCCGCCATGCCCAATCGATGGCGCT 1728
1621 GAGGCCCTGGTCCCGTGGTCCCGTGTGCACTGTCACTGTGCGCGTGGGATCCGGGAGC 1680
1729 GAGGCCCTGGTCCCGTGGTCCCGTGTGCACTGTCACTGTGCGCGTGGGATCCGGGAGC 1788
1681 GCACCGGGTCTCAACAGCGCTGAGCCCTCAGTACGAGGAGGAGGCTGCGGTGGGGATG 1740
1789 GCACCGGGTCTCAACAGCGCTGAGCCCTCAGTACGAGGAGGAGGCTGCGGTGGGGATG 1848
1741 TGACGAGCGTCAAGTGTGCAACAGAGAGTGTGCCCCGTGAGTGTCTTTATCCAAACC 1800
1849 TGACGAGCGTCAAGTGTGCAACAGAGAGTGTGCCCCGTGAGTGTCTTTATCCAAACC 1908
1801 CTTGCTTCCGGGAGCCAGTGCAGCAGTTCCTCCGATGGTCTGCTATCGGCTCT 1860
1909 CTTGCTTCCGGGAGCCAGTGCAGCAGTTCCTCCGATGGTCTGCTATCGGCTCT 1968
1861 GCCTGTGGGCTTTCTTTGGGCAATGGCACCCACTGTGAGGACCTGACGAGTGTGCCCTGG 1920
1969 GCCTGTGGGCTTTCTTTGGGCAATGGCACCCACTGTGAGGACCTGACGAGTGTGCCCTGG 2028
1921 TCCCGGACATCTGCTTCTCCACGACAGGTGCTGCTGTGTCAACACTCAGCTTGGCT 1980
2029 TCCCGGACATCTGCTTCTCCACGACAGGTGCTGCTGTGTCAACACTCAGCTTGGCT 2088
1981 TCCACTGCTTCCCTGCTCCCGCCCGATACAGAGGGAACCCAGCCCGTCCGGGCTCGGCTGG 2040
2089 TCCACTGCTTCCCTGCTCCCGCCCGATACAGAGGGAACCCAGCCCGTCCGGGCTCGGCTGG 2148
2041 AAGCAGCAGACGAGAAAGCAAGTGTGAGCCCGGAAACCCATGCAAGGACAGACAC 2100
2149 AAGCAGCAGACGAGAAAGCAAGTGTGAGCCCGGAAACCCATGCAAGGACAGACAC 2208
2101 ACAACTGCCCAAGCAGCGGAGTGTATCTACCTGGGCACTTTCAGCGACCCCATGTACA 2160
2209 ACAACTGCCCAAGCAGCGGAGTGTATCTACCTGGGCACTTTCAGCGACCCCATGTACA 2268
2161 AGTGGAGTCCACAGACAGGCTA CGCGGGCGACGGGCTCATCTGCGGGGAGGACTCGGACC 2220
2269 AGTGGAGTCCACAGACAGGCTA CGCGGGCGACGGGCTCATCTGCGGGGAGGACTCGGACC 2328
2221 TGGAGCGCTGGCCCAACTCAATCTGTGTGCGCCACCAAGCGCACTTACCACTGATCA 2280
2329 TGGAGCGCTGGCCCAACTCAATCTGTGTGCGCCACCAAGCGCACTTACCACTGATCA 2388
2281 AGGATAACTGCCCCCACTCTGCCAAATTTCTGGGCAGGAAAGACTTTTGACAGGACGGGATTG 2340

2389 AGGATAACTGCCCCCACTCTGCCAAATTTCTGGGAGGAAAGCTTTTGACAGGACGGGATTG 2448
2341 GCGATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
2449 GCGATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2508
2401 AGCTCTCTTTCAATCCCGCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460
2509 AGCTCTCTTTCAATCCCGCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2568
2461 ACAACTGCCCTTACGTGCACAAACCTCCAGATGATGATGATGATGATGATGATGATGATGATGATG 2520
2569 ACAACTGCCCTTACGTGCACAAACCTCCAGATGATGATGATGATGATGATGATGATGATGATGATG 2628
2521 AGCTCTCTCTCGTGGACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
2629 AGCTCTCTCTCGTGGACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2688
2581 ACCTCTACACACTGACGAGGAGACCGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640
2689 ACCTCTACACACTGACGAGGAGACCGATGATGATGATGATGATGATGATGATGATGATGATGATG 2748
2641 ACTGCCCTCTGGTGCACAAACCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
2749 ACTGCCCTCTGGTGCACAAACCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2808
2701 AGTGTGACAAACGAGGACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
2809 AGTGTGACAAACGAGGACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2868
2761 CCTACATCTCCAAACGAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
2869 CCTACATCTCCAAACGAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2928
2821 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880
2929 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2988
2881 ACCCAGACCGAGGAGCTTGGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
2989 ACCCAGACCGAGGAGCTTGGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3048
2941 ACAATGACAAACATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
3049 ACAATGACAAACATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3108
3001 CAGACTTTCAGGAACTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
3109 CAGACTTTCAGGAACTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3168
3061 CCAACTGGGCTCAATTCGCCATCAAGGCAAGAGCTGATGATGATGATGATGATGATGATGATGATG 3120
3169 CCAACTGGGCTCAATTCGCCATCAAGGCAAGAGCTGATGATGATGATGATGATGATGATGATGATG 3228
3121 GCATCGCTGTAGGTTTTCAGGAGTTTTCGGCTGTGGACTTTCAGTGGCAGCATTTCTACCTGAA 3180
3229 GCATCGCTGTAGGTTTTCAGGAGTTTTCGGCTGTGGACTTTCAGTGGCAGCATTTCTACCTGAA 3288
3181 ACATGACCGGAGCAGCAGCTATGCTCGGCTTTCGCTTTTGTGTACAGTCAAGCAGCGCT 3240
3289 ACATGACCGGAGCAGCAGCTATGCTCGGCTTTCGCTTTTGTGTACAGTCAAGCAGCGCT 3348
3241 TCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
3349 TCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3408
3301 CCTATGGCTACTCCGGGCTGTCCCTCAAGGTGGTGAATCCACCAACCGGGGACCGGGCGAGC 3360
3409 CCTATGGCTACTCCGGGCTGTCCCTCAAGGTGGTGAATCCACCAACCGGGGACCGGGCGAGC 3468
3361 ACCTGAGGACCGCTGTGGCACACCGGGGAAACCGCGGGGACGGTGGAACTTTATGGC 3420


```

2y 5580 TTATGTTTACATGTCACAAATTTTACCACTGAAACCCCTGACCTTAGCTAGAACCTCAT 5639
db 5680 TTAATGTTTACATGTCACAAATTTTACCACTGAAACCCCTGACCTTAGCTAGAACCTCAT 5739
2y 5640 TTTTAAAGATTACACAGGAATTAATTTGTAAGAAAGGTTTCT 5684
db 5740 TTTTAAAGATTACACAGGAATTAATTTGTAAGAAAGGTTTCT 5784

RESULT 5
JS-10-240-425-1280
: Sequence 1280, Application US/10240425
: Publication No. US20040033502A1
: GENERAL INFORMATION:
: APPLICANT: Williams, Amanda
: APPLICANT: Bolland, Joseph F.
: APPLICANT: Lord, Reginald V.
: APPLICANT: Alvarez, Chris
: APPLICANT: Wetzel, Jon C.
: APPLICANT: Scherz, Uwe
: APPLICANT: Vockley, Joseph G.
: TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
: FILE REFERENCE: 44921-5026
: CURRENT APPLICATION NUMBER: US/10/240,425
: CURRENT FILING DATE: 2002-09-30
: PRIOR APPLICATION NUMBER: PCT/US01/09847
: PRIOR FILING DATE: 2001-03-28
: PRIOR APPLICATION NUMBER: US 60/193,446
: PRIOR FILING DATE: 2000-03-31
: NUMBER OF SEQ ID NOS: 1588
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1280
: LENGTH: 5784
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20040033502A1 L12350
JS-10-240-425-1280

Query Match 97.9%; Score 5576.6; DB 12; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

2y 1 GACTACGCTGCATGACGAGGCGGTCTCTCGCTCCAGCAGAGCTCGCGCTTCTGACTC 60
db 109 GAGCATCTGCACTGACGAGGCGGTCTCTCGCTCCAGCAGAGCTCGCGCTTCTGACTC 168
2y 61 GGTCCGGAACACTGAACCCAGTCATCACTGCATCTTTTGGCAACCGAGAGCTCAGCTG 120
db 169 GGTCCGGAACACTGAACCCAGTCATCACTGCATCTTTTGGCAACCGAGAGCTCAGCTG 228
2y 121 CAGGAGCAGGATGGTCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
db 229 CAGGAGCAGGATGGTCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
2y 181 AAGCTGTCACGAGACAAAGACAGACCTTTCAGCTTTCAGTATCAGCAACATCAACC 240
db 289 AAGCTGTCACGAGACAAAGACAGACCTTTCAGCTTTCAGTATCAGCAACATCAACC 348
2y 241 GCAAGACCATTTGGCCCAAGCAGTTCCGCGGCGCCGACCCCGGCTGCGGCTTACCGCT 300
db 349 GCAAGACCATTTGGCCCAAGCAGTTCCGCGGCGCCGACCCCGGCTGCGGCTTACCGCT 408
3y 301 TCGTGGCTTTGACTATCATCCACCGGTGAACGAGATGACCTCAGCAAGATCACCAGA 360
db 409 TCGTGGCTTTGACTATCATCCACCGGTGAACGAGATGACCTCAGCAAGATCACCAGA 468
3y 361 TCATGCGGCAAGAGGGCTTCTCTCAGCGGCCAGCTCAAGCAGAGCGCAAGTCCA 420
db 469 TCATGCGGCAAGAGGGCTTCTCTCAGCGGCCAGCTCAGCAGAGCGCAAGTCCA 528
3y 421 GGGGACGCTTGGCTCTGAGGAGGCGCCCGGTCTCTCCACAGAGCATTCGAGATCGTCT 480

```

```

db 529 GGGGACGCTTGTGGCTCTGGAGGCGCCCGGTCTCTCCACAGAGCAGTTCCGATCGTCT 588
qy 481 CCACGGGCGCCGCGACACGCTGATCTCACTACTGATTTGACGCGACCCGCGATGTGG 540
db 589 CCACGGGCGCCGCGACACGCTGATCTCACTACTGATTTGACGCGACCCGCGATGTGG 648
qy 541 TCTCCCTGGAGGACGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
db 649 TCTCCCTGGAGGACGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
qy 601 CTGGCGAGACCTCAGCTTGGACGCTGGGCTGCGACCTCATAGACAGCTTCCCTCTGGACG 660
db 709 CTGGCGAGACCTCAGCTTGGACGCTGGGCTGCGACCTCATAGGACCACTGCTCTGGACG 768
qy 661 AGCCCTTCTACGACACCTGCGCGGAAAGAGCCGATGTACGCTGCGCCAAAGCTCTG 720
db 769 AGCCCTTCTACGACACCTGCGCGGAAAGAGCCGATGTACGCTGCGCCAAAGCTCTG 828
qy 721 CCAGAGAGTCACTTCAAGGAGTTTGTCTTCAAGACGTCCTCACTAGTGTGTAAGAACTCTG 780
db 829 CCAGAGAGTCACTTCAAGGAGTTTGTCTTCAAGACGTCCTCACTAGTGTGTAAGAACTCTG 888
qy 781 TGGAGATATTCTAAGCAAGAGGTTTCCCAAGAGCCAGGAGCTCAGATCAACGCCA 840
db 889 TGGAGATATTCTAAGCAAGAGGTTTCCCAAGAGCCAGGAGCTCAGATCAACGCCA 948
qy 841 TCAGTGAGAACACAGAGACGCTGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
db 949 TCAGTGAGAACACAGAGACGCTGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1008
qy 901 CCAGCTCAGAGAGGAGGCGCGAGGTGTGCGAACGCTCGTGGAGAGCTGGGAAACATGG 960
db 1009 CCAGCTCAGAGAGGAGGCGCGAGGTGTGCGAACGCTCGTGGAGAGCTGGGAAACATGG 1068
qy 961 TCCAGAGCTCTCGGGGCTCCAGCTCTCTGTAACAGCTCAGCGAGAACCTCAAGAGAG 1020
db 1069 TCCAGAGCTCTCGGGGCTCCAGCTCTCTGTAACAGCTCAGCGAGAACCTCAAGAGAG 1128
qy 1021 TGTGGAATGATAAACAGTTTCTCTGGAGGCTCATTTGGTGGCCCTCTTAAGACAAAGGAACA 1080
db 1129 TGTGGAATGATAAACAGTTTCTCTGGAGGCTCATTTGGTGGCCCTCTTAAGACAAAGGAACA 1188
qy 1081 TGTGAGCTTGTGGCAGGATGCGCGGTCTTTTGGGAAATGAAACCTGGTGGTGGTGGTGG 1140
db 1189 TGTGAGCTTGTGGCAGGATGCGCGGTCTTTTGGGAAATGAAACCTGGTGGTGGTGGTGG 1248
qy 1141 GGTGACCACTGCTGACCTGCAAGAAATTTAAACCATTTGGCCACCAATCACTGCGCCGC 1200
db 1249 GGTGACCACTGCTGACCTGCAAGAAATTTAAACCATTTGGCCACCAATCACTGCGCCGC 1308
qy 1201 CTGCAACTGCGCCAGTCCATCTTTGGAAGGCAATGCTGCGCTTCTGCTTCCACT 1260
db 1309 CTGCAACTGCGCCAGTCCATCTTTGGAAGGCAATGCTGCGCTTCTGCTTCCACT 1368
qy 1261 CGGTGGAAGGAGGCTGCTCGTGGGAGAGTGGACCCAGTGGCTCGCTGCTGCTGCTGCTG 1320
db 1369 CGGTGGAAGGAGGCTGCTCGTGGGAGAGTGGACCCAGTGGCTCGCTGCTGCTGCTGCTG 1428
qy 1321 GTGGCTCTGGGACCCAGCAGAGGCGCGTCTCTGTGAGCTCACCAGCAACACCTGCTTGG 1380
db 1429 GTGGCTCTGGGACCCAGCAGAGGCGCGTCTCTGTGAGCTCACCAGCAACACCTGCTTGG 1488
qy 1381 GGCCTCCATCCAGACGGGCTTGCAGTCTGACGAGTGTGACACCCGCAATCCGGCAGG 1440
db 1489 GGCCTCCATCCAGACGGGCTTGCAGTCTGACGAGTGTGACACCCGCAATCCGGCAGG 1548
qy 1441 AGCGGGCTGGAGCCACTGTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
db 1549 AGCGGGCTGGAGCCACTGTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1608
qy 1501 ATATCAGCAGCATCGTCTCTGCAACTCCCGAGTGGCCCGACATGGGGGCAAGATTGCA 1560
db 1609 ATATCAGCAGCATCGTCTCTGCAACTCCCGAGTGGCCCGACATGGGGGCAAGATTGCA 1668

```


2Y	1561	AAGGGAGTGGCCGGGAGACCAAAAGCCTGCAGGGCGCCCATCGATCGATGGCCGT	1620
Db	1669	AAGGGAGTGGCCGGGAGACCAAAAGCCTGCAGGGCGCCCATCGATGGCCGT	1728
2Y	1621	GGAGCCCTGGTCCCGTGGTCCGCTGCACCTGTGCGGTGGAGTCCGGAGC	1680
Db	1729	GGAGCCCTGGTCCCGTGGTCCGCTGCACCTGTGCGGTGGAGTCCGGAGC	1788
2Y	1681	GCACCCGGGTCTCAACAGCCTTGAGCTCAGTACGGAGGGAAGGCTCGTGGGGATG	1740
Db	1789	GCACCCGGGTCTCAACAGCCTTGAGCTCAGTACGGAGGGAAGGCTCGTGGGGATG	1848
2Y	1741	TGCAGGAGGTCAAGTGTGCAACAGAGGAGCTGCCCGTGGATGCTGTTATCAAC	1800
Db	1849	TGCAGGAGGTCAAGTGTGCAACAGAGGAGCTGCCCGTGGATGCTGTTATCAAC	1908
QY	1801	CTTGCTTCCCGGAGGCCAGTGCAGCAGCTTCCCGATGGGTCTGTCATCGGTCCT	1860
Db	1909	CTTGCTTCCCGGAGGCCAGTGCAGCAGCTTCCCGATGGGTCTGTCATCGGTCCT	1968
QY	1861	GCCTGTGGCTTCTTGGGCAATGGCACCACTGTGAGGACCTGGACGAGTGCCCTG	1920
Db	1969	GCCTGTGGCTTCTTGGGCAATGGCACCACTGTGAGGACCTGGACGAGTGCCCTG	2028
QY	1921	TCGCCACATCTGCTTCTCCACAGCAAGTGCTCGCTGTGCAACACTCAGCCTGGCT	1980
Db	2029	TCGCCACATCTGCTTCTCCACAGCAAGTGCTCGCTGTGCAACACTCAGCCTGGCT	2088
QY	1981	TCACCTGCTGCCCTGCCCGCCCGATACAGAGGGAACAGCCGTCGGGTCCGCTGG	2040
Db	2089	TCACCTGCTGCCCTGCCCGCCCGATACAGAGGGAACAGCCGTCGGGTCCGCTGG	2148
QY	2041	AAGCAGCCAAAGACGGAAAGCAAGTGTGAGCGCCCGAAAAACCATGCAAGGACAAGACAC	2100
Db	2149	AAGCAGCCAAAGACGGAAAGCAAGTGTGAGCGCCCGAAAAACCATGCAAGGACAAGACAC	2208
QY	2101	ACAACTGCGCAACAGCAGCGGAGTGCACTTACTGGGCCACTTCAGGAGCCCATGTACA	2160
Db	2209	ACAACTGCGCAACAGCAGCGGAGTGCACTTACTGGGTCACTTCAGCGACCCCATGTACA	2268
QY	2161	AGTCGAGTGCCACAGACAGGCTACCGCGGCCACCGGCTCATCTCGGGGAGGACTCGGACC	2220
Db	2269	AGTCGAGTGCCACAGACAGGCTACCGCGGCCACCGGCTCATCTCGGGGAGGACTCGGACC	2328
QY	2221	TGAGCGCTGGCCCAACCTCAATCTGTGTGTGGCCACCAAGCCACTACACTGCATCA	2280
Db	2329	TGAGCGCTGGCCCAACCTCAATCTGTGTGTGGCCACCAAGCCACTACACTGCATCA	2388
QY	2281	AGGATAACTGCCCCCATCTGCCAAATCTCGGCAAGAACTTGAACAAGACGGGATTG	2340
Db	2389	AGGATAACTGCCCCCATCTGCCAAATCTCGGCAAGAACTTGAACAAGACGGGATTG	2448
QY	2341	CGGATGCTGTGATGAGTGAAGATGAATAAGACGGTGTGACGGATGAGAAGACACTGCC	2400
Db	2449	CGGATGCTGTGATGAGTGAAGATGAATAAGACGGTGTGACGGATGAGAAGACACTGCC	2508
QY	2401	AGCTCTCTTCAATCCCGCCAGGCTGACTATGACAAAGGATGAGTTGGGGAACGCTGTG	2460
Db	2509	AGCTCTCTTCAATCCCGCCAGGCTGACTATGACAAAGGATGAGTTGGGGAACGCTGTG	2568
QY	2461	ACAACTGCCCTTACGTGACAAACCTTGCCAGATCGACACAGACAACAATGGAGAGGCTG	2520
Db	2569	ACAACTGCCCTTACGTGACAAACCTTGCCAGATCGACACAGACAACAATGGAGAGGCTG	2628
QY	2521	ACGCTGTCTCGTGGACATTGATGGGACGATGTCTTCAATGAACGAGACAATTTGTCCT	2580
Db	2629	ACGCTGTCTCGTGGACATTGATGGGACGATGTCTTCAATGAACGAGACAATTTGTCCT	2688
QY	2581	ACGTCTTAAACACTGAACAGAGGACACGGATGTGTGACGGTGTGGGGATCACTGTGACA	2640
Db	2689	ACGTCTTAAACACTGAACAGAGGACACGGATGTGTGACGGTGTGGGGATCACTGTGACA	2748

2641	ACTGCCCTGGTGCACAAACCTGNACAGACGGACGTGGCAATGACCTGTTGGGACC	2700
2749	ACTGCCCTGGTGCACAAACCTGNACAGACGGACGTGGCAATGACCTGTTGGGACC	2808
2701	AGTGTGCAACAAACGAGGACATAGATGACGCGCCACAGAAACACAGGACAACTGCC	2760
2809	AGTGTGCAACAAACGAGGACATAGATGACGCGCCACAGAAACACAGGACAACTGCC	2868
2761	CCTACATCTCMAACGCCAACAGAGTGCACCATGACAGAGACGGCCAGGCGACGCGTGTG	2820
2869	CCTACATCTCMAACGCCAACAGAGTGCACCATGACAGAGACGGCCAGGCGACGCGTGTG	2928
2821	ACCCTGATGATGACAAACGATGGCTCCCCGATGACAGGGAACAACTGCCGCTGTGTTCA	2880
2929	ACCCTGATGATGACAAACGATGGCTCCCCGATGACAGGGAACAACTGCCGCTGTGTTCA	2988
2881	ACCCAGACACGAGGACCTTGGACGGTGTGACGCGGTGATATTTGTAAGATGATTTTG	2940
2989	ACCCAGACACGAGGACCTTGGACGGTGTGACGCGGTGATATTTGTAAGATGATTTTG	3048
2941	ACAATGACAAACATCCAGATATTTGATGATGTGTCTTGAAACAAATGCCATCAGTGAGA	3000
3049	ACAATGACAAACATCCAGATATTTGATGATGTGTCTTGAAACAAATGCCATCAGTGAGA	3108
3001	CAGACTTCAGGAACCTTCAGATGGTCCCTTGGATCCCAAGGGACACCCAAATTGATC	3060
3109	CAGACTTCAGGAACCTTCAGATGGTCCCTTGGATCCCAAGGGACACCCAAATTGATC	3168
3061	CCAACTGGGTCAATTCCGCATCAAGGCAAGGAGCTGGTTCAGACGCCAACTCGGACCCCG	3120
3169	CCAACTGGGTCAATTCCGCATCAAGGCAAGGAGCTGGTTCAGACGCCAACTCGGACCCCG	3228
3121	GCATCGCTGTAGTCTTTCAGCAGATTTGGTCTGTGACCTTCAGTGGGCACATTCACGTAA	3180
3229	GCATCGCTGTAGTCTTTCAGCAGATTTGGTCTGTGACCTTCAGTGGGCACATTCACGTAA	3288
3181	ACACTGACCGGACGACGACTATGCTGGCTTCGCTTTGGTTTACAGTCAAGCAGCCGCT	3240
3289	ACACTGACCGGACGACGACTATGCTGGCTTCGCTTTGGTTTACAGTCAAGCAGCCGCT	3348
3241	TCATGTGTGTGATGTGGAAAGCAGGTGACGACAGCTACTTGGGAGGACACAGCCACGCGGG	3300
3349	TCATGTGTGTGATGTGGAAAGCAGGTGACGACAGCTACTTGGGAGGACACAGCCACGCGGG	3408
3301	CCTATGGCTACTCCGCGGTGCCACACGGGGAAACGCGCGGGCAGGTGCGAAACCTTATGGC	3360
3409	CCTATGGCTACTCCGCGGTGCCACACGGGGAAACGCGCGGGCAGGTGCGAAACCTTATGGC	3468
3361	ACCTGAGGAAACGCGCTGTGGCACAACGGGGAAACGCGCGGGCAGGTGCGAAACCTTATGGC	3420
3469	ACCTGAGGAAACGCGCTGTGGCACAACGGGGAAACGCGCGGGCAGGTGCGAAACCTTATGGC	3528
3421	AGACCCCAAGGAACATTTGGCTGGAAAGGACTACACGGCTTATAGTGGGCACCTGACTCACA	3480
3529	AGACCCCAAGGAACATTTGGCTGGAAAGGACTACACGGCTTATAGTGGGCACCTGACTCACA	3588
3481	GGCCCAAGACTGGCTACATCAGAGCTTATAGTGATGAAAGGAAAAACAGTTCATGGCAGACT	3540
3589	GGCCCAAGACTGGCTACATCAGAGCTTATAGTGATGAAAGGAAAAACAGTTCATGGCAGACT	3648
3541	CAGGACCTATCTATGACGAAACCTAGCTGGCGGGCGGTGGGTCTATTTGTCCTCTCTC	3600
3649	CAGGACCTATCTATGACGAAACCTAGCTGGCGGGCGGTGGGTCTATTTGTCCTCTCTC	3708
3601	AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGAGATATTTAAACAAAGATTG	3660
3709	AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGAGATATTTAAACAAAGATTG	3768
3661	CTGCATTTCCGGAATGCCCTGTGATGCCATGGTCCCTAGACACCTCAGTTTCATTTGTGG	3720
3769	CTGCATTTCCGGAATGCCCTGTGATGCCATGGTCCCTAGACACCTCAGTTTCATTTGTGG	3828
3721	TCCTGTGGGCTTCTCTCTTAGCAGACACCTCCCTGTCCCTTGACCTTAACTCTGATGGTTC	3780


```

; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo sapiens
JS-10-060-036-149

```

Query Match 97.9%; Score 5576.6; DB 14; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

Qy		1	GACTACGCTGCATCGAGGGCCGGTCTCTCGCTCCAGCAGAGCGCTCGGCTTTTCTCACTC	60
Db		109	GAGCATCTCTGCACTGAGGGCCGGTCTCTCGCTCCAGCAGAGCGCTCGGCTTTTCTCACTC	168
Qy		61	GGTCCGGAACACTGAACAACAGTCATCACTGCATCTTTTTTGCCAACACGAGAGCTCAAGCTG	120
Db		169	GGTCCGGAACACTGAACAACAGTCATCACTGCATCTTTTTTGCCAACACGAGAGCTCAAGCTG	228
Qy		121	CAGGAGCGAGGATGGTCTGGAGGCTGGTCTGTCTGGCTCTGTGGGTGTGGCCCGAGCACGC	180
Db		229	CAGGAGCGAGGATGGTCTGGAGGCTGGTCTGTCTGGCTCTGTGGGTGTGGCCCGAGCACGC	288
Qy		181	AAGCTGGTCAACCAGGACAAAGAACAAGACCTTCGACCTTTTCAGTATCAGCAAACATCAACC	240
Db		289	AAGCTGGTCAACCAGGACAAAGAACAAGACCTTCGACCTTTTCAGTATCAGCAAACATCAACC	348
Qy		241	GCAAGACCATTTGGGCCCAAGCAGTTCCGGGGCCCCAGCCCCTGGGCTCCGGCTTACCGCT	300
Db		349	GCAAGACCATTTGGGCCCAAGCAGTTCCGGGGCCCCAGCCCCTGGGCTTACCGCTTACCGCT	408
Qy		301	TCGTGCGCTTTGACTACATCCCAACCGGTGAACGCAGATGACCTCAGCAAGATCACCAAGA	360
Db		409	TCGTGCGCTTTGACTACATCCCAACCGGTGAACGCAGATGACCTCAGCAAGATCACCAAGA	468
Qy		361	TCATGGCGCAGAGGAGGGCTTCTCTCAGGCCCCAGCTCAGCAGGACGGCAAGTCCA	420
Db		469	TCATGGCGCAGAGGAGGGCTTCTCTCAGGCCCCAGCTCAGCAGGACGGCAAGTCCA	528
Qy		421	GGGSCACGCTTTGGCTCTCGAAGGCCCCGGTCTCTCCAGAGGCAGTTTCAGATCGTCT	480
Db		529	GGGSCACGCTTTGGCTCTCGAAGGCCCCGGTCTCTCCAGAGGCAGTTTCAGATCGTCT	588
Qy		481	CCACGGCCCGCGGACACGCTGGATCTCACTACTGGATTGACGGCACCCGGCATGTGG	540
Db		589	CCACGGCCCGCGGACACGCTGGATCTCACTACTGGATTGACGGCACCCGGCATGTGG	648
Qy		541	TCTCCCTGGAGGACGTGGCCCTGCTGACTGCGAGTGAAGAACGTCAACCGTCAGGTGG	600
Db		649	TCTCCCTGGAGGACGTGGCCCTGCTGACTGCGAGTGAAGAACGTCAACCGTCAGGTGG	708
Qy		601	CTGGCGAGACCTACAGCTTGCACGTGGGCTCGACCTCATAGACAGCTTCGCTCTGACGC	660
Db		709	CTGGCGAGACCTACAGCTTGCACGTGGGCTCGACCTCATAGACAGCTTCGCTCTGACGC	768
Qy		661	AGCCCTTCTACGACACCTGAGCGCGGAAAAGACCGGATGTACGTGGCCAAAGGCTCTG	720
Db		769	AGCCCTTCTACGACACCTGAGCGCGGAAAAGACCGGATGTACGTGGCCAAAGGCTCTG	828
Qy		721	CCAGAGAGAGTCACCTTCAGGGGTTTGCCTTCAGAACGCTCCACTAGTGTTTGAAAACCTG	780
Db		829	CCAGAGAGAGTCACCTTCAGGGGTTTGCCTTCAGAACGCTCCACTAGTGTTTGAAAACCTG	888
Qy		781	TGGAAGATATTCTAAGCAAGAGGGTTCCGACGACGACCGCGGAGCTGAGATCAACGCCA	840
Db		889	TGGAAGATATTCTAAGCAAGAGGGTTCCGACGACGACCGCGGAGCTGAGATCAACGCCA	948
Qy		841	TCAGTGAACAACAGAGACGCTGCGCCCTCGCATGTCCACACGAGTACCTGGGCC	900
Db		949	TCAGTGAACAACAGAGACGCTGCGCCCTCGCATGTCCACACGAGTACCTGGGCC	1008

901	QY	901	CCAGCTCAGAGAGGAGGCCGAGGTTGTCGGAACCGTCTGTCGAGGAGCTCGGAAACATGG	960
1009	DB	1009	CCAGCTCGGAGAGAGGAGGCCGAGGTTGTCGGAACCGTCTGTCGAGGAGCTCGGAAACATGG	1068
961	QY	961	TCAGAGAGCTCTCGGCGCTCCACGTCCTCTGTGAACCAAGCTCAGCGGAGAACTCAAGAGAG	1020
1069	DB	1069	TCAGAGAGCTCTCGGCGCTCCACGTCCTCTGTGAACCAAGCTCAGCGGAGAACTCAAGAGAG	1128
1021	QY	1021	TGTCGAATGATTAACCAAGTTTCTCTGGGAGCTCATTGTGGCGCTCTTAAGACACAGGACA	1080
1129	DB	1129	TGTCGAATGATTAACCAAGTTTCTCTGGGAGCTCATTGTGGCGCTCTTAAGACACAGGACA	1138
1081	QY	1081	TGTCAGCTTCTGCTGCAGAGATGGCCGGTCTTTTGGCGAAAAATGAACCTGGGTGGTGACA	1140
1189	DB	1189	TGTCAGCTTCTGCTGCAGAGATGGCCGGTCTTTTGGCGAAAAATGAACCTGGGTGGTGACA	1248
1141	QY	1141	GCTGCACACAGTGTACTCTGCAGAAATTTAAACCAATTTGCCACCAATCACCTGCCCGC	1200
1249	DB	1249	GCTGCACACAGTGTACTCTGCAGAAATTTAAACCAATTTGCCACCAATCACCTGCCCGC	1308
1201	QY	1201	CTGCAACTCTGCGCCAGTCCATCCTTTGTGGAAAGCGAATGCTGCCCTTCCTGCTCCACT	1260
1309	DB	1309	CTGCAACTCTGCGCCAGTCCATCCTTTGTGGAAAGCGAATGCTGCCCTTCCTGCTCCACT	1368
1261	QY	1261	CGGTGGAAGTGAAGAGGCGTGGTCTCCGTGGGACAGTGGACCCAGTGTCTCCGTGACGT	1320
1369	DB	1369	CGGTGGAAGTGAAGAGGCGTGGTCTCCGTGGGACAGTGGACCCAGTGTCTCCGTGACGT	1428
1321	QY	1321	GTGGCTCTGCGGACCCACAGCAGAGAGGCGGTCTCTGTGACGTCAACAGCAACACTGCTTG	1380
1429	DB	1429	GTGGCTCTGCGGACCCACAGCAGAGAGGCGGTCTCTGTGACGTCAACAGCAACACTGCTTG	1488
1381	QY	1381	GGCCCTCCATCTCAGACACGGGCTTGACGTCTGACAGTGTGACACCGCATCCGGCAGG	1440
1489	DB	1489	GGCCCTCGATCTCAGACACGGGCTTGACGTCTGACAGTGTGACACCGCATCCGGCAGG	1548
1441	QY	1441	ACGGCGGCTGGAGCCACTGGTCACTTGGTCTTCTATGCTGTGTGACCTGTGAGTTGCA	1500
1549	DB	1549	ACGGCGGCTGGAGCCACTGGTCACTTGGTCTTCTATGCTGTGTGACCTGTGAGTTGCA	1608
1501	QY	1501	ATATCAACAGCATCCGTCTCTGCAACTCCGCCAGTGCCTCCAGATGGGGGCAAGAAATGCA	1560
1609	DB	1609	ATATCAACAGCATCCGTCTCTGCAACTCCGCCAGTGCCTCCAGATGGGGGCAAGAAATGCA	1668
1561	QY	1561	AAGGAGTGGCCGGAGACAAAGCCTGCACGGCGCCCCATGCCCCAATCGATGGCGCT	1620
1669	DB	1669	AAGGAGTGGCCGGAGACAAAGCCTGCACGGCGCCCCATGCCCCAATCGATGGCGCT	1728
1621	QY	1621	GGAGCCCTGGTCCCGTGGTCCGCTGACACTGTACACTGTGTCGGGTGGGATCCGGGAGC	1680
1729	DB	1729	GGAGCCCTGGTCCCGTGGTCCGCTGACACTGTACACTGTGTCGGGTGGGATCCGGGAGC	1788
1681	QY	1681	GCACCCGGTCTGCAACAGCCCTGAGCCTCAGTACGAGGGGAAGCCCTCGTGGGGGATG	1740
1789	DB	1789	GCACCCGGTCTGCAACAGCCCTGAGCCTCAGTACGAGGGGAAGCCCTCGTGGGGGATG	1848
1741	QY	1741	TGAGGAGCGTCAAGTGTGCAACAGAGGAGCTGCCCGGTGATGGCTTTATTCCAACC	1800
1849	DB	1849	TGAGGAGCGTCAAGTGTGCAACAGAGGAGCTGCCCGGTGATGGCTTTATTCCAACC	1908
1801	QY	1801	CGTGTCTCCCGGAGCCAGTGCAGAGCTTCCCGATGGGTCTGTGGTTCATGCGGCTCCT	1860
1909	DB	1909	CGTGTCTCCCGGAGCCAGTGCAGAGCTTCCCGATGGGTCTGTGGTTCATGCGGCTCCT	1968
1861	QY	1861	GCCTGTGGGCTCTCTGGGCATATGGCAACCACTGTGAGACTCTGGACAGTGTGCCCTGG	1920
1969	DB	1969	GCCTGTGGGCTCTCTGGGCATATGGCAACCACTGTGAGACTCTGGACAGTGTGCCCTGG	2028
1921	QY	1921	TCCCGACATCTGTTCTTCCACAGCAAGGTGGCTCGCTGTGTCAACTCACTGACCTGGCT	1980
2029	DB	2029	TCCCGACATCTGTTCTTCCACAGCAAGGTGGCTCGCTGTGTCAACTCACTGACCTGGCT	2088

y 241 GCAAGACCAATTGGCGCAAGCAGTTCGGCGGCGCCGACCCCGCGGTGCGGGTTACCGCT 300
 b 349 GCAAGACCAATTGGCGCAAGCAGTTCGGCGGCGCCGACCCCGCGGTGCGGGTTACCGCT 408
 y 301 TCGTGGCTTTGACTACATCCCAACCGGTGAAACGACAGATGACCTCAGCAAGATCAACAAGA 360
 b 409 TCGTGGCTTTGACTACATCCCAACCGGTGAAACGACAGATGACCTCAGCAAGATCAACAAGA 468
 y 361 TCATGGCGGAGAGAGGGCTTCCTTCACGCGCGAGCTCAAGCAGAGACGCGCAAGTCCA 420
 b 469 TCATGGCGGAGAGAGGGCTTCCTTCACGCGCGAGCTCAAGCAGAGACGCGCAAGTCCA 528
 y 421 GGCGCACCGTGTGGCTCTGGAAGGGCCCGGTCTCTCCAGAGGAGTTCAGAGATCGTCT 480
 b 529 GGCGCACCGTGTGGCTCTGGAAGGGCCCGGTCTCTCCAGAGGAGTTCAGAGATCGTCT 588
 y 481 CCAAACGGCCCGCGGACACGCTGGATCTCACTACTGGAATTGACGGCACCCCGGCAATGG 540
 b 589 CCAAACGGCCCGCGGACACGCTGGATCTCACTACTGGAATTGACGGCACCCCGGCAATGG 648
 y 541 TCTCCCTGGAGACGTCGCGCTGGCTGACTCGCAGTGAAGAACGTCACCGTGCAGGTGG 600
 b 649 TCTCCCTGGAGACGTCGCGCTGGCTGACTCGCAGTGAAGAACGTCACCGTGCAGGTGG 708
 y 601 CTGGCGAGACCTACAGCTTGCACGCTGGCTGCGAAGCTCATAGACAGCTTCGCTCTGGACG 660
 b 709 CTGGCGAGACCTACAGCTTGCACGCTGGCTGCGAAGCTCATAGACAGCTTCGCTCTGGACG 768
 y 661 AGCCCTTCTACGACACCTGCAAGCGGCGGAAAGCGGATGTACCTGGCCCAAGGCTCTG 720
 b 769 AGCCCTTCTACGACACCTGCAAGCGGCGGAAAGCGGATGTACCTGGCCCAAGGCTCTG 828
 y 721 CCAGAGAGAGTCACTTCAGGGGTTTCTTCAGAAAGTCCACCTAGTGTGTTGAAACTCTG 780
 b 829 CCAGAGAGAGTCACTTCAGGGGTTTCTTCAGAAAGTCCACCTAGTGTGTTGAAACTCTG 888
 y 781 TGGAGATATTCTAAGCAGAGAGGTTGCGAGAGGCGGAGGCGAGGCTGAGATCAAGCCA 840
 b 889 TGGAGATATTCTAAGCAGAGAGGTTGCGAGAGGCGGAGGCGAGGCTGAGATCAAGCCA 948
 y 841 TCAGTCAGAAACACAGAGACGCTGCGGCTGGGCTCCGATGTCAACACCGAGTACGTGGGCC 900
 b 949 TCAGTCAGAAACACAGAGACGCTGCGGCTGGGCTCCGATGTCAACACCGAGTACGTGGGCC 1008
 y 901 CAGCTCAGAGAGAGGCGCGAGGTGTGCAAGCTCTGTCGAGAGAGCTGGGAAACATGG 960
 b 1009 CAGCTCAGAGAGAGGCGCGAGGTGTGCAAGCTCTGTCGAGAGAGCTGGGAAACATGG 1068
 y 961 TCAGAGAGCTCTCGGGCTCCAGCTCTGCTGAAACAGCTCAGCGAGAACCTCAAGAGAG 1020
 b 1069 TCAGAGAGCTCTCGGGCTCCAGCTCTGCTGAAACAGCTCAGCGAGAACCTCAAGAGAG 1128
 y 1021 TGTGGAATGATAACAGTTTCTCTGGAGGCTCATTTGGTGGCCCTCTTAAGACAAGAAACA 1080
 b 1129 TGTGGAATGATAACAGTTTCTCTGGAGGCTCATTTGGTGGCCCTCTTAAGACAAGAAACA 1188
 y 1081 TGTGAGCTTCTGCGAGGATGGCGGTTCTTTGCGGAATGAAAGTGGGTGGGACA 1140
 b 1189 TGTGAGCTTCTGCGAGGATGGCGGTTCTTTGCGGAATGAAAGTGGGTGGGACA 1248
 y 1141 GCTGCAACCGTGTACTGCAAGAAATTTAAACCAATTTGCCACCAATCACCCTGCCCGC 1200
 b 1249 GCTGCAACCGTGTACTGCAAGAAATTTAAACCAATTTGCCACCAATCACCCTGCCCGC 1308
 y 1201 CTGCAACCTGCGCAGTCCATCTCTTGTGGAAGGCGAATGCTGCCCTCTCTGCTCCACT 1260
 b 1309 CTGCAACCTGCGCAGTCCATCTCTTGTGGAAGGCGAATGCTGCCCTCTCTGCTCCACT 1368
 y 1261 CGGTGACGCTGAGAGGGGCTGTCTCCGTGGGAGAGTGGACCCAGTCTCCGTGACGT 1320
 b 1369 CGGTGACGCTGAGAGGGGCTGTCTCCGTGGGAGAGTGGACCCAGTCTCCGTGACGT 1428
 y 1321 GTGGCTCTGGGACCCGACAGAGAGGCGGTCTCTGTGACGTCAACGCAACACCTGCTGG 1380

Db 1429 GTGGCTCTGGGACCCGACGAGAGAGGCGGTCTGTGACGTCAACGACCAACCTGCTGG 1488
 Qy 1381 GGCCCTCCATCCAGACACACGGGCTTGAGTCTGAGCAAGTGTGACACCCGATCCGCGAGG 1440
 Db 1489 GGCCCTCGATCCAGACACACGGGCTTGAGTCTGAGCAAGTGTGACACCCGATCCGCGAGG 1548
 Qy 1441 ACGGCGCTGGAGCCACTGGTCACTTGGTCTTCATGCTCTGTGACTGTGAGTGGGATGGCA 1500
 Db 1549 ACGGCGCTGGAGCCACTGGTCACTTGGTCTTCATGCTCTGTGACTGTGAGTGGGATGGCA 1608
 Qy 1501 ATATCACACGATCCGCTCTGCAACTCCCCAGTGGCCCCAGATGGGGGGCAAGAAATGCA 1560
 Db 1609 ATATCACACGATCCGCTCTGCAACTCCCCAGTGGCCCCAGATGGGGGGCAAGAAATGCA 1668
 Qy 1561 AAGGAGTGGCCGGAGACCAAGACCTGCCAGGGCCCCCAATCGCATGGGCGCT 1620
 Db 1669 AAGGAGTGGCCGGAGACCAAGACCTGCCAGGGCCCCCAATCGCATGGGCGCT 1728
 Qy 1621 GGAGCCCTGGTCCCGTGGTCCGCTGCACTGTCACTGTGCGGTGGGATCCGGGAGC 1680
 Db 1729 GGAGCCCTGGTCCCGTGGTCCGCTGCACTGTCACTGTGCGGTGGGATCCGGGAGC 1788
 Qy 1681 GCACCCGGTCTGCAACAGCCCTGAGCTCAGTACGAGAGGAGGCTGCGTGGGGATG 1740
 Db 1789 GCACCCGGTCTGCAACAGCCCTGAGCTCAGTACGAGAGGAGGCTGCGTGGGGATG 1848
 Qy 1741 TGCAAGAGCGTCAAGTGTGCAACAGAGAGTGGCCCGTGGATGGCTGTTATCCAACC 1800
 Db 1849 TGCAAGAGCGTCAAGTGTGCAACAGAGAGTGGCCCGTGGATGGCTGTTATCCAACC 1908
 Qy 1801 CTTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTCTGGTCAATGCGGTCTCT 1860
 Db 1909 CTTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTCTGGTCAATGCGGTCTCT 1968
 Qy 1861 GCCTGTGGCTTCTTGGGCAATGGCAACCTGAGGACCTGAGACCTGAGTGGCCCTGG 1920
 Db 1969 GCCTGTGGCTTCTTGGGCAATGGCAACCTGAGGACCTGAGACCTGAGTGGCCCTGG 2028
 Qy 1921 TCCCGACATCTGCTTCTCCACGAGCAAGTGTGCTCGTGTGTCAACACTCAGCCTGGCT 1980
 Db 2029 TCCCGACATCTGCTTCTCCACGAGCAAGTGTGCTCGTGTGTCAACACTCAGCCTGGCT 2088
 Qy 1981 TCCACTGCTTCCCTCCCGCGGATACAGGGGACAGCCGCTCGGGGTGGCCCTGG 2040
 Db 2089 TCCACTGCTTCCCTCCCGCGGATACAGGGGACAGCCGCTCGGGGTGGCCCTGG 2148
 Qy 2041 AAGCAGCAAGACGGAAGCAAGTGTGTGAGCCCGAAGAACCCATGCAAGGACAAAGAC 2100
 Db 2149 AAGCAGCAAGACGGAAGCAAGTGTGTGAGCCCGAAGAACCCATGCAAGGACAAAGAC 2208
 Qy 2101 ACACTGCCACAGCAGCGCGGATGCTACTTACCTGGCCACTTCAGGACCCCATGTACA 2160
 Db 2209 ACACTGCCACAGCAGCGCGGATGCTACTTACCTGGGTCACTTCAGGACCCCATGTACA 2268
 Qy 2161 AGTCGAGTGCACAGAGGCTACGCGGCGACGCGGTCTATCTCGCGGAGGACTTCGAGCC 2220
 Db 2269 AGTCGAGTGCACAGAGGCTACGCGGCGACGCGGTCTATCTCGCGGAGGACTTCGAGCC 2328
 Qy 2221 TGGACGCTGGCCCAACCTCAATCTGGTCTGGCGCACCAAGCCCACTTACCTGATCA 2280
 Db 2329 TGGACGCTGGCCCAACCTCAATCTGGTCTGGCGCACCAAGCCCACTTACCTGATCA 2388
 Qy 2281 AGGATACTGCCCACTCTGCCAAATTCGGGAGGAGACTTTGACAGGAGCGGATG 2340
 Db 2389 AGGATACTGCCCACTCTGCCAAATTCGGGAGGAGACTTTGACAGGAGCGGATG 2448
 Qy 2341 GCGATGCTGTGATGATGACGATGACCAATGACGCTGTGACCGGATGAGAGGACCAATGCC 2400
 Db 2449 GCGATGCTGTGATGATGACGATGACCAATGACGCTGTGACCGGATGAGAGGACCAATGCC 2508
 Qy 2401 AGCTCTCTTCAATCCCGGAGCTGACTATGACAGGATGAGGTGGGAGCCGCTGTG 2460

2509	AGCTCTCTTCAATCCCGCCAGCGTGCATATGCAAGAGTGAAGTTGGGACCGCGTGTG	2566
2461	AAACTGCCCTTTACGTGTCACAAACCTTGCCAGATGCACACAGACAAACAATGGAGAGGGTG	2520
2569	ACAACTGCCCTTTACGTGTCACAAACCTTGCCAGATGCACACAGACAAACAATGGAGAGGGTG	2628
2521	ACGCTCTGCTCCGTGGGACATTGATGGGGACGATGTCTTCAATGAAACAGACAAATTGTCCT	2580
2629	ACGCTCTGCTCCGTGGGACATTGATGGGGACGATGTCTTCAATGAAACAGACAAATTGTCCT	2688
2581	ACGTCTTAAACATGTACACGAGGGACACGGATGGTGACCGGTGGGGGATCACTGTGACA	2640
2689	ACGTCTTAAACATGTACACGAGGGACACGGATGGTGACCGGTGGGGGATCACTGTGACA	2748
2641	ACTGCCCTCTGGTGCACAAACCTTGACACAGACCGACGTGGCAATGACCTTGTTTGGGGAC	2700
2749	ACTGCCCTCTGGTGCACAAACCTTGACACAGACCGACGTGGCAATGACCTTGTTTGGGGAC	2808
2701	AGTGTGACAAACACGAGGACATAGATGACGACGGCCACACGAAACAACAGGACCAACTGCC	2760
2809	AGTGTGACAAACACGAGGACATAGATGACGACGGCCACACGAAACAACAGGACCAACTGCC	2868
2761	CTTACATCTCCAAACGGCCAAACAGGCTGACCATGACAGACAGCGCCAGGCGACGCGCTGTG	2820
2869	CTTACATCTCCAAACGGCCAAACAGGCTGACCATGACAGACAGCGCCAGGCGACGCGCTGTG	2928
2821	ACCTGTATGATGACACGATGGGTGCCCGATGACACAGGACCAACTGCCGCTGTGTTCAC	2880
2929	ACCTGTATGATGACACGATGGGTGCCCGATGACACAGGACCAACTGCCGCTGTGTTCAC	2988
2881	ACCCAGACACGAGGAGGACTTGGACCGGTGATGGACCGGGTGATATTTCTAAAGATGATTTTG	2940
2989	ACCCAGACACGAGGAGGACTTGGACCGGTGATGGACCGGGTGATATTTCTAAAGATGATTTTG	3048
2941	ACAATGACAAATCCAGATATTGATGATGTGTCTCTGAAAAACAATGCCATCAGTGA	3000
3049	ACAATGACAAATCCAGATATTGATGATGTGTCTCTGAAAAACAATGCCATCAGTGA	3108
3001	CAGACTTCAGGAACTTCCAGATGGTCCCTTGGATCCCAAAGGGACACCCAAATTTGATC	3060
3109	CAGACTTCAGGAACTTCCAGATGGTCCCTTGGATCCCAAAGGGACACCCAAATTTGATC	3168
3061	CGAACTGGGTCAATCCGCATCAGGCAGAGCTGTTTCAGACAGCCCACTCGGACCCCG	3120
3169	CGAACTGGGTCAATCCGCATCAGGCAGAGCTGTTTCAGACAGCCCACTCGGACCCCG	3228
3121	GCATCGCTGTAGTGTTTTGAACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTTACGTAA	3180
3229	GCATCGCTGTAGTGTTTTGAACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTTACGTAA	3288
3181	ACACTGACCGGACGAGACTATGCCGCTTCGCTCTTGGTTACCAAGTCAAGCAGCCGCT	3240
3289	ACACTGACCGGACGAGACTATGCCGCTTCGCTCTTGGTTACCAAGTCAAGCAGCCGCT	3348
3241	TCTATGTGGTGATGTGGAACAGGTGACGACACCTACTCGGAGGACCAACCCACGCGG	3300
3349	TCTATGTGGTGATGTGGAACAGGTGACGACACCTACTCGGAGGACCAACCCACGCGG	3408
3301	CCATATGCTACTCCGGCGTCCCTCAAGTGTGTGAATCCACACGGGAGACGGGCGAGC	3360
3409	CCATATGCTACTCCGGCGTCCCTCAAGTGTGTGAATCCACACGGGAGACGGGCGAGC	3468
3361	ACCTGAGGAACCGGCTGTGGCACACGGGGAACACGCCGGGCGAGGTGCGAACTTTATGCC	3420
3469	ACCTGAGGAACCGGCTGTGGCACACGGGGAACACGCCGGGCGAGGTGCGAACTTTATGCC	3528
3421	ACGACCCCGGAACTTGGCTTGGAGGACTACACGGCTTATAGTGTGCACTTCACTCACA	3480
3529	ACGACCCCGGAACTTGGCTTGGAGGACTACACGGCTTATAGTGTGCACTTCACTCACA	3588
3481	GGCCCAAGACTGGCTACATCAGAGTCTTAGTGTGATGAAGAAACAGGTTCATGGCAGACT	3540
3589	GGCCCAAGACGGGTACATCAGAGTCTTAGTGTGATGAAGAAACAGGTTCATGGCAGACT	3648

QY	3541	CAGACCTATCTATGACCAAACTAGACGCTGGCGGGGGCTGGGCTATATTGTGCTTCTCTC	3560
DB	3549	CAGACCTATCTATGACCAAACTAGACGCTGGCGGGGGCTGGGCTATATTGTGCTTCTCTC	3708
QY	3601	AAGAAATGGTCTATTTCTCAGACTCAAGTACGAATGCGAGAGATATTAAACAAGATTG	3660
DB	3709	AAGAAATGGTCTATTTCTCAGACTCAAGTACGAATGCGAGAGATATTAAACAAGATTG	3768
QY	3661	CTGATTTCCGGGAATGCCCTGTGCAATGCCATGGTCCCTAGACACCTCAGTTCATTGTGG	3720
DB	3769	CTGATTTCCGGGAATGCCCTGTGCAATGCCATGGTCCCTAGACACCTCAGTTCATTGTGG	3828
QY	3721	TCCTTGTGGCTTCTCTCTAGCAGACACCTCCCTGTCCCTTGACCTTAACTCATAGTTC	3780
DB	3829	TCCTTGTGGCTTCTCTCTAGCAGACACCTCCCTGTCCCTTGACCTTAACTCATAGTTC	3888
QY	3781	TTCACTTCCTGCAGCAACCCCAAAACCCAAAGTGCCTTCAGAGATATAATCAATGGAAC	3840
DB	3889	TTCACTTCCTGCAGCAACCCCAAAACCCAAAGTGCCTTCAGAGATATAATCAATGGAAC	3948
QY	3841	GCAGAGATGAACATCTAACCCACTAGAGGAAAACAGTTTGGTGATATAGAGACTTTATG	3900
DB	3949	TCAGAGATGAACATCTAACCCACTAGAGGAAAACAGTTTGGTGATATAGAGACTTTATG	4008
QY	3901	TGGAGTGAATAATGGGCATGCCATTACATTGCTTTTCTTTGTTTAAAAAGATGAC	3960
DB	4009	TGGAGTGAATAATGGGCATGCCATTACATTGCTTTTCTTTGTTTAAAAAGATGAC	4068
QY	3961	GTTTACATATAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTTGAAGGGAATA	4020
DB	4069	GTTTACATATAAATGTAATTACTTATTGTATTTATGTGTATATGGAGTTGAAGGGAATA	4128
QY	4021	CTGTGCATAAGCCATTATGATAAATTAAAGCATGAAAAATTTGCTGAACACTTTTCGTG	4080
DB	4129	CTGTGCATAAGCCATTATGATAAATTAAAGCATGAAAAATTTGCTGAACACTTTTCGTG	4188
QY	4081	CTTAAAGTTGTCACTATTCTTGTAATTAGAGTTGCTCTACAAATGACACACAAATCCCGCTA	4140
DB	4189	CTTAAAGTTGTCACTATTCTTGTAATTAGAGTTGCTCTACAAATGACACACAAATCCCGCTA	4248
QY	4141	AATAAATTAATAACAAGGGTCAATTTCAAAATTTGAAGTAATGTTTATAGTAGGAGATTA	4200
DB	4249	AATAAATTAATAACAAGGGTCAATTTCAAAATTTGAAGTAATGTTTATAGTAGGAGATTA	4308
QY	4201	GAAGACAACAGGCATAGCAAAATGACATTAAGCTACCGNTAACTTAATCGGAACATGTAATA	4260
DB	4309	GAAGACAACAGGCATAGCAAAATGACATTAAGCTACCGNTAACTTAATCGGAACATGTAATA	4368
QY	4261	CAGTTACAAAAATAAAGCAACTCTCTCTTTGTGCTCAAAATGAAAGCCCTCATGTGCAGTA	4320
DB	4369	CAGTTACAAAAATAAAGCAACTCTCTCTTTGTGCTCAAAATGAAAGCCCTCATGTGCAGTA	4428
QY	4321	GAGATGAGTTTCATCAAGAAACAACATCCITGCAAAATGGGTGTGATCGGTTCCAGAT	4380
DB	4429	GAGATGAGTTTCATCAAGAAACAACATCCITGCAAAATGGGTGTGATCGGTTCCAGAT	4488
QY	4381	GTGATTTGGCAAAACCTCATTTAAAGTAAAGGTTAGCAGAGCAAAAGTCGGTGCCTTTAG	4440
DB	4489	GTGATTTGGCAAAACCTCATTTAAAGTAAAGGTTAGCAGAGCAAAAGTCGGTGCCTTTAG	4548
QY	4441	CTGCTGCTGTGCGGCTGTGGGTGTGCGGGAGGCTCTGTGCTGAGCTTCCTTCCCAGCTT	4500
DB	4549	CTGCTGCTGTGCGGCTGTGGGTGTGCGGGAGGCTCTGTGCTGAGCTTCCTTCCCAGCTT	4608
QY	4501	TGCTGCTGAGAGGAACACAGAGCAGACGACAGCGCGGAAAAAGCGCATCTAAACGGCTAT	4560
DB	4609	TGCTGCTGAGAGGAACACAGAGCAGACGACAGCGCGGAAAAAGCGCATCTAAACGGCTAT	4668
QY	4561	CTAGGCTTTGGTAACTCGGACAAGTTGCTTTTACCTGATTTCGATGATACATTTCAATTA	4620
DB	4669	CTAGGCTTTGGTAACTCGGACAAGTTGCTTTTACCTGATTTCGATGATACATTTCAATTA	4728

4621 GGTCCAGTATAAATATTTTGTAAATATTTTAAAGTGACATATAGAATGCACTCCATT 4680
4729 GGTTCAGATATAAATATTTTGTAAATATTTTAAAGTGACATATAGAATGCACTCCATT 4788
4681 TACCAGTAACTTATTTTAAATATGCTAGTACACATATAGTATATTTTCTAGAACACA 4740
4789 TACCAGTAACTTATTTTAAATATGCTAGTACACATATAGTATATTTTCTAGAACACA 4848
4741 AACATCTAATAGTATATATCTGTGAAATATGAGGCTTGATATATATAGTTGTCAAC 4800
4849 AACATCTAATAGTATATATCTGTGAAATATGAGGCTTGATATATATAGTTGTCAAC 4908
4801 GATGAGCATGCTAGAGCTGTAAACAGATACATAGAGATATAGGAGTTATGATGG 4860
4909 GATGAGCATGCTAGAGCTGTAAACAGATACATAGAGATATAGGAGTTATGATGG 4968
4861 AACCTTAAATATATATGTTGCCAGCGATTTTGTATCAATATTTGTACTGTATCTATC 4920
4969 AACCTT-AAATATATATGTTGCCAGCGATTTTGTATCAATATTTGTACTGTATCTATC 5027
4921 TGTGTATATGGAATCTTTTAAATTCAAACGCTGAAAAA-GAATCAGCATTTAGTCTGCC 4979
5028 TGTGTATATGGAATCTTTTAAATTCAAACGCTGAAAAAGCAATCAGCATTTAGTCTGCC 5087
4980 AGGCACACCAATAATCAGTCATGTGTAATATGCAACAAGTTTGTATTTTGTATTTT 5039
5088 AGGCACACCAATAATCAGTCATGTGTAATATGCAACAAGTTTGTATTTTGTATTTT 5147
5040 TTTTGTGTTGTTGTTTGTATTTTAAAGTTGCAATGATCTTTCTGAGGAAATAGTCA 5099
5148 TTTTGTGTTGTTGTTTGTATTTTAAAGTTGCAATGATCTTTCTGAGGAAATAGTCA 5203
5100 CTCATCCCACTCACATAAGGGTTTGTAGTAAAGAGAGTCTGTCTGTGATCATGGATAG 5159
5204 CTCATCCCACTCACATAAGGGTTTGTAGTAAAGAGTCTGTCTGTGATCATGGATAG 5263
5160 GGGGCAAAATCTTTTCCCTTCTGTAAATAGTATCATATTTCTATGCAAAACAGGAAC 5219
5264 GGGGCAAAATCTTTTCCCTTCTGTAAATAGTATCATATTTCTATGCAAAACAGGAAC 5323
5220 AATCCATATCTTAAAGTATACATGTCATTTTGTATTAATTTTGTATTTTGTATTT 5279
5324 GATCCATATCTTAAAGTATACATGTCATTTTGTATTAATTTTGTATTTTGTATTT 5383
5280 CTTTGAAGTTGATCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5339
5384 CTTTGAAGTTGATCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5440
5340 GCTGTATTCGGAGACCAACGAGCTTGGGATCTTCAATTAATGATGAGTCTGCAAC 5399
5441 GCTGTATTCGGAGAC-CAACGAGAGCTTGGGATCTTCAATTAATGATGAGTCTGCAAC 5499
5400 AGCGTGCAGGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5459
5500 AGCGTGCAGGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5559
5460 GATGATGTGAATATTTAGATATGATACATATTTTGTAAATATTTATGTTTCTTAAAC 5519
5560 GATGATGTGAATATTTAGATATGATACATATTTTGTAAATATTTATGTTTCTTAAAC 5619
5520 AAATTTATCGTATAGTTGATGAAACGTCATGTTGTTTGTGCAAGACTGTAATATTTAT 5579
5620 AAATTTATCGTATAGTTGATGAAACGTCATGTTGTTTGTGCAAGACTGTAATATTTAT 5679
5580 TTATGTTTCAATGTTGCAAAATTTTCAACATGAAACCTGCACTTAGTATGAACTCTCAT 5639
5680 TTATGTTTCAATGTTGCAAAATTTTCAACATGAAACCTGCACTTAGTATGAACTCTCAT 5739
5640 TTTTAAAGATTAACACAGGAAATTAATTTGTAATAAAGGTTTCT 5684
5740 TTTTAAAGATTAACACAGGAAATTAATTTGTAATAAAGGTTTCT 5784

RESULT 8
US-10-017-724-1
; Sequence 1, Application US/10017724
; Publication No. US20030099958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: NMI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-017-724-1
Query Match 97.9%; Score 5576.6; DB 14; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;
QY 1 GACTACCTCTGACTGACAGGCGCGTCTCTCGCTCCAGCAGAGCTGCGCTTTCTGACTC 60
DB 109 GAGCATCTGACTGACAGGCGCGTCTCTCGCTCCAGCAGAGCTGCGCTTTCTGACTC 168
QY 61 GGTCCGAAACACTGAAACCAAGTATCATCTGCATCTTTTGGCAAAACAGGAGCTGAGCTG 120
DB 169 GGTCCGAAACACTGAAACCAAGTATCATCTGCATCTTTTGGCAAAACAGGAGCTGAGCTG 228
QY 121 CAGAGCAGAGTGGTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 229 CAGAGCAGAGTGGTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
QY 181 AAGTGTCTCACCAGGCAAAAGACACGACTTTCACCTTTTTCAGTATCAGCAACATCAACC 240
DB 289 AAGTGTCTCACCAGGCAAAAGACACGACTTTCAGTATCAGCAACATCAACC 348
QY 241 GCAGACATTTGGCGGCAAGCAGTTCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 300
DB 349 GCAGACATTTGGCGGCAAGCAGTTCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 408
QY 301 TCGTGCCTTTTGACTACATCCCAACCGGTGAACGACGATGACCTCAGCAAGATCACCAGA 360
DB 409 TCGTGCCTTTTGACTACATCCCAACCGGTGAACGACGATGACCTCAGCAAGATCACCAGA 468
QY 361 TCATGCGGCAAGAGGAGGCTTCTTCTCAGCGGCCAGCTCAGCAGGAGCGGCAAGTCCA 420
DB 469 TCATGCGGCAAGAGGAGGCTTCTTCTCAGCGGCCAGCTCAGCAGGAGCGGCAAGTCCA 528
QY 421 GGGGCAAGCTTTTGGCTCTGAGGCGGCGGCGGCTCTCCAGAGGCGAGTTCGAGATCGTCT 480
DB 529 GGGGCAAGCTTTTGGCTCTGAGGCGGCGGCGGCTCTCCAGAGGCGAGTTCGAGATCGTCT 588
QY 481 CCACAGCGCGCGGGAACACGCTGATCTACCTATCTGATGATGAGCGCACCCCGCATGTGG 540
DB 589 CCACAGCGCGCGGGAACACGCTGATCTACCTATCTGATGATGAGCGCACCCCGCATGTGG 648
QY 541 TCTCCCTGGAGGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 649 TCTCCCTGGAGGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
QY 601 CTGCGGAGACTACAGCTTGTGCACTGGGCTGCGACTCTATAGACAGCTTCTGCTGAGCG 660
DB 709 CTGCGGAGACTACAGCTTGTGCACTGGGCTGCGACTCTATAGACAGCTTCTGCTGAGCG 768
QY 661 AGCCCTTCTACGAGCAGCTGCGGCGGGAAGAGCGGATGATGCTGCTGCTGCTGCTGCTGCTG 720
DB 769 AGCCCTTCTACGAGCAGCTGCGGCGGGAAGAGCGGATGATGCTGCTGCTGCTGCTGCTGCTG 828

721 CCAGAGAGTCACTTCAGGGTGTGTTTCAGAACTGCTCAGTGTGTTGAAATCTGTG 780
 829 CCAGAGAGTCACTTCAGGGTGTGTTTCAGAACTGCTCAGTGTGTTGAAATCTGTG 888
 781 TGAAGATATCTTAAGCAAGAGGTTCAGCAAGGCGCCAGGAGCTGAGTCAACGCCA 840
 889 TGAAGATATCTTAAGCAAGAGGTTCAGCAAGGCGCCAGGAGCTGAGTCAACGCCA 948
 841 TCAGTGAGAACACAGAGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 900
 949 TCAGTGAGAACACAGAGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 1008
 901 CGAGCTCAGAGAGAGGCGCCAGAGGTTCAGCAAGGCGCTCGCTCGAGAGCTGGAACA 960
 1009 CCAGCTCGGAGAGAGGCGCCAGAGGTTCAGCAAGGCGCTCGCTCGAGAGGCTGGAACA 1068
 961 TCAGAGAGCTCTCGGGGCTCCAGCTCTCGTGAACAGAGCTCAGCGAGAACTCAAGAGAG 1020
 1069 TCAGAGAGCTCTCGGGGCTCCAGCTCTCGTGAACAGAGCTCAGCGAGAACTCAAGAGAG 1128
 1021 TGTGGAATGATACCAAGTTCCTCGGAGGCTCATTTGGTGGCCCTCTTAAGACAGAGAAC 1080
 1129 TGTGGAATGATACCAAGTTCCTCGGAGGCTCATTTGGTGGCCCTCTTAAGACAGAGAAC 1188
 1081 TGTGAGCTTCTGCGCAGAGTGGCGGTTCTTTCGGGAAATGAAAGCTGGGTGGGACA 1140
 1189 TGTGAGCTTCTGCGCAGAGTGGCGGTTCTTTCGGGAAATGAAAGCTGGGTGGGACA 1248
 1141 GTTGACACAGTGTACTGCAAGAAATTTAAACCAATTTGCGAACCAATCACTGCGCCGC 1200
 1249 GCTGCAACAGTGTACTGCAAGAAATTTAAACCAATTTGCGAACCAATCACTGCGCCGC 1308
 1201 CTGCAACCTCGCCAGTCACTCTTTGTGGAAGCGCAATGCTCCCTCTCTGCTCCACT 1260
 1309 CTGCAACCTCGCCAGTCACTCTTTGTGGAAGCGCAATGCTCCCTCTCTGCTCCACT 1368
 1261 CGGTGACGCTGAGAGGGTGTGCTCCGTGGGACAGTGGACCCAGTGTCTCGTGAAGT 1320
 1369 CGGTGACGCTGAGAGGGTGTGCTCCGTGGGACAGTGGACCCAGTGTCTCGTGAAGT 1428
 1321 GTGGCTGTGGACCCAGCAGAGAGGCGGTCTGAGCTGACGTCACAGCAACACTGCTGG 1380
 1429 GTGGCTGTGGACCCAGCAGAGAGGCGGTCTGAGCTGACGTCACAGCAACACTGCTGG 1488
 1381 GGCCCTCCATCCAGACACGGGCTGTGAGTCTGAGCAAGTGTGACCCGATCCGGCAGG 1440
 1489 GGCCCTCCATCCAGACACGGGCTGTGAGTCTGAGCAAGTGTGACCCGATCCGGCAGG 1548
 1441 ACGGGCTGTGGACCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 1549 ACGGGCTGTGGACCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1608
 1501 ATATCACACGATCCGCTCTGCAACTCCCGAGTGGCCAGATGGGGGGCAAGAAATGCA 1560
 1609 ATATCACACGATCCGCTCTGCAACTCCCGAGTGGCCAGATGGGGGGCAAGAAATGCA 1668
 1561 AAGGAGTGGCGGGGACCAAGCTGTGCAAGGCGCCGATGCGCCCAATCGATGGCGCT 1620
 1669 AAGGAGTGGCGGGGACCAAGCTGTGCAAGGCGCCGATGCGCCCAATCGATGGCGCT 1728
 1621 GGAGCCCTGTGCTCCCGTGTGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 1729 GGAGCCCTGTGCTCCCGTGTGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1788
 1681 GCACCCGGGCTGTGCAACAGGCTGTGAGCTCAGTACGAGAGAGAGGCTGCGTGGGGATG 1740
 1789 GCACCCGGGCTGTGCAACAGGCTGTGAGCTCAGTACGAGAGAGAGGCTGCGTGGGGATG 1848
 1741 TGCAGGAGCGTCAAGTGTGCAACAGGAGAGCTGCGCGGTGAGTGTGTTATCCAAACC 1800
 1849 TGCAGGAGCGTCAAGTGTGCAACAGGAGAGCTGCGCGGTGAGTGTGTTATCCAAACC 1908

QY 1801 CCTCTTCCCGGAGCCAGTGTGAGCAGCTTCCCGATGGGTCTGTGTATGCGGTCTCT 1860
 Db 1909 CCTCTTCCCGGAGCCAGTGTGAGCAGCTTCCCGATGGGTCTGTGTATGCGGTCTCT 1968
 QY 1861 GCCCTGTGGGCTTCTTGGGCAATGGGCAATGGGCAATGGGCAATGGGCAATGGGCAATGG 1920
 Db 1969 GCCCTGTGGGCTTCTTGGGCAATGGGCAATGGGCAATGGGCAATGGGCAATGGGCAATGG 2028
 QY 1921 TCCCGGACATCTGCTTCTCCACAGCAAGTGTGCTGTGTGTCAACACTCAGCCTGGCT 1980
 Db 2029 TCCCGGACATCTGCTTCTCCACAGCAAGTGTGCTGTGTGTCAACACTCAGCCTGGCT 2088
 QY 1981 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 Db 2089 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2148
 QY 2041 AAGCAGCAAGACAGGAAAGCAAGTGTGTGAGCGGCAAGGCAAGGCAAGGCAAGGCAAG 2100
 Db 2149 AAGCAGCAAGACAGGAAAGCAAGTGTGTGAGCGGCAAGGCAAGGCAAGGCAAGGCAAG 2208
 QY 2101 ACAAAGTCCACAGCAGCGGAGTGCATCTACCTGGGCACTTACAGGACCCCATGTACA 2160
 Db 2209 ACAAAGTCCACAGCAGCGGAGTGCATCTACCTGGGCACTTACAGGACCCCATGTACA 2268
 QY 2161 AGTGGAGTGTCCAGACAGGCTAGCGGGGCGACGGGCTCATCTGGGGGAGGACTTCGGACC 2220
 Db 2269 AGTGGAGTGTCCAGACAGGCTAGCGGGGCGACGGGCTCATCTGGGGGAGGACTTCGGACC 2328
 QY 2221 TGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
 Db 2329 TGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2388
 QY 2281 AGGATAAAGTGGGCAAGTGTGAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 2340
 Db 2389 AGGATAAAGTGGGCAAGTGTGAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 2448
 QY 2341 CGGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
 Db 2449 CGGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2508
 QY 2401 AGCTCTCTTCAATCCCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
 Db 2509 AGCTCTCTTCAATCCCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2568
 QY 2461 ACAAAGTGGGCAAGTGTGAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 2520
 Db 2569 ACAAAGTGGGCAAGTGTGAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 2628
 QY 2521 ACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
 Db 2629 ACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2688
 QY 2581 ACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
 Db 2689 ACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2748
 QY 2641 ACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
 Db 2749 ACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2808
 QY 2701 AGTGTGCAACACAGGAGATAGATGACAGGCGCAACAGGCAACACAGGCAACACAGGCAAC 2760
 Db 2809 AGTGTGCAACACAGGAGATAGATGACAGGCGCAACAGGCAACACAGGCAACACAGGCAAC 2868
 QY 2761 CCTACATCTCCAGCGCAACAGGAGTGCATGACAGAGCGGCGGCGGCGGCGGCGGCGGCG 2820
 Db 2869 CCTACATCTCCAGCGCAACAGGAGTGCATGACAGAGCGGCGGCGGCGGCGGCGGCGGCG 2928
 QY 2821 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880
 Db 2929 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2988
 QY 2881 ACCCAGACCGAGGAGCTTGGACCGGTGATGATGATGATGATGATGATGATGATGATGAT 2940

1201 CTGAACTGCGCAGTCCATCCTTTGTGAAGGCGAATGCTGCCCTTCTCTGCTCCACT 1260
 1309 CTGCAACTGGCCAGTCCATCCTTTGTGAAGGCGAATGCTGCCCTTCTCTGCTCCACT 1368
 1261 CGGTGAGCGGTGAGGAGGCTGTCTCCGTGGGCGAGTGGACCCAGTCTCGGTGAGGT 1320
 1369 CGGTGAGCGGTGAGGAGGCTGTCTCCGTGGGCGAGTGGACCCAGTCTCGGTGAGGT 1428
 1321 GTGGCTCTGGGACCCAGCAGAGAGGCGGTCTCTGACGTCAACAGCAACACTGCTGG 1380
 1429 GTGGCTCTGGGACCCAGCAGAGAGGCGGTCTCTGACGTCAACAGCAACACTGCTGG 1488
 1381 GGCCCTCTCAATCCAGCAACCGGCTTGCAGTCTGAGCAAGTGTGACACCCGCAATCCGGCAGG 1440
 1489 GGCCCTCTCAATCCAGCAACCGGCTTGCAGTCTGAGCAAGTGTGACACCCGCAATCCGGCAGG 1548
 1441 ACGGCGCTGGAGCCACTGTGTCACTTGGTCTCTGACGTCAACAGCAACACTGCTGG 1500
 1549 ACGGCGCTGGAGCCACTGTGTCACTTGGTCTCTGACGTCAACAGCAACACTGCTGG 1608
 1501 ATATCAACGCATCCGTCTCTGCAATCCGCCAGTGCCTCCAGATGGGGGCAAGATTGCA 1560
 1609 ATATCAACGCATCCGTCTCTGCAATCCGCCAGTGCCTCCAGATGGGGGCAAGATTGCA 1668
 1561 AAGGAGTGGCGGGAGACCAAGCCTGCGAGGGCGCCATGCGCCCAATCGATGCGCGCT 1620
 1669 AAGGAGTGGCGGGAGACCAAGCCTGCGAGGGCGCCATGCGCCCAATCGATGCGCGCT 1728
 1621 GAGGCCCTCTGCTCCCGTGTGCGGCTGCACTGTCACTGTGCGGCTGGGATCCGGGAGC 1680
 1729 GAGGCCCTCTGCTCCCGTGTGCGGCTGCACTGTCACTGTGCGGCTGGGATCCGGGAGC 1788
 1681 GCACCGGCTGTGCAACAGCCCTGAGCCTCAGTACCGAGGGAAGGCTCGGTGGGGATG 1740
 1789 GCACCGGCTGTGCAACAGCCCTGAGCCTCAGTACCGAGGGAAGGCTCGGTGGGGATG 1848
 1741 TGCAGAGCGCTCAGATGTGCAAAAGAGGAGCTGCCCGCTGTGATGCTGTTATCCAAAC 1800
 1849 TGCAGAGCGCTCAGATGTGCAAAAGAGGAGCTGCCCGCTGTGATGCTGTTATCCAAAC 1908
 1801 CTTGCTTCCGGGAGCCAGTGCAGAGCTTCCCGATGGGTCTGTCATCGGGCTCT 1860
 1909 CTTGCTTCCGGGAGCCAGTGCAGAGCTTCCCGATGGGTCTGTCATCGGGCTCT 1968
 1861 GCCCTGTGGCTTCTTGGGCAATGGCAACCACTGTGAGGACCTGAGAGTGTGCCCTGG 1920
 1969 GCCCTGTGGCTTCTTGGGCAATGGCAACCACTGTGAGGACCTGAGAGTGTGCCCTGG 2028
 1921 TCCCGGACATCTGCTTCTCCACGAGAGGTGCTCGCTGTGTCAACACTCAGCCTGGCT 1980
 2029 TCCCGGACATCTGCTTCTCCACGAGAGGTGCTCGCTGTGTCAACACTCAGCCTGGCT 2088
 1981 TCCACTGCTGCTGCTGCCCGCCGATACAGAGGGAACAGCCCGTGGGGTCCGGCTGG 2040
 2089 TCCACTGCTGCTGCTGCCCGCCGATACAGAGGGAACAGCCCGTGGGGTCCGGCTGG 2148
 2041 AAGCAGCCAGAGCGAAAGCAAGTGTGAGGCCGGAACCCATGCAAGGACCAAGACAC 2100
 2149 AAGCAGCCAGAGCGAAAGCAAGTGTGAGGCCGGAACCCATGCAAGGACCAAGACAC 2208
 2101 ACGACTGCCCAAGCAGCGAGTGCATCTACCTGGGCCACTTTCAGCGACCCCATGTACA 2160
 2209 ACGACTGCCCAAGCAGCGAGTGCATCTACCTGGGGTCACTTCAGCGACCCCATGTACA 2268
 2161 AGTCGAGTGCAGACAGGCTTACCGGGCGACGGGCTCATCTCGGGGAGGATCCGAGC 2220
 2269 AGTCGAGTGCAGACAGGCTTACCGGGCGACGGGCTCATCTCGGGGAGGATCCGAGC 2328
 2221 TGGAGGCTGCGCCCAACTCAATCTGCTCTCGGCCCAACCGCCTACCTACCTGCTGATCA 2280
 2329 TGGAGGCTGCGCCCAACTCAATCTGCTCTCGGCCCAACCGCCTACCTACCTGCTGATCA 2388

2281 AGGATAACTGCCCCCATCTGCCAAATTTCTGGCAGGAGACTTTTGACAAGGACGGGATTG 2340
 2389 AGGATAACTGCCCCCATCTGCCAAATTTCTGGCAGGAGACTTTTGACAAGGACGGGATTG 2448
 2341 GCGATGCTGTGATGATGAGATGACATGACGGTGTGACCGATGAGAGGACAACTGACC 2400
 2449 GCGATGCTGTGATGATGAGATGACATGACGGTGTGACCGATGAGAGGACAACTGACC 2508
 2401 AGCTCTCTCTTCAATCCCGCCGAGCTGACTATGACAAAGGATGAGTTGGGAGACCGCTGTG 2460
 2509 AGCTCTCTCTTCAATCCCGCCGAGCTGACTATGACAAAGGATGAGTTGGGAGACCGCTGTG 2568
 2461 ACGACTGCTTACGTCAGTCAACCCCTGCCAGATCGACACAGCAACAAATGGAGAGGCTG 2520
 2569 ACGACTGCTTACGTCAGTCAACCCCTGCCAGATCGACACAGCAACAAATGGAGAGGCTG 2628
 2521 ACGCTCTCTCGTGGACCAATTTGATGGGACGATGTCTTCAATGAACGAGCAATTTGTCCT 2580
 2629 ACGCTCTCTCGTGGACCAATTTGATGGGACGATGTCTTCAATGAACGAGCAATTTGTCCT 2688
 2581 ACGTCTACACACTGACAGAGGACACGGATGATGACGGTGTGGGGGATCACTGTGACA 2640
 2689 ACGTCTACACACTGACAGAGGACACGGATGATGACGGTGTGGGGGATCACTGTGACA 2748
 2641 ACTGCCCTCTGGTGCACAAACCCCTGACAGACCGACGTGACAAATGACCTTTGTTGGGACC 2700
 2749 ACTGCCCTCTGGTGCACAAACCCCTGACAGACCGACGTGACAAATGACCTTTGTTGGGACC 2808
 2701 AGTGTGACAAACAGAGACATAGATGACAGCGCCACACAGACCAACAGGACAACTGCC 2760
 2809 AGTGTGACAAACAGAGACATAGATGACAGCGCCACACAGACCAACAGGACAACTGCC 2868
 2761 CCTACATCTCCAAACCGCAACCCAGGCTGACATGACAGAGCGGCGAGGGGACACCTGTG 2820
 2869 CCTACATCTCCAAACCGCAACCCAGGCTGACATGACAGAGCGGCGAGGGGACACCTGTG 2928
 2821 ACCCTGATGATGACAAAGTGGCTTCCCGATGACAGGACCACTGCGGCTTGTGTCA 2880
 2929 ACCCTGATGATGACAAAGTGGCTTCCCGATGACAGGACCACTGCGGCTTGTGTCA 2988
 2881 ACCCAGACCGAGGAGCTTTGACCGGTGATGACCGGGTGTATTTGTAAGATGATTTTG 2940
 2989 ACCCAGACCGAGGAGCTTTGACCGGTGATGACCGGGTGTATTTGTAAGATGATTTTG 3048
 2941 ACAATGACAAACATCCAGATATTGATGATGTCTCTGAAACAAATGCCATCAGTGA 3000
 3049 ACAATGACAAACATCCAGATATTGATGATGTCTCTGAAACAAATGCCATCAGTGA 3108
 3001 CAGACTTCAGAACTTCCAGATGCTCCCTTGGATCCCAAGGGACACCCAAATTTGATC 3060
 3109 CAGACTTCAGAACTTCCAGATGCTCCCTTGGATCCCAAGGGACACCCAAATTTGATC 3168
 3061 CCAACTGGGTCAATTCGCCATCAAGGCAAGGAGCTGGTTTCAGACAGCCAACTCGGACCCCG 3120
 3169 CCAACTGGGTCAATTCGCCATCAAGGCAAGGAGCTGGTTTCAGACAGCCAACTCGGACCCCG 3228
 3121 GCATCGCTGATGATTTGACGAGTTGGTCTGTGGACTTCAGTGGGACATTTCTACGTAA 3180
 3229 GCATCGCTGATGATTTGACGAGTTGGTCTGTGGACTTCAGTGGGACATTTCTACGTAA 3288
 3181 ACATGACCGGGACGACGACTATGCGGCTTCTGCTTTGTTTACAGTCAAGAGCGGCT 3240
 3289 ACATGACCGGGACGACGACTATGCGGCTTCTGCTTTGTTTACAGTCAAGAGCGGCT 3348
 3241 TCTATGCTGATGATGGAGCAGGTGACGACGACTACTTGGGAGGACCGACCCACGGGG 3300
 3349 TCTATGCTGATGATGGAGCAGGTGACGACGACTACTTGGGAGGACCGACCCACGGGG 3408
 3301 CCTATGGCTACTTCGGGCGTGTCCCTCAAGGTGTGAACTCCACACCGGGACCGGCGGAGC 3360
 3409 CCTATGGCTACTTCGGGCGTGTCCCTCAAGGTGTGAACTCCACACCGGGACCGGCGGAGC 3468
 3361 ACCTGAGGAAACGCGCTGTGGCAGACAGGGGGAACACCGCGGGCAGGTGCGAACCTTATGGC 3420

Db 3469 ACCTGAGGAACGGCTGTGGCAACCGGGGAAACCGCGGGGAGGTCGAAACCTTATGGC 3528
 3471 ACACACCCAGGAAACATTTGGTGGAAAGGACTTACACGGCTTATAGGTGGACCTGACTCACA 3480
 3473 TGCTGCTGAGAGAAACGAGAGACGACGACGCGGAAAGGCGCATTAACGCGGTAT 4668
 3475 ACACACCCAGGAAACATTTGGTGGAAAGGACTTACACGGCTTATAGGTGGACCTGACTCACA 3588
 3477 GGCCCAAGACTGGGTACATCAGAGTCTTAGTGATGAAGAAACAGGTGATGGGAGACT 3540
 3479 GGCCCAAGACCGGTACATCAGAGTCTTAGTGATGAAGAAACAGGTGATGGGAGACT 3648
 3481 CAGGACCTATCTATGACCAACCTACGCTGGCGGGGCTGGGTCTATTGTGCTTCTCTC 3600
 3483 CAGGACCTATCTATGACCAACCTACGCTGGCGGGGCTGGGTCTATTGTGCTTCTCTC 3708
 3485 AAGAAATGGTCTATTCTCAGACCTCAGTACGAAATGCAGAGATATTAAACAGATTTG 3660
 3487 AAGAAATGGTCTATTCTCAGACCTCAGTACGAAATGCAGAGATATTAAACAGATTTG 3768
 3489 CTGCATTTCCGGCAATGCCCTGTGCATGCCATCGTCCCTAGACACCTCAGTTCAATTTGG 3720
 3491 CTGCATTTCCGGCAATGCCCTGTGCATGCCATCGTCCCTAGACACCTCAGTTCAATTTGG 3828
 3493 TCCTTGGGCTTCTCTCTAGCAGCACTCTCTGCTCCCTTGAACCTTAACTCTGATGGTTC 3888
 3495 TCCTTGGGCTTCTCTCTAGCAGCACTCTCTGCTCCCTTGAACCTTAACTCTGATGGTTC 3780
 3497 TTCAACCTCTGCGCAGCAACCCCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3840
 3499 TTCAACCTCTGCGCAGCAACCCCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAAC 3948
 3501 GCAGAGATGAACATCTAACCCCACTAGAGGAAACAGTTTGGTGTATATGAGACTTTATG 3900
 3503 TCAGAGATGAACATCTAACCCCACTAGAGGAAACAGTTTGGTGTATATGAGACTTTATG 4008
 3505 TGGAGTGAATTTGGGATGCCATTCATATGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3960
 3507 TGGAGTGAATTTGGGATGCCATTCATATGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 4068
 3509 GTTTTACATATAAATGTAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4128
 3511 GTTTTACATATAAATGTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4020
 3513 CTGTGCAATAGCCATTTATGATAAATTAAGCATGAAATATTTCTGACCTTTTCTTTTCTTT 4080
 3515 CTGTGCAATAGCCATTTATGATAAATTAAGCATGAAATATTTCTGACCTTTTCTTTTCTTT 4188
 3517 CTAAAGTTGTCACTATTCTTTGAAATTAAGAGTTGCTCTACAAATGACACACAAATCCCGCTA 4140
 3519 CTAAAGTTGTCACTATTCTTTGAAATTAAGAGTTGCTCTACAAATGACACACAAATCCCGCTA 4248
 3521 AATAAATTAACAGGGTCAATTCAAATTTGAAGTAAATTTAGTAAAGGAGATTA 4200
 3523 AATAAATTAACAGGGTCAATTCAAATTTGAAGTAAATTTAGTAAAGGAGATTA 4308
 3525 GAAGCAACAGGCATAGCAATGACATAAGCTACCGATTAACTAAATCGGAACATGTAATA 4368
 3527 CAGTTAATAAATAAAGCACTCTCTCTGCTCTACAAATGAAAGCCCTCATGTGAGATTA 4320
 3529 CAGTTAATAAATAAAGCACTCTCTCTGCTCTACAAATGAAAGCCCTCATGTGAGATTA 4428
 3531 GAGATGCAATTTCAATCAAGAAACAAACATCTCTGCAATGGGTGTGATGGGTTCCAGAT 4380
 3533 GAGATGCAATTTCAATCAAGAAACAAACATCTCTGCAATGGGTGTGATGGGTTCCAGAT 4488
 3535 GTGATTTGGCAAAACCTCATTAAAGTAAAGGTTAGCAGAGCAAGGTGCGGTCTTTAG 4440
 3537 GTGATTTGGCAAAACCTCATTAAAGTAAAGGTTAGCAGAGCAAGGTGCGGTCTTTAG 4548
 3539 CTGCTGCTTGGCGCTGTGGTGTGGGAGGCTCTGCTGCTGAGCTTCTTCCCGAGCTT 4500

Db 4549 CTGCTGCTTGTGCGGTGTGCGGTGGGAGGCTCTCTGCTGAGCTTCTTCCCGAGCTT 4608
 4551 TGCTGCTGAGAGAAACGAGAGACGCAACGCGCGGAAAGGCGCATCTAAGCGGTAT 4560
 4553 TGCTGCTGAGAGAAACGAGAGACGCAACGCGCGGAAAGGCGCATCTAAGCGGTAT 4668
 4555 CTAGGCTTTGGTAACTCGGACAAAGTTGCTTTTACCTGATTTGATGATACATTTCAITAA 4620
 4557 CTAGGCTTTGGTAACTCGGACAAAGTTGCTTTTACCTGATTTGATGATACATTTCAITAA 4728
 4559 GGTTCAGATTATAAATATTGTTTAAATATTATTAAGTGACTATAGAAATGCAATCCCAT 4580
 4561 GGTTCAGATTATAAATATTGTTTAAATATTATTAAGTGACTATAGAAATGCAATCCCAT 4788
 4563 TACCAGTAACCTTATTTTAAATATGCTTAGTAACACATATGATGATATAATTTCTAGAAACA 4740
 4565 TACCAGTAACCTTATTTTAAATATGCTTAGTAACACATATGATGATATAATTTCTAGAAACA 4848
 4567 AACATCTAAATAGTATATAATCTCTGTGAAATATGAGGCTTGATAATATTAGGTGTGCAC 4800
 4569 AACATCTAAATAGTATATAATCTCTGTGAAATATGAGGCTTGATAATATTAGGTGTGCAC 4908
 4571 GATGAAGCATCTAGAAAGCTGTAACAGATACATAGAGAAATTAATGAGAGTTTATGATGG 4860
 4573 GATGAAGCATCTAGAAAGCTGTAACAGATACATAGAGAAATTAATGAGAGTTTATGATGG 4968
 4575 AACCTTAAATATAATATTGTTGCCAGCAATTTTATTTCAATTTTGTACTGTTATCTATC 4920
 4577 AACCTTAAATATAATATTGTTGCCAGCAATTTTATTTCAATTTTGTACTGTTATCTATC 5027
 4579 TGCTGTATATGGAATTTCTTTTAAATTTCAACGCTGAAAACGAAATCAGATTTAGTCTTGCC 4979
 4581 TGCTGTATATGGAATTTCTTTTAAATTTCAACGCTGAAAACGAAATCAGATTTAGTCTTGCC 5087
 4583 AGGCACACCCCAATTAATCAGTCATGTGTAATATGACAAAGTTTGTGTTTTGTTTTT 5039
 4585 AGGCACACCCCAATTAATCAGTCATGTGTAATATGACAAAGTTTGTGTTTTGTTTTT 5147
 4587 TTTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 5099
 4589 TTTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 5203
 4591 CTCTATCCCACTCCACATAAAGGGTTAGTAAGAGAGTCTGTCTGTCTGTATGATGGATAG 5159
 4593 CTCTATCCCACTCCACATAAAGGGTTAGTAAGAGAGTCTGTCTGTCTGTATGATGGATAG 5263
 4595 GGCGCAAAATCTTTTCCCTTTCTGTTAAAGTATCACAATTTCTATGCCAAACAGGAAC 5219
 4597 GGCGCAAAATCTTTTCCCTTTCTGTTAAAGTATCACAATTTCTATGCCAAACAGGAAC 5323
 4599 AATCCATAACTTTAGTCTTAAATGTACACATTTGCAATTTGATAAAATTAATTTGTTGTT 5279
 4601 GATCCATAACTTTAGTCTTAAATGTACACATTTGCAATTTGATAAAATTAATTTGTTGTT 5383
 4603 CTTTGAAGTTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5339
 4605 CTTTGAAGTTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5440
 4607 GCTGTATTTCCCGAGCAACGAGGTTGGGATGACTTCAITTAATGATGAGACGTGTCAAC 5399
 4609 GCTGTATTTCCCGAGCAACGAGGTTGGGATGACTTCAITTAATGATGAGACGTGTCAAC 5499
 4611 AGCGTGCAGGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5459
 4613 AGCGTGCAGGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5559
 4615 GATGATGGAATATTAGAAATGTAATTTTGTAAATTTTATGTTGTTTCTAAAC 5519
 4617 GATGATGGAATATTAGAAATGTAATTTTGTAAATTTTATGTTGTTTCTAAAC 5619
 4619 AAATTTATGATAGGTTGATGAAACGTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5579
 4621 AAATTTATGATAGGTTGATGAAACGTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5679


```

5580 TTATGTTTACATGGTCAAAATTTACCACTGAAACCCCTGCACTTAGCTAGAACCTCAT 5639
5680 TTATGTTTACATGGTCAAAATTTACCACTGAAACCCCTGCACTTAGCTAGAACCTCAT 5739
5640 TTTTAAAGATTACACAGGAATAAATTTGTAAGAAAGGTTTTCT 5684
5740 TTTTAAAGATTACACAGGAATAAATTTGTAAGAAAGGTTTTCT 5784

RESULT 10
JS-10-301-822-202
: Sequence 202, Application US/10301822
: Publication No. US20030148410A1
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: APPLICANT: Berger, Allison
: APPLICANT: Guillemette, Tracy L.
: APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Schlegel, Robert
: APPLICANT: Monahan, John E.
: APPLICANT: Thibodeau, Stephen N.
: APPLICANT: BURGART, Lawrence J.
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
: TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: FILE REFERENCE: MEMO1-029P2RNM
: CURRENT APPLICATION NUMBER: US/10/301,822
: CURRENT FILING DATE: 2002-11-21
: PRIOR APPLICATION NUMBER: US 60/339,971
: PRIOR FILING DATE: 2001-12-10
: PRIOR APPLICATION NUMBER: US 60/361,978
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/381,988
: PRIOR FILING DATE: 2002-05-20
: NUMBER OF SEQ ID NOS: 228
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 202
: LENGTH: 5784
: TYPE: DNA
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (240)...(3758)
JS-10-301-822-202

Query Match 97.9%; Score 5576.6; DB 14; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

2y 1 GACTACGCTGCACTGAGGCGCGTCTCTGCTCCAGCAGAGCTGGCGCTTCTGACTC 60
Db 109 GAGCATCTGCACTGAGGCGCGTCTCTGCTCCAGCAGAGCTGGCGCTTCTGACTC 168
2y 61 GGTCCGGAACACTGAAACCACTGATCATCTGCTCTTGGCAACCCAGAGCTCAGCTG 120
Db 169 GGTCCGGAACACTGAAACCACTGATCATCTGCTCTTGGCAACCCAGAGCTCAGCTG 228
2y 121 CAGAGGAGGAGTGGTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 229 CAGAGGAGGAGTGGTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
Qy 181 AAGCTGTGTCCACAGGAGAAAGACAGACCTTTCGACCTTTTCAGTATCAGCAACATCAACC 240
Db 289 AAGCTGTGTCCACAGGAGAAAGACAGACCTTTCGACCTTTTCAGTATCAGCAACATCAACC 348
Qy 241 GCAAGACCATTTGGCCCAAGCAGTTCGCGGCGCCGAGCCCGCGGTGCGCGCTTACCGCT 300
Db 349 GCAAGACCATTTGGCCCAAGCAGTTCGCGGCGCCGAGCCCGCGGTGCGCGCTTACCGCT 408
Qy 301 TCGTGGCGCTTTGATACATCCCGGTGACGAGATGACCTCAGCAAGATCACCACAGA 360
Db 409 TCGTGGCGCTTTGATACATCCCGGTGACGAGATGACCTCAGCAAGATCACCACAGA 468

```

```

361 TCATGCGGCAAGAGAGGGCTTCTTCTCTCAGGCCCAGCTCAAGCAGGACGGCAAGTCCA 420
Db TCATGCGGCAAGAGAGGGCTTCTTCTCTCAGGCCCAGCTCAAGCAGGACGGCAAGTCCA 528
Qy 421 GGGCAGCGCTTGGCTCTCGAGGCGCCCGGTCTCTCCAGAGGCACTTCGAGATCGTCT 480
Db 529 GGGCAGCGCTTGGCTCTCGAGGCGCCCGGTCTCTCCAGAGGCACTTCGAGATCGTCT 588
Qy 481 CCAACGGCCCCGCGGACACGCTGGATCTCACTACTCGATTGACGGACCCGCGCATGTGG 540
Db 589 CCAACGGCCCCGCGGACACGCTGGATCTCACTACTCGATTGACGGACCCGCGCATGTGG 648
Qy 541 TCTCCCTGGAGAGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 649 TCTCCCTGGAGAGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
Qy 601 CTGGCAGACCTCAGAGCTTGCACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 709 CTGGCAGACCTCAGAGCTTGCACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
Qy 661 AGCCCTTCTACGAGACCTGCGAGGCGGAAAGAGCGGATGTAGTGGCCAAAGGCTCTG 720
Db 769 AGCCCTTCTACGAGACCTGCGAGGCGGAAAGAGCGGATGTAGTGGCCAAAGGCTCTG 828
Qy 721 CCAGAGAGAGTCACTTCAGGGGTTTGTCTTCAGAACTGCTGCTGCTGCTGCTGCTGCTG 780
Db 829 CCAGAGAGAGTCACTTCAGGGGTTTGTCTTCAGAACTGCTGCTGCTGCTGCTGCTGCTG 888
Qy 781 TGGAGATATTCTAAGCAAGAGGTTGCCAGCAAGGCGGAGCTGAGATCAACGCCA 840
Db 889 TGGAGATATTCTAAGCAAGAGGTTGCCAGCAAGGCGGAGCTGAGATCAACGCCA 948
Qy 841 TCAGTGAGAACACAGAGACCTGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 949 TCAGTGAGAACACAGAGACCTGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
Qy 901 CCAGCTCAGAGAGAGGCGCGAGTGTGCGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 1009 CCAGCTCAGAGAGAGGCGCGAGTGTGCGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
Qy 961 TCCAGGAGCTCTCGGGGCTCCACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 1069 TCCAGGAGCTCTCGGGGCTCCACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1128
Qy 1021 TGTGCAATGATAACAGGTTCTCTGGAGCTCATTTGGTGGCTTCTTAAGCAAGGAACA 1080
Db 1129 TGTGCAATGATAACAGGTTCTCTGGAGCTCATTTGGTGGCTTCTTAAGCAAGGAACA 1188
Qy 1081 TGTGCACTTGTGCGAGAGTGGCGGTTCTTTGCGGAAATGAAACGTTGGTGGTGGACA 1140
Db 1189 TGTGCACTTGTGCGAGAGTGGCGGTTCTTTGCGGAAATGAAACGTTGGTGGTGGACA 1248
Qy 1141 GGTGCAACAGTGTGCTGCAAGAAATTTAAACCAATTTGCGCAACCAATCACTGCGCGC 1200
Db 1249 GGTGCAACAGTGTGCTGCAAGAAATTTAAACCAATTTGCGCAACCAATCACTGCGCGC 1308
Qy 1201 CTGCAACCTGCGCAGTCCATCTTGTGGAGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1309 CTGCAACCTGCGCAGTCCATCTTGTGGAGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1368
Qy 1261 CGGTGGAGCGGTGAGAGGCTGGTCTCGCTGGGCGAGAGTGGAGCCAGTGTCTCCGTGAGCT 1320
Db 1369 CGGTGGAGCGGTGAGAGGCTGGTCTCGCTGGGCGAGAGTGGAGCCAGTGTCTCCGTGAGCT 1428
Qy 1321 GTGGCTCTGGAGCCAGCAGAGAGCGGCTCTGCTGAGCTCAGCAGCAACCACTGCTTGG 1380
Db 1429 GTGGCTCTGGAGCCAGCAGAGAGCGGCTCTGCTGAGCTCAGCAGCAACCACTGCTTGG 1488
Qy 1381 GGCCCTTCCATCCAGACAGCGGCTTGCAGTGTGAGCAAGTGTGACACCCCGCATCCGGCAGG 1440
Db 1489 GGCCCTTCCATCCAGACAGCGGCTTGCAGTGTGAGCAAGTGTGACACCCCGCATCCGGCAGG 1548

```


2y 1441 ACGCCGCTGGAGCCATGCTCACTTGGTCTTCACTGCTCTGTGAACCTGTGGAGTTGGCA 1500
2b 1549 ACGCCGCTGGAGCCATGCTCACTTGGTCTTCACTGCTCTGTGAACCTGTGGAGTTGGCA 1608
2y 1501 ATATCACAGCATCCGCTCTGTGAACCTCCCACTGCCCCAGATGGGGGGCAAGATTGCA 1560
2b 1609 ATATCACAGCATCCGCTCTGTGAACCTCCCACTGCCCCAGATGGGGGGCAAGATTGCA 1668
2y 1561 AAGGAGTGGCCGGAGAACCAAGCTGTCAGGGCGCCCCCATGCCAAATCGATGGCCGCT 1620
2b 1669 AAGGAGTGGCCGGAGAACCAAGCTGTCAGGGCGCCCCCATGCCAAATCGATGGCCGCT 1728
2y 1621 GGAGCCCTGTCCTCCCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
2b 1729 GGAGCCCTGTCCTCCCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1788
2y 1681 GCACCCGGGTGCAACAGAGCCCTGAGCCTCAGTACGAGGAGAAAGGCTCGCTGGGGGATG 1740
2b 1789 GCACCCGGGTGCAACAGAGCCCTGAGCCTCAGTACGAGGAGAAAGGCTCGCTGGGGGATG 1848
2y 1741 TGCAGGAGCTCAGATGTGCAACAGAGGAGCTGCCCGGTGGATGCTGTTTATCCAAC 1800
2b 1849 TGCAGGAGCTCAGATGTGCAACAGAGGAGCTGCCCGGTGGATGCTGTTTATCCAAC 1908
2y 1801 CCTGCTTCCCGGAGCCAGTGCAGAGCTTCCCGATGGGTCTCTGCTCATGCGGCTCCT 1860
2b 1909 CCTGCTTCCCGGAGCCAGTGCAGAGCTTCCCGATGGGTCTCTGCTCATGCGGCTCCT 1968
2y 1861 GCCCTGTGGGCTTCTTGGGCAATGGCAACCACTGTGAGGAGCTGGACGATGTCCTCTG 1920
2b 1969 GCCCTGTGGGCTTCTTGGGCAATGGCAACCACTGTGAGGAGCTGGACGATGTCCTCTG 2028
2y 1921 TCCCGGACATCTGCTTCTCCACAGCAAGGTGCTCGCTGCTGTCAACACTCAGCCTGGCT 1980
2b 2029 TCCCGGACATCTGCTTCTCCACAGCAAGGTGCTCGCTGCTGTCAACACTCAGCCTGGCT 2088
2y 1981 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
2b 2089 TCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2148
2y 2041 AAGCAGCCAGACGAGAAAGCAAGTGTGAGCCCGGAAACCCATGCAAGGCAAGACAC 2100
2b 2149 AAGCAGCCAGACGAGAAAGCAAGTGTGAGCCCGGAAACCCATGCAAGGCAAGACAC 2208
2y 2101 ACAATGCCAACAACGAGGAGTGCATCTACTGGGCCACTTCAGGCAACCCATGTACA 2160
2b 2209 ACAATGCCAACAACGAGGAGTGCATCTACTGGGCCACTTCAGGCAACCCATGTACA 2268
2y 2161 AGTGGAGTGCAGACAGGCTACGCGGGCGACGGGCTCATCTGGGGAGGACTCGGACC 2220
2b 2269 AGTGGAGTGCAGACAGGCTACGCGGGCGACGGGCTCATCTGGGGAGGACTCGGACC 2328
2y 2221 TGGAGGCTGGCCCAACCTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
2b 2329 TGGAGGCTGGCCCAACCTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2388
2y 2281 AGGATACTGCCCCCATCTGCAAAATTTGCGGAGGAGCTTTCAGAGGAGGAGTTG 2340
2b 2389 AGGATACTGCCCCCATCTGCAAAATTTGCGGAGGAGCTTTCAGAGGAGGAGTTG 2448
2y 2341 GCGATGCTGTGATGATGACGATGACATGACGCTGTCGCGCCACCAACGCGACCTAC 2400
2b 2449 GCGATGCTGTGATGATGACGATGACATGACGCTGTCGCGCCACCAACGCGACCTAC 2508
2y 2401 AGCTCTCTTCAATCCCGCCAGGCTGACTATGACAGGATGAGTTGGGAGCCGCTGTG 2460
2b 2509 AGCTCTCTTCAATCCCGCCAGGCTGACTATGACAGGATGAGTTGGGAGCCGCTGTG 2568
2y 2461 ACAATGCTCTTACGTGCACCAACCTGCCCCAGATGACACAGACCAACATGAGAGGGTG 2520
2b 2569 ACAATGCTCTTACGTGCACCAACCTGCCCCAGATGACACAGACCAACATGAGAGGGTG 2628
2y 2521 AGCCCTGCTCCGTGGAATTTGATGGGAGGATGCTTCTCAATGAACGAGACAAATTTGCCCT 2580

Db 2629 ACGCCGCTCCGTGGACATTTGATGGGACGATGCTTCAATGAACGAGACAAATTTGCCCT 2688
Qy 2581 ACCTCTACAAACACTGACACAGAGGACACCGATGCTGACCGGTGGGGGATCCTGTGACA 2640
Db 2689 ACCTCTACAAACACTGACACAGAGGACACCGATGCTGACCGGTGGGGGATCCTGTGACA 2748
Qy 2641 ACTGCCCTCCGTGGACAAACCTGACACAGACCGGATGACGATGACCTTTGTTGGGACC 2700
Db 2749 ACTGCCCTCCGTGGACAAACCTGACACAGACCGGATGACGATGACCTTTGTTGGGACC 2808
Qy 2701 AGTGTGACAAACAGAGACATAGATGACGACCGCCACAGAAACACAGAGACAACTGCC 2760
Db 2809 AGTGTGACAAACAGAGACATAGATGACGACCGCCACAGAAACACAGAGACAACTGCC 2868
Qy 2761 CCTACATCTCCAAACGCGCAACAGGCTGACATGACAGAGCGGACCGGACCGCTGTG 2820
Db 2869 CCTACATCTCCAAACGCGCAACAGGCTGACATGACAGAGCGGACCGGACCGCTGTG 2928
Qy 2821 ACCCTGATGATGACAAACGATGGCTGCCGATGACAGGACAACTGCCGGCTTGTGTCA 2880
Db 2929 ACCCTGATGATGACAAACGATGGCTGCCGATGACAGGACAACTGCCGGCTTGTGTCA 2988
Qy 2881 ACCCAGACAGAGAGACTTGGACCGGTGATGACGCGGTGATATTTGTAAGATGATTTG 2940
Db 2989 ACCCAGACAGAGAGACTTGGACCGGTGATGACGCGGTGATATTTGTAAGATGATTTG 3048
Qy 2941 ACAATGACAAACATCCAGATATTTGATGATGCTCTGTAACAACTGCCCATCAGTGAGA 3000
Db 3049 ACAATGACAAACATCCAGATATTTGATGATGCTCTGTAACAACTGCCCATCAGTGAGA 3108
Qy 3001 CAGACTTCAGAACTTCCAGATGCTCCCTTGGATCCCAAGAGGACCAACCCAAATTTGATC 3060
Db 3109 CAGACTTCAGAACTTCCAGATGCTCCCTTGGATCCCAAGAGGACCAACCCAAATTTGATC 3168
Qy 3061 CCAACTGGCTCATTCGCCATCAAGCAGGAGCTGTTTCAGACAGCAACCTCGGACCCCG 3120
Db 3169 CCAACTGGCTCATTCGCCATCAAGCAGGAGCTGTTTCAGACAGCAACCTCGGACCCCG 3228
Qy 3121 GCATCGCTGTAGTTTGAACGAGTTGGCTGTGAGCTTCAGTGGCACATTTACGTA 3180
Db 3229 GCATCGCTGTAGTTTGAACGAGTTGGCTGTGAGCTTCAGTGGCACATTTACGTA 3288
Qy 3181 ACACGTACCGGAGACGACACTATCGCGCTTCGCTTGGTTACCGTTCAGGACCGCT 3240
Db 3289 ACACGTACCGGAGACGACACTATCGCGCTTCGCTTGGTTACCGTTCAGGACCGCT 3348
Qy 3241 TCTATGCTGTGATGTGGAAGCAGAGTGCAGACACTTCTGGGAGGACCCAGCCACGCGG 3300
Db 3349 TCTATGCTGTGATGTGGAAGCAGAGTGCAGACACTTCTGGGAGGACCCAGCCACGCGG 3408
Qy 3301 CCTATGGCTACTCCCGCGTGTCCCTCAAGGTGGTAACTCCACACGGGAGCGGCGAGC 3360
Db 3409 CCTATGGCTACTCCCGCGTGTCCCTCAAGGTGGTAACTCCACACGGGAGCGGCGAGC 3468
Qy 3361 ACCTGAGGAAACGCGTGTGGCACACGGGGAACACGCGGGGAGGTGCGAACCTTATGGC 3420
Db 3469 ACCTGAGGAAACGCGTGTGGCACACGGGGAACACGCGGGGAGGTGCGAACCTTATGGC 3528
Qy 3421 ACAGCCCAAGGAAACATTTGGCTGGAAGGACTACAGGCTATAGTGGCACCTGACTACA 3480
Db 3529 ACAGCCCAAGGAAACATTTGGCTGGAAGGACTACAGGCTATAGTGGCACCTGACTACA 3588
Qy 3481 GGCCCAAGACTGGCTTACATCAGAGTCTTGTGATGAAGGAAACAGGTCTATGGCAGACT 3540
Db 3589 GGCCCAAGACTGGCTTACATCAGAGTCTTGTGATGAAGGAAACAGGTCTATGGCAGACT 3648
Qy 3541 CAGGACCTTATGACCAACCTACGCTGGCGGCGCTGGTCTATTTGCTTCTCTC 3600
Db 3649 CAGGACCTTATGACCAACCTACGCTGGCGGCGCTGGTCTATTTGCTTCTCTC 3708
Qy 3601 AAGAAATGCTTATTTCTCAGACCTCAAGTACGAGATATTTAAACAGATTTG 3660

3709 AAGAAATGGTCTATTCTCAGACCTCAAGTACGAATGCGAGAGATATTAAACAGAGTTG 3768
3661 CTCATTTCCGGCAATGCCCCGTGTCATGCGTCCCTAGACACCTCAGTTCAATGTGG 3720
3769 CTGCAATTTCCGGCAATGCCCCGTGTCATGCGTCCCTAGACACCTCAGTTCAATGTGG 3828
3721 TCCTGTGGCTTCTCTCTAGCAGCCTCCTGTCGCTCCCTGACCTTAACCTGATGGTTC 3780
3829 TCCTTGGGCTTCTCTCTAGCAGCCTCCTGTCGCTCCCTGACCTTAACCTGATGGTTC 3888
3781 TTCACCTCTGCCAGCAACCCCAACCCCAAGTCCCTTACAGAGATAAATATCAATGGAA 3840
3889 TTCACCTCTGCCAGCAACCCCAACCCCAAGTCCCTTACAGAGATAAATATCAATGGAA 3948
3841 GCGAGATGACATCTAAACCCCTAGAGGAAACAGTTTGGTGATATATGACACTTATG 3900
3949 TCAGAGATGAACATCTAAACCCCTAGAGGAAACAGTTTGGTGATATATGACACTTATG 4008
3901 TGGAGTGAATAATGGGCATGCCATTAATGCTTTTCTGTTTGTGTTTAAAGAAATGAC 3960
4009 TGGAGTGAATAATGGGCATGCCATTAATGCTTTTCTGTTTGTGTTTAAAGAAATGAC 4068
3961 GTTTACATATAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4020
4069 GTTTACATATAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4128
4021 CTGTGATAGCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4080
4129 CTGTGATAGCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4188
4081 CTTAAAGTTGCTACTATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4140
4189 CTTAAAGTTGCTACTATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4248
4141 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4200
4249 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4308
4201 GAAGACAACAGGATAGCAAAATGACATAAGTACCGATTAACTAATCGGAAATGTA 4260
4309 GAAGACAACAGGATAGCAAAATGACATAAGTACCGATTAACTAATCGGAAATGTA 4368
4261 CAGTTACAAATAATGACAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4320
4369 CAGTTACAAATAATGACAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4428
4321 GAGATGAGTTTCATCAAGAAACAAACATCTTTCGAAATGGGTGATCGGTTCCAGAT 4380
4429 GAGATGAGTTTCATCAAGAAACAAACATCTTTCGAAATGGGTGATCGGTTCCAGAT 4488
4381 GTGGATTTGCAAAACCTCTAATTAAGTAAAGTTAGCAGAGCAAGTCCGCTGCTTAG 4440
4489 GTGGATTTGCAAAACCTCTAATTAAGTAAAGTTAGCAGAGCAAGTCCGCTGCTTAG 4548
4441 CTGTGCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4500
4549 CTGTGCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4608
4501 TGCTGCTGAGAGAACCGAG 4560
4609 TGCTGCTGAGAGAACCGAG 4668
4561 CTAGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4620
4669 CTAGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4728
4621 GGTTCAGTTTATAAATTTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4680
4729 GGTTCAGTTTATAAATTTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4788
4681 TACAGTAACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4740
4789 TACAGTAACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4848

RESULT 11
US-10-008-093-3
; Sequence 3, Application US/10008093
; Publication No. US20030166017A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeannette Just
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION.

4741 AACATCTAATAAGATATATAATCTCTGGAATAATGAGGCTTGATATAATATTAGGTGTGCAC 4800
4849 AACATCTAATAAGATATATAATCTCTGGAATAATGAGGCTTGATATAATATTAGGTGTGCAC 4908
4801 GATGAAGCATGCTAGAGCTGTAAACAGAAATACATAGAGAATAATAGGAGTTTATGATGG 4860
4909 GATGAAGCATGCTAGAGCTGTAAACAGAAATACATAGAGAATAATAGGAGTTTATGATGG 4968
4861 AACCTTAAATATATAATATGTTGCGCAGCGATTTTAAATTAATTTGTTTACTGTATATATC 4920
4969 AACCTTAAATATATAATATGTTGCGCAGCGATTTTAAATTAATTTGTTTACTGTATATATC 5027
4921 TGCTGTATATGGAATCTCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4979
5028 TGCTGTATATGGAATCTCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5087
4980 AGGCACACCAATTAATCAGTCATGTGTAATATGACAAAGTTTGTGTTTGTGTTTGTGTTT 5039
5088 AGGCACACCAATTAATCAGTCATGTGTAATATGACAAAGTTTGTGTTTGTGTTTGTGTTT 5147
5040 TTTGTTGGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 5099
5148 TTTGTTGGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 5203
5100 CTCAATCCCACTCCACATAGGGGTTTAAAGAGAGTCTGCTGCTGATGATGATG 5159
5204 CTCAATCCCACTCCACATAGGGGTTTAAAGAGAGTCTGCTGCTGATGATGATG 5263
5160 GGGCAATCTTTTCCCTTCTGTTAATAGTCATCACAATTTCTATGCCAACAAGAAC 5219
5264 GGGCAATCTTTTCCCTTCTGTTAATAGTCATCACAATTTCTATGCCAACAAGAAC 5323
5220 AATCCATAAATCTTAACTGTAATGATACATTTGATGATAAATTAATTTGTTGTTT 5279
5324 GATCCATTAATCTTAACTGTAATGATACATTTGATGATAAATTAATTTGTTGTTT 5383
5280 CTTTGAAGTTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5339
5384 CTTTGAAGTTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5440
5340 GCTGATTTCCCGAGACCAAGAGCGTTGGGATACCTTCAATAATGAGGAGCTGTCAAC 5399
5441 GCTGATTTCCCGAGACCAAGAGCGTTGGGATACCTTCAATAATGAGGAGCTGTCAAC 5499
5400 AGCTGAGGTTTCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5459
5500 AGCTGAGGTTTCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5559
5460 GATGATGTAATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5519
5560 GATGATGTAATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5619
5520 AAATTTATGCTATAGTTGATGAAACGTCATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5579
5620 AAATTTATGCTATAGTTGATGAAACGTCATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5679
5580 TTATGCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5639
5680 TTATGCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5739
5640 TTTTAAAGATTAAACACAGGAAATAATTTGTAATAAAGGTTTCT 5684
5740 TTTTAAAGATTAAACACAGGAAATAATTTGTAATAAAGGTTTCT 5784

; TITLE OF INVENTION: ASSESSMENT, PREVENTION AND THERAPY OF
 ; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
 ; FILE REFERENCE: MRI-026
 ; CURRENT APPLICATION NUMBER: US/10/008,093
 ; CURRENT FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: US 60/248,185
 ; PRIOR FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: US 60/257,417
 ; PRIOR FILING DATE: 2000-12-22
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5784
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-008-093-3

Query Match 97.9%; Score 5576.6; DB 14; Length 5784;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;
 1 GACTAGCTGCACTGACGGGCGGTCTCTGCTCCAGCAGAGCTGGCCCTTCTGACTC 60
 109 GAGCATCTGCACTGACGGGCGGTCTCTGCTCCAGCAGAGCTGGCCCTTCTGACTC 168
 61 GGTCCGGAACACTGAACACAGTCACTGATCTTTTGGCAACACAGAGCTCAGCTG 120
 169 GGTCCGGAACACTGAACACAGTCACTGATCTTTTGGCAACACAGAGCTCAGCTG 228
 121 CAGGAGCAGAGTGTCTGAGGCGTCTCTGCTGCTGCTCTGCTGCTGCTGCTGCTG 180
 229 CAGGAGCAGAGTGTCTGAGGCGTCTCTGCTGCTGCTCTGCTGCTGCTGCTGCTG 288
 181 AAGCTGTTACACAGACAAAGACAGCTCTGACCTTTTTCAGTATCAGCAACATCAACC 240
 289 AAGCTGTTACACAGACAAAGACAGCTCTGACCTTTTTCAGTATCAGCAACATCAACC 348
 241 GCAAGACATTGGCGCCAAAGCAGTTCCCGGCGCGGACCCCGGCGTGCCTTACCGCT 300
 349 GCAAGACATTGGCGCCAAAGCAGTTCCCGGCGCGGACCCCGGCGTGCCTTACCGCT 408
 301 TCGTGGCTTTGACTACATCCACCGGTGAACGAGATGACTCAGCAAGATCAACAGA 360
 409 TCGTGGCTTTGACTACATCCACCGGTGAACGAGATGACTCAGCAAGATCAACAGA 468
 361 TCATCGGCGAGAGGAGGCTTCTTCTCAAGGCGGCGGCTCAAGCAGGACGGCAAGTCCA 420
 469 TCATCGGCGAGAGGAGGCTTCTTCTCAAGGCGGCGGCTCAAGCAGGACGGCAAGTCCA 528
 421 GGGGACCGTGTGCTGCTGAGGCGCGGCTCTCTCCAGAGGAGTTCGAGATCGTCT 480
 529 GGGGACCGTGTGCTGCTGAGGCGCGGCTCTCTCCAGAGGAGTTCGAGATCGTCT 588
 481 CCAAGGCGCGCGGACAGCTGATCTCACTACTGATTTGAAGGACCCCGGATGTGG 540
 589 CCAAGGCGCGCGGACAGCTGATCTCACTACTGATTTGAAGGACCCCGGATGTGG 648
 541 TCTCCCTGAGAGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 649 TCTCCCTGAGAGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
 601 CTGGGAGACCTTACAGCTTTCAGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 660
 709 CTGGGAGACCTTACAGCTTTCAGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 768
 661 AGCCCTTTCAGAGCACTGACAGGCGGAAAGAGCCGATGTATCGTGGCCAAAGGCTCTG 720
 769 AGCCCTTTCAGAGCACTGACAGGCGGAAAGAGCCGATGTATCGTGGCCAAAGGCTCTG 828
 721 CCAGAGAGAGTCACTTCAGGGGTTGCTTCAGAAAGTCCAGCTCCTAGTGTTCGAAACTCTG 780
 829 CCAGAGAGAGTCACTTCAGGGGTTGCTTCAGAAAGTCCAGCTCCTAGTGTTCGAAACTCTG 888

QY 781 TGGAGATATTCTTAAGCAAGAGGGTTCAGAGCAAGGCGCAGGAGCTGAGATCAACGCCA 840
 DB 889 TGGAGATATTCTTAAGCAAGAGGGTTCAGAGCAAGGCGCAGGAGCTGAGATCAACGCCA 948
 QY 841 TCAGTGAAGAACACAGAGACGCTGCGCTGGGTCCGCATGTCAACACCGAGTACGTGGGCC 900
 DB 949 TCAGTGAAGAACACAGAGACGCTGCGCTGGGTCCGCATGTCAACACCGAGTACGTGGGCC 1008
 QY 901 CCAGCTCAGAGAGGAGGCGCGAGGTGTGCGAACGCTCTGCGAGAGAGCTGGGAAACATGG 960
 DB 1009 CCAGCTCAGAGAGGAGGCGCGAGGTGTGCGAACGCTCTGCGAGAGAGCTGGGAAACATGG 1068
 QY 961 TCCAGGAGCTCTCGGGGCTCCACGCTCTGCGAACGCTCAGCGAGAACCTCAAGAGAG 1020
 DB 1069 TCCAGGAGCTCTCGGGGCTCCACGCTCTGCGAACGCTCAGCGAGAACCTCAAGAGAG 1128
 QY 1021 TGTGGAATGATAACCAAGTTCTCTGGGAGCTCATTTGGTGGCCCTCTTAAGACAAGAAACA 1080
 DB 1129 TGTGGAATGATAACCAAGTTCTCTGGGAGCTCATTTGGTGGCCCTCTTAAGACAAGAAACA 1188
 QY 1081 TGTGAGCTTGTGGCAGGATGCGCGTCTTTTGGGAAATGAAACGTGGGTGGTGACA 1140
 DB 1189 TGTGAGCTTGTGGCAGGATGCGCGTCTTTTGGGAAATGAAACGTGGGTGGTGACA 1248
 QY 1141 GCTGCACCACTGTACCTGCAAGAAATTTAAACCAATTTGGCCACCAATCACTCCCGCC 1200
 DB 1249 GCTGCACCACTGTACCTGCAAGAAATTTAAACCAATTTGGCCACCAATCACTCCCGCC 1308
 QY 1201 CTGCAACCTGCGCCAGTCCATCTTTTGGAGGGAATGCTGCCCTTCTTCCCTCCACT 1260
 DB 1309 CTGCAACCTGCGCCAGTCCATCTTTTGGAGGGAATGCTGCCCTTCTTCCCTCCACT 1368
 QY 1261 CGGTGACCGTGTGAGGAGGCTGCTCTCGTGGGACAGTGGACCCAGTCTCTCGTGA 1320
 DB 1369 CGGTGACCGTGTGAGGAGGCTGCTCTCGTGGGACAGTGGACCCAGTCTCTCGTGA 1428
 QY 1321 GTGGCTCTGGACCCACAGAGAGGCGGTCTGTGACGTCAACAGCAACACTCTCTGG 1380
 DB 1429 GTGGCTCTGGACCCACAGAGAGGCGGTCTGTGACGTCAACAGCAACACTCTCTGG 1488
 QY 1381 GGGCTCTCACTCCAGACACAGGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCGCATCCGGCAGG 1440
 DB 1489 GGGCTCTCACTCCAGACACAGGGGCTTGCAGTCTGAGCAAGTGTGACACCCGCGCATCCGGCAGG 1548
 QY 1441 AGCGGCTGTGAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 DB 1549 AGCGGCTGTGAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1608
 QY 1501 ATATACACGCACTCCGCTCTGCAACTCCCGAGTGGCCCGCAGATGGGGGCAAGAAATTGCA 1560
 DB 1609 ATATACACGCACTCCGCTCTGCAACTCCCGAGTGGCCCGCAGATGGGGGCAAGAAATTGCA 1668
 QY 1561 AAGGAGTGGCGGAGACCAAGGCTGCGAGGGCGCCCGCATGCGCCAAATCGATGGCGCT 1620
 DB 1669 AAGGAGTGGCGGAGACCAAGGCTGCGAGGGCGCCCGCATGCGCCAAATCGATGGCGCT 1728
 QY 1621 GAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 DB 1729 GAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1788
 QY 1681 GCACCCGGTCTGCAACAGCCCTGAGCTTCAGTACGAGGGAAGGCTGCTGCTGGGGATG 1740
 DB 1789 GCACCCGGTCTGCAACAGCCCTGAGCTTCAGTACGAGGGAAGGCTGCTGCTGGGGATG 1848
 QY 1741 TGCAGGAGCTCAGATGTGCAACAGAGAGCTGCGCGTGGATGCTGCTTTATCCAAAC 1800
 DB 1849 TGCAGGAGCTCAGATGTGCAACAGAGAGCTGCGCGTGGATGCTGCTTTATCCAAAC 1908
 QY 1801 CTTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTGCTGCTGCTGCTGCTGCTGCTG 1860
 DB 1909 CTTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTGCTGCTGCTGCTGCTGCTGCTG 1968
 QY 1861 GCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGACAGTGTGCTGCTGCTG 1920

Db 1969 GCCCTGTGGGCTTCTTGGCAATGGCAACCACTGTGAGGACCTTGGACGAGTGTGCCCTGG 2028
 2y 1921 TCCCGGACATCTGTCTTCCACAGCAAGGTGCTCTGTCTGTCAACACTCAGCTGGCT 1980
 Db 2029 TCCCGGACATCTGTCTTCCACAGCAAGGTGCTCTGTCTGTCAACACTCAGCTGGCT 2088
 2y 1981 TCCACTGCTGCTTCCCGGCCCCCGATACAGAGGAAACAGCCGCTGCGGGTGGGCTGG 2040
 Db 2089 TCCACTGCTGCTTCCCGGCCCCCGATACAGAGGAAACAGCCGCTGCGGGTGGGCTGG 2148
 2y 2041 AAGCAGCAGCAAGCAAGCAAGTGTGTGAGCCGCAAAACCCATGCAAGCAAGACAC 2100
 Db 2149 AAGCAGCAGCAAGCAAGCAAGTGTGTGAGCCGCAAAACCCATGCAAGCAAGACAC 2208
 2y 2101 ACAACTGCCAAGCAGCGGAGTGCATCTACTGGGCCACTTTCAGCGACCCCATGTACA 2160
 Db 2209 ACAACTGCCAAGCAGCGGAGTGCATCTACTGGGGTCACTTCAGCGACCCCATGTACA 2268
 2y 2161 AGTCGAGTGCAGACAGGCTACGCGGCGACGCGCTCATCTCGGGGAGACTCGGAC 2220
 Db 2269 AGTCGAGTGCAGACAGGCTACGCGGCGACGCGCTCATCTCGGGGAGACTCGGAC 2328
 2y 2221 TGGACGCTGGCCCCAACCCTCAATCTGTCTGCGCCACCAACGCACTTACCACTGCATCA 2280
 Db 2329 TGGACGCTGGCCCCAACCCTCAATCTGTCTGCGCCACCAACGCACTTACCACTGCATCA 2388
 2y 2281 AGGATACCTGCCCCCATCTGCCAATCTCGGCGAGAGACTTTGACNAGGACGGATTTG 2340
 Db 2389 AGGATACCTGCCCCCATCTGCCAATCTCGGCGAGAGACTTTGACNAGGACGGATTTG 2448
 2y 2341 GCGATGCTGTGATGATGACGATGACAAATGACGGTGTGACCGGATGAGAGGACAACTGCC 2400
 Db 2449 GCGATGCTGTGATGATGACGATGACAAATGACGGTGTGACCGGATGAGAGGACAACTGCC 2508
 2y 2401 AGCTCCTCTTCAATCCCGGACGCTGACTATGACAGGATGAGTTGGGACCGCTGTG 2460
 Db 2509 AGCTCCTCTTCAATCCCGGACGCTGACTATGACAGGATGAGTTGGGACCGCTGTG 2568
 2y 2461 ACAACTGCCCTTACGTGCACAAACCTGCCAGATCGACACAGACAACAAATGGAGGGGTG 2520
 Db 2569 ACAACTGCCCTTACGTGCACAAACCTGCCAGATCGACACAGACAACAAATGGAGGGGTG 2628
 2y 2521 ACGCTGCTCGGTGGACATTTGATGGGACGATGTCTTCAATGAAACAGACAATTTGCCCT 2580
 Db 2529 ACGCTGCTCGGTGGACATTTGATGGGACGATGTCTTCAATGAAACAGACAATTTGCCCT 2688
 2y 2581 ACGTCTACAACTGACAGAGGACACGATGGTACGGTGTGGGGATCACTGTGACA 2640
 Db 2689 ACGTCTACAACTGACAGAGGACACGATGGTACGGTGTGGGGATCACTGTGACA 2748
 2y 2641 ACTGCCCTGGTGACAACCCCTGACAGACGACGATGGGACAAATGACCTTTGGGGACC 2700
 Db 2749 ACTGCCCTGGTGACAACCCCTGACAGACGACGATGGGACAAATGACCTTTGGGGACC 2808
 2y 2701 AGTGTGACAACAGAGGACATGATGACAGCGCCACAGACGACCAACAGGACCACTGCC 2760
 Db 2809 AGTGTGACAACAGAGGACATGATGACAGCGCCACAGACGACCAACAGGACCACTGCC 2868
 2y 2761 CCTACATCTCCAAACGCAACAGGCTGACCATGACAGAGCGCCAGGCGACGCTGTG 2820
 Db 2869 CCTACATCTCCAAACGCAACAGGCTGACCATGACAGAGCGCCAGGCGACGCTGTG 2928
 2y 2821 ACCCTGATGATGACAAAGTGGGCTCCCATGACAGGAGCACTCCGCTGTGTTCA 2880
 Db 2929 ACCCTGATGATGACAAAGTGGGCTCCCATGACAGGAGCACTCCGCTGTGTTCA 2988
 2y 2881 ACCCAGACCGAGGACTTGGACGGTGTGATGAGCGGGGTGATTTTGTAAAGATGATTTG 2940
 Db 2989 ACCCAGACCGAGGACTTGGACGGTGTGATGAGCGGGGTGATTTTGTAAAGATGATTTG 3048
 2y 2941 ACAATGACAACTCCAGATATTGATGATGTGTCTGAAAACAAATGCCATCAGTGAGA 3000

Db 3049 ACAATGACAACTCCAGCATATTGATGATGTGTCTGTAATAAACAATGCCATCAGTGAGA 3108
 3001 CAGACTTCAGAAACTTCCAGATGGTCCCTTGGATCCCAAAGGGACCAACCAATTTGATC 3060
 Db 3109 CAGACTTCAGAAACTTCCAGATGGTCCCTTGGATCCCAAAGGGACCAACCAATTTGATC 3168
 3061 CCAACTGGGTCAATTCGCCCATCAAGCAAGGAGCTGGTTTCAGACAGCCAACTCGGACCCCG 3120
 Db 3169 CCAACTGGGTCAATTCGCCCATCAAGCAAGGAGCTGGTTTCAGACAGCCAACTCGGACCCCG 3228
 3121 GCATCGCTGTAGTTTTCAGAGTTTGGTCTGTGGACTTCAGTGGACATTTCTACGTAA 3180
 Db 3229 GCATCGCTGTAGTTTTCAGAGTTTGGTCTGTGGACTTCAGTGGACATTTCTACGTAA 3288
 3181 ACACTGACCGGACGACACTATGCTGGCTTCGTCTTTGGTTACAGTCAAGCAGCCGCT 3240
 Db 3289 ACACTGACCGGACGACACTATGCTGGCTTCGTCTTTGGTTACAGTCAAGCAGCCGCT 3348
 3241 TCTATGCTGTGATGTGGAAGCAGAGTGCAGCAGACTCTCTGGGAGACCAAGCCCGCGGG 3300
 Db 3349 TCTATGCTGTGATGTGGAAGCAGAGTGCAGCAGACTCTCTGGGAGACCAAGCCCGCGGG 3408
 3301 CCTATGGCTACTCCGGCTGTCCCTCAAGGTGGTGAACCTCCACCAAGGGACGCGCGAGC 3360
 Db 3409 CCTATGGCTACTCCGGCTGTCCCTCAAGGTGGTGAACCTCCACCAAGGGACGCGCGAGC 3468
 3361 ACCTGAGGAAACGCGCTGTGGCACAACGCGGACACGCGGGGAGTGCAGACCTTATGGC 3420
 Db 3469 ACCTGAGGAAACGCGCTGTGGCACAACGCGGAGAACCGCGGGGAGTGCAGACCTTATGGC 3528
 3421 ACGACCCAGGAAACATTTGGCTGGAAGACTACACGGGCTATAGGTGGCACCTGACTCACA 3480
 Db 3529 ACGACCCAGGAAACATTTGGCTGGAAGACTACACGGGCTATAGGTGGCACCTGACTCACA 3588
 3481 GGCCCAAGACTGGCTACTACAGTCTTAGTGCATGAAGGAAACAGGTCAATGGCAGACT 3540
 Db 3589 GGCCCAAGACTGGCTACTACAGTCTTAGTGCATGAAGGAAACAGGTCAATGGCAGACT 3648
 3541 CAGACCTTATCTATGACCAAACTACGCTGGCGGGCGGCTGGTCTATTTGCTTCTCTC 3600
 Db 3649 CAGACCTTATCTATGACCAAACTACGCTGGCGGGCGGCTGGTCTATTTGCTTCTCTC 3708
 3601 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGAGATTTTAAACAGATTG 3660
 Db 3709 AAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGACAGAGATTTTAAACAGATTG 3768
 3661 CTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCAATTGG 3720
 Db 3769 CTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCAATTGG 3828
 3721 TCCTTGTGGCTTCTCTCTAGACGACCTCCTGTGCTTGAACCTTAACCTCTGATGGTTC 3780
 Db 3829 TCCTTGTGGCTTCTCTCTAGACGACCTCCTGTGCTTGAACCTTAACCTCTGATGGTTC 3888
 3781 TTCACCTCCTCCAGCAACCCCAACCCAGTCTTTCAGAGGATAAATATCAATGGAAC 3840
 Db 3889 TTCACCTCCTCCAGCAACCCCAACCCAGTCTTTCAGAGGATAAATATCAATGGAAC 3948
 3841 GCAGAGTGAACATCTAACCCACCTAGAGGAAACAGATTGCTGATATATGAGACTTTATG 3900
 Db 3949 TCAGAGTGAACATCTAACCCACCTAGAGGAAACAGATTGCTGATATATGAGACTTTATG 4008
 3901 TGGAGTGAACATTTGGGCAATGCAATTTGCTTTTCTTTTGTGTTTAAAGAAATGAC 3960
 Db 4009 TGGAGTGAACATTTGGGCAATGCAATTTGCTTTTCTTTTGTGTTTAAAGAAATGAC 4068
 3961 GTTACATATATAAATGAATTTACTTATTGTATTATGTTATGTTATGTTATGTTATGTTATG 4020
 Db 4069 GTTACATATATAAATGAATTTACTTATTGTATTATGTTATGTTATGTTATGTTATGTTATG 4128
 4021 CTGTGCAATACCCATTTATGATAAATTAAGCATGAAAATATTGCTGAACTACTTTTGGTG 4080
 Db 4129 CTGTGCAATACCCATTTATGATAAATTAAGCATGAAAATATTGCTGAACTACTTTTGGTG 4188

121 CAGAGGCGAGGATGGCTCTGGAGGCTGGTCTCTGTGTGCTCTGTGGGTGTGGCGCAGCAGC 180
122 CAGAGGCGAGGATGGCTCTGGAGGCTGGTCTCTGTGTGCTCTGTGGGTGTGGCGCAGCAGC 288
181 AAGCTGGTCAACAGGACAAAGACACAGCTTCCAGCTTTTTCAGTATCAGCAACATCAACC 240
289 AAGCTGGTCAACAGGACAAAGACACAGCTTCCAGCTTTTTCAGTATCAGCAACATCAACC 348
241 GCAAGACCAATGGCGGCAAGCAATTCGGGGGGCCGACCCCGCGGTGCGGCTTACCGCT 300
349 GCAAGACCAATGGCGGCAAGCAATTCGGGGGGCCGACCCCGCGGTGCGGCTTACCGCT 408
301 TCGTGGCTTTGACTACATCCACCGGTGAACGACATGACCTCAGCAAGATCAACAGA 360
409 TCGTGGCTTTGACTACATCCACCGGTGAACGACATGACCTCAGCAAGATCAACAGA 468
361 TCATGGCGGAGAGAGGGCTTCTTCTCAACGCGCCAGCTCAAGCAGGACGCAAGTCCA 420
469 TCATGGCGGAGAGAGGGCTTCTTCTCAACGCGCCAGCTCAAGCAGGACGCAAGTCCA 528
421 GGGGCAAGCTTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGCAAGTTCGAGATCGTCT 480
529 GGGGCAAGCTTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGCAAGTTCGAGATCGTCT 588
481 CCAACGCGCCCGCGGACACGCTGGATCTCACTTCTGATTCAGCGCACCCCGGCAATGG 540
589 CCAACGCGCCCGCGGACACGCTGGATCTCACTTCTGATTCAGCGCACCCCGGCAATGG 648
541 TCTCCCTGGAGGACGTCGGCTGGCTGACTCGCAGTGGAGACGTCACCGTGCAGGTGG 600
649 TCTCCCTGGAGGACGTCGGCTGGCTGACTCGCAGTGGAGACGTCACCGTGCAGGTGG 708
601 CTGGCGAGACCTACAGCTTGCAGCTGGGTGCGACCTCATAGACAGCTTCGCTCTGGAG 660
709 CTGGCGAGACCTACAGCTTGCAGCTGGGTGCGACCTCATAGACAGCTTCGCTCTGGAG 768
661 AGCCCTTTCAGGACGCTCAGCGGGAAGAGCGGATGATAGTGGCCAAAGGCTCTG 720
769 AGCCCTTTCAGGACGCTCAGCGGGAAGAGCGGATGATAGTGGCCAAAGGCTCTG 828
721 CCAGAGAGCTCACTTCAGGGGTTGCTTCAGAAACGTCACACCTAGTGTGAAACCTCTG 780
829 CCAGAGAGCTCACTTCAGGGGTTGCTTCAGAAACGTCACACCTAGTGTGAAACCTCTG 888
781 TGAAGATATTCAGCAAGAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCA 840
889 TGAAGATATTCAGCAAGAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCA 948
841 TCAGTGAGAACACAGAGACGCTCGCTGGTCCGATGTACACCGAGTACGTGGGC 900
949 TCAGTGAGAACACAGAGACGCTCGCTGGTCCGATGTACACCGAGTACGTGGGC 1008
901 CCAGCTCAGAGAGAGCCCGAGGTGTGAAACGCTCTGCGAGGAGCTGGGAAACATGG 960
1009 CCAGCTCAGAGAGAGCCCGAGGTGTGAAACGCTCTGCGAGGAGCTGGGAAACATGG 1068
961 TCCAGAGGCTCTCGGGCTCCAGCTCTCTGTAACAGCTCAGCGAGAACCTCAAGAGAG 1020
1069 TCCAGAGGCTCTCGGGCTCCAGCTCTCTGTAACAGCTCAGCGAGAACCTCAAGAGAG 1128
1021 TGTGGAATGATAACCAATTTCTCTGGAGCTCAATTTGGTGGCCCTTCTTAAGACAAGAA 1080
1129 TGTGGAATGATAACCAATTTCTCTGGAGCTCAATTTGGTGGCCCTTCTTAAGACAAGAA 1188
1081 TGTGAGCTCTGCGAGGATGGCGGTCTCTTTCGGGAATGAACGTGGGTGGTGA 1140
1189 TGTGAGCTCTGCGAGGATGGCGGTCTCTTTCGGGAATGAACGTGGGTGGTGA 1248
1141 GCTGCAACAGCTGTACCTGCAAGAAATTTAAACCAATTTGCCACCAATCAGCTGCCGC 1200
1249 GCTGCAACAGCTGTACCTGCAAGAAATTTAAACCAATTTGCCACCAATCAGCTGCCGC 1308

QY 1201 CTGCAACCTGGCGCAGTCCATCTTTGTGGAAGCGGAATGCTGCCCTTCTGCTCCACT 1260
Db 1309 CTGCAACCTGGCGCAGTCCATCTTTGTGGAAGCGGAATGCTGCCCTTCTGCTCCACT 1368
QY 1261 CGGTGGACGGTGAAGAGGGTGGTCTCCGTGGGAGAGTGGACCCAGTGTCTCGTGACGT 1320
Db 1369 CGGTGGACGGTGAAGAGGGTGGTCTCCGTGGGAGAGTGGACCCAGTGTCTCGTGACGT 1428
QY 1321 GTGGCTCTGGACCCAGCAGAGAGCCGGTCTCTGTGACGTCAACAGCAACACCTGCTTGG 1380
Db 1429 GTGGCTCTGGACCCAGCAGAGAGCCGGTCTCTGTGACGTCAACAGCAACACCTGCTTGG 1488
QY 1381 GGCCTCTCATCCAGACACGGCTTGCAGTCTGAGCAAGTGTGACCCCGCATCCGGCAGG 1440
Db 1489 GGCCTCTCATCCAGACACGGCTTGCAGTCTGAGCAAGTGTGACCCCGCATCCGGCAGG 1548
QY 1441 ACGGCGGTGAGGACCACTGGTACCTTGGTCTTCACTCTGTGACCTGTGGAGTTGGCA 1500
Db 1549 ACGGCGGTGAGGACCACTGGTACCTTGGTCTTCACTCTGTGACCTGTGGAGTTGGCA 1608
QY 1501 ATATCACACGATCCGTCTCTGCAACTCCCGAGTCCCAGATGGGGGGCAAGAAATTGCA 1560
Db 1609 ATATCACACGATCCGTCTCTGCAACTCCCGAGTCCCAGATGGGGGGCAAGAAATTGCA 1668
QY 1561 AAGGAGTGGCGGGAGACCAAGCCTGCCAGGGCGCCCATGCCCCAATCGATGGCGCT 1620
Db 1669 AAGGAGTGGCGGGAGACCAAGCCTGCCAGGGCGCCCATGCCCCAATCGATGGCGCT 1728
QY 1621 GGAGCCCTGTGCTCCCGTGGTGGCTGCACTGTGCGGTGGGATCCGGGAGC 1680
Db 1729 GGAGCCCTGTGCTCCCGTGGTGGCTGCACTGTGCGGTGGGATCCGGGAGC 1788
QY 1681 GCACCCGGTGTCAACAGACGCTGAGCTCAGTACGAGGAAAGGCTGCTGGGGGATG 1740
Db 1789 GCACCCGGTGTCAACAGACGCTGAGCTCAGTACGAGGAAAGGCTGCTGGGGGATG 1848
QY 1741 TGCAGGACGCTCAGATGTCAACAGAGGAGCTGCCCGGTGGATGGCTTTATTCRAACC 1800
Db 1849 TGCAGGACGCTCAGATGTCAACAGAGGAGCTGCCCGGTGGATGGCTTTATTCRAACC 1908
QY 1801 CCTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTGTGATGCGGTCTCT 1860
Db 1909 CCTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTGTGATGCGGTCTCT 1968
QY 1861 GCCTGTGGGCTTCTGGGCAATGGCAACCACTGTGAGGACCTGGAGAGTGTGCCCTGG 1920
Db 1969 GCCTGTGGGCTTCTGGGCAATGGCAACCACTGTGAGGACCTGGAGAGTGTGCCCTGG 2028
QY 1921 TCCCGGACATCTGCTTCTCCACCAAGAGTGGCTCGCTGTGTCAAACACTCAGCTTGGCT 1980
Db 2029 TCCCGGACATCTGCTTCTCCACCAAGAGTGGCTCGCTGTGTCAAACACTCAGCTTGGCT 2088
QY 1981 TCCACTGCTGCTTCCCGCCCGGATACAGAGGAAACCGCTGCGGGTGGGCTGG 2040
Db 2089 TCCACTGCTGCTTCCCGCCCGGATACAGAGGAAACCGCTGCGGGTGGGCTGG 2148
QY 2041 AAGCAGCAAGACGGAAGCAAGTGTGAGCCGCAAAACCCATGCAAGGACAAAGACAC 2100
Db 2149 AAGCAGCAAGACGGAAGCAAGTGTGAGCCGCAAAACCCATGCAAGGACAAAGACAC 2208
QY 2101 ACAACTGCCACAAGCAGCGGAGTGCATCTACTTGGGCCATTTCAGGACCCCATGTACA 2160
Db 2209 ACAACTGCCACAAGCAGCGGAGTGCATCTACTTGGGTCTACTTCAGGACCCCATGTACA 2268
QY 2161 AGTGGAGTGCACAGGCTTACCGGGGCAACGGGCTCATCTGCGGGGAGACTTCGGACC 2220
Db 2269 AGTGGAGTGCACAGGCTTACCGGGGCAACGGGCTCATCTGCGGGGAGACTTCGGACC 2328
QY 2221 TGGACGGTGGCCCAACCTCAATCTGTGTGGGCCAACAGCGCCACCTACCTGTGATCA 2280
Db 2329 TGGACGGTGGCCCAACCTCAATCTGTGTGGGCCAACAGCGCCACCTACCTGTGATCA 2388
QY 2281 AGGATACTGCCCCCATCTGCCAAATTTCTGGGAGGAAAGACTTTTGACAAAGGACGGATTG 2340

2389	db	AGGATAACCTGCCCCCACTGCCCCAAATCTCTGGGCAGGAAGACTTTTGACAAGGACGGGATTG	2448
2341	zy	GGGATGCCCTGTGATGATGACGATGACAATGACGGTGTGACCGATGAGAAAGGACAACCTGCC	2400
2449	db	GGGATGCCCTGTGATGATGACGATGACAATGACGGTGTGACCGATGAGAAAGGACAACCTGCC	2508
2401	zy	AGCTCCTCTTCATCCCGCCACGAGCTGACTATGACAAAGGATGAGGTTGGGGACCGCTGTG	2460
2509	db	AGCTCCTCTTCATCCCGCCACGAGCTGACTATGACAAAGGATGAGGTTGGGGACCGCTGTG	2568
2461	zy	ACAACTGCCCTTACGTGCAAAACCTCTGCCAGATCGACACAGACAACATGGAGAGGGTGTG	2520
2569	db	ACAACTGCCCTTACGTGCAAAACCTCTGCCAGATCGACACAGACAACATGGAGAGGGTGTG	2628
2521	zy	ACGCTCTGCTCCGTGGACATTGATGGGGACGATGCTTCAATGAACAGACAAATTGTCCTCT	2580
2629	db	ACGCTCTGCTCCGTGGACATTGATGGGGACGATGCTTCAATGAACAGACAAATTGTCCTCT	2688
2581	zy	ACGCTTACAACTGACAGAGGACAACCGATGGTGAACGGTGTGGGGATCACTGTGACA	2640
2689	db	ACGCTTACAACTGACAGAGGACAACCGATGGTGAACGGTGTGGGGATCACTGTGACA	2748
2641	zy	ACTGCCCCCTGTGTGCACAAACCTCTACAGACCGAGTGGCAATGACCTTGTTTGGGGAC	2700
2749	db	ACTGCCCCCTGTGTGCACAAACCTCTACAGACCGAGTGGCAATGACCTTGTTTGGGGAC	2808
2701	zy	AGTGTGACAACACAGAGGACATAGATGACGACGGCCACAGAAACAACAGGACAACCTGCC	2760
2809	db	AGTGTGACAACACAGAGGACATAGATGACGACGGCCACAGAAACAACAGGACAACCTGCC	2868
2761	Qy	CCTACATCTCCACGGCCAAACAGCTGACCATGACAGAGACGGCCAGGCGACGCTGTG	2820
2869	db	CCTACATCTCCACGGCCAAACAGCTGACCATGACAGAGACGGCCAGGCGACGCTGTG	2928
2821	Qy	ACCTTGATGATCAACAGATGGCGTCCCGATGACAGGGACAACCTGCGGCTTGTGTTCA	2880
2929	db	ACCTTGATGATCAACAGATGGCGTCCCGATGACAGGGACAACCTGCGGCTTGTGTTCA	2988
2881	zy	ACCCAGACACAGGAGGACTTCGACGGTGATGGAACGGGTGATATTGTAAAGATGATTTTG	2940
2989	db	ACCCAGACACAGGAGGACTTCGACGGTGATGGAACGGGTGATATTGTAAAGATGATTTTG	3048
2941	Qy	ACAATGACAACATCCAGATATTGATGATGTGTGCTGAAAAACAATGCCATCAAGTGAGA	3000
3049	db	ACAATGACAACATCCAGATATTGATGATGTGTGCTGAAAAACAATGCCATCAAGTGAGA	3108
3001	Qy	CAGACTTCAGAACTCCAGATGGTCCCTTGATCCCAAGGGACACCCCAAAATGATC	3060
3109	db	CAGACTTCAGAACTCCAGATGGTCCCTTGATCCCAAGGGACACCCCAAAATGATC	3168
3061	Qy	CCAACTGGGTCAATTCGCCATCAAGGCAGAGCTGGTTGACAGCGCAACTCGGACCCCG	3120
3169	db	CCAACTGGGTCAATTCGCCATCAAGGCAGAGCTGGTTGACAGCGCAACTCGGACCCCG	3228
3121	Qy	GCATCGCTGTAGGTTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTCTACGTAA	3180
3229	db	GCATCGCTGTAGGTTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTCTACGTAA	3288
3181	Qy	ACACTGACCGGGACGACGACTATGACCGCGCTTCGTCTTTGGTTACAGTCAAGCAGCGCT	3240
3289	db	ACACTGACCGGGACGACGACTATGACCGCGCTTCGTCTTTGGTTACAGTCAAGCAGCGCT	3348
3241	Qy	TCTATGTGGTGTGATGGAAGCAGGTTGACGACCTACTGGAGGACCAACCCACGCGGG	3300
3349	db	TCTATGTGGTGTGATGGAAGCAGGTTGACGACCTACTGGAGGACCAACCCACGCGGG	3408
3301	Qy	CCTATGCTACTCCGGCGTTCCTCAAGGTGTGAACTCCACACGCGGACCGGGCAGC	3360
3409	db	CCTATGCTACTCCGGCGTTCCTCAAGGTGTGAACTCCACACGCGGACCGGGCAGC	3468
3361	Qy	ACCTGAGGAAACGGCTGTGGCACACGGGAAACACGCGCGGGAGGTGCGAAACCTTATGGC	3420

D	b	3469	A	C	T	G	A	G	A	C	G	G	T	G	G	C	A	C	A	C	G	G	G	G	A	C	A	C	G	G	G	G	A	C	A	C	G	G	G	G	A	C	A	C	T	T	A	T	G	G		3520								
Q	y	3421	A	C	A	C	C	C	C	A	G	A	A	C	A	T	T	G	G	T	G	A	A	C	T	A	C	A	C	G	G	C	T	A	T	A	G	T	G	C	A	C	T	A	C	T	G	A	C		3480									
D	b	3529	A	C	A	C	C	C	C	A	G	A	A	C	A	T	T	G	G	T	G	A	A	C	T	A	C	A	C	G	G	C	T	A	T	A	G	T	G	C	A	C	T	A	C	T	G	A	C		3588									
Q	y	3481	G	G	C	C	A	A	G	A	C	T	G	C	T	A	C	A	T	C	A	G	A	G	T	C	T	T	A	G	T	G	A	T	G	A	A	G	A	A	A	C	A	A	C	A	G	T	C	A	T	G	C	A	G	A	C	T		3540
D	b	3589	G	G	C	C	A	A	G	A	C	C	G	S	T	A	C	A	T	C	A	G	A	G	T	C	T	T	A	G	T	G	A	T	G	A	A	G	A	A	A	C	A	A	C	A	G	T	C	A	T	G	C	A	G	A	C	T		3648
Q	y	3541	C	A	G	A	C	T	A	T	A	T	A	C	A	A	A	C	T	A	C	T	G	C	T	G	C	G	G	G	G	G	C	T	A	C	A	A	C	C	T	A	T	T	G	T	C	T	T	C	T	C	T	C	T	C		3600		
D	b	3649	C	A	G	A	C	T	A	T	A	T	A	C	A	A	A	C	T	A	C	T	G	C	T	G	C	G	G	G	G	C	T	A	T	T	G	T	C	A	T	T	G	T	C	T	C	T	C		3708									
Q	y	3601	A	A	G	A	A	T	G	G	T	C	T	A	T	T	C	T	C	A	G	A	C	T	C	A	A	G	T	P	A	C	A	A	T	G	C	A	G	A	T	A	T	T	A	A	C	A	A	G	A	T	T	G		3660				
D	b	3709	A	A	G	A	A	T	G	G	T	C	T	A	T	T	C	T	C	A	G	A	C	T	C	A	A	G	T	P	A	C	A	A	T	G	C	A	G	A	T	A	T	T	A	A	C	A	A	G	A	T	T	G		3768				
Q	y	3661	C	T	G	A	T	T	C	G	G	A	A	T	G	C	C	T	G	C	A	T	G	C	A	T	G	C	C	T	A	G	C	A	T	G	C	T	A	G	A	C	C	T	A	G	C	T	A	T	G	C	T		3720					
D	b	3769	C	T	G	A	T	T	C	G	G	A	A	T	G	C	C	T	G	C	A	T	G	C	A	T	G	C	C	T	A	G	C	A	T	G	C	T	A	G	A	C	C	T	A	G	C	T	A	T	G	C	T		3828					
Q	y	3721	T	C	T	T	G	G	C	T	C	T	C	T	A	G	C	A	C	C	T	C	T	G	A	C	C	T	T	G	A	C	C	T	T	A	A	C	T	A	C	T	A	C	T	G	A	T	T	G		3780								
D	b	3829	T	C	T	T	G	G	C	T	C	T	C	T	A	G	C	A	C	C	T	C	T	G	A	C	C	T	T	G	A	C	C	T	T	A	A	C	T	A	C	T	G	A	T	T	G		3888											
Q	y	3781	T	T	C	A	C	T	C	T	G	C	A	G	A	A	C	C	C	C	A	A	C	C	C	C	A	A	C	C	C	A	A	C	C	C	C	A	A	C	C	C	C	A	A	C	A	A	C	A		3840								
D	b	3889	T	T	C	A	C	T	C	T	G	C	A																																															

2Y	4501	TGCTGCCTGAGAGAAACCGAGAGCAGCGCACGGCCGGAAAAAGCGCATCTAAACGGTAT	4560
3b	4609	TGCTGCCTGAGAGGAACCAAGAGCAGCGCACAGGCCGAAAAGCGCATCTAAACGGGTAT	4668
2Y	4561	CTAGGCTTTGGTAACCTGCGGACAAGTTGCTTTTACCTGATTTCATGATGATCATTTCAATAA	4620
3b	4669	CYAGGCTTTGGTAACCTGCGGACAAGTTGCTTTTACCTGATTGATGATCATTTCAATAA	4728
2Y	4621	GGTTCAGATTATAAATAATTTTTGTTATAATTTATTAAGTGACTATAGAAATGCAACTCCATT	4680
3b	4729	GGTTCAGATTATAAATAATTTTTGTTATAATTTATTAAGTGACTATAGAAATGCAACTCCATT	4788
2Y	4681	TACCAGTAACCTTATTTTAAATATGCGCTAGTAAACACATATGCTAGTAAATTTCTAGAACA	4740
Db	4789	TACCAGTAACCTTATTTTAAATATGCGCTAGTAAACACATATGCTAGTAAATTTCTAGAACA	4848
2Y	4741	AACATCTAATAAGTATATAATCTCTGGGAAAATATGAGGCTTGATATAATTAGGTTGTCAC	4800
Db	4849	AACATCTAATAAGTATATAATCTCTGGGAAAATATGAGGCTTGATATAATTAGGTTGTCAC	4908
2Y	4801	GATTGAACATGCTAGAACCTGTAAACGAAATACATAGAGAATAATGAGGAGTTTATCATGG	4860
3b	4909	GATGAACATGCTAGAACCTGTAAACGAAATACATAGAGAATAATGAGGAGTTTATGATGG	4968
2Y	4861	AACCTTAAATATATAATGTTGCCAGCGAATTTAGTTCAAATATTTGTTACTGTTATCTATC	4920
Db	4969	AACCTT-AAATATATAATGTTGCCAGCGAATTTAGTTCAAATATTTGTTACTGTTATCTATC	5027
2Y	4921	TGCTGTATATGGAAATCTTTTAAATTCAAACGCTGAAAA-GAATCAGCATTTAGCTTTGCC	4979
Db	5028	TGCTGTATATGGAAATCTTTTAAATTCAAACGCTGAAAA-CGAATCAGCATTTAGCTTTGCC	5087
2Y	4980	AGGCACACCCAATAATCAGTCATGTGTAATAATGCAACAAGTTGTTTGTGTTTGTGTTTT	5039
3b	5088	AGGCACACCCAATAATCAGTCATGTGTAATAATGCAACAAGTTGTTTGTGTTTGTGTTTT	5147
2Y	5040	TTTGTTGGTTGGTTGTTTGTGTTTGTGTTTAAAGTTGCATGACTCTCTGCGAGAAATAGTCA	5099
Db	5148	TTTGTTGGTTGG---GTTTTTTTGCTTTAAGTTGCATGATCTTTCTGCGAGAAATAGTCA	5203
QY	5100	CTCATCCACTCCACATAAAGGGTTTAGTAAGAGAAGTCGTGCTGATGATGATGATGATG	5159
Db	5204	CTCATCCACTCCACATAAAGGGTTTAGTAAGAGAAGTCGTGCTGATGATGATGATGATG	5263
QY	5160	GGGGCAAAATCTTTTTCCCCTTCTGTTTAAAGTCATCAATCTCTATGCCAAACAGGAAC	5219
Db	5264	GGGGCAAAATCTTTTTCCCCTTCTGTTTAAAGTCATCAATCTCTATGCCAAACAGGAAC	5323
2Y	5220	AATCCATAACTTTAGTCTTAATGTPACACATGTCATTTTGATATAAATTAATTTTGTGTTTT	5279
Db	5324	GATCCATAACTTTAGTCTTAATGTPACACATGTCATTTTGATATAAATTAATTTTGTGTTTT	5383
2Y	5280	CCATTGAGGTTGATCGTTGTGTTCTGTTTGTGTCACATTTTACTTTTTTGGGTGTTGGA	5339
Db	5384	CCATTGAGGTTGATCGTTG--TGTTGTTGTCGCACTTTTACTTTTTTGGGTGTTGGA	5440
2Y	5340	GCTGTATTCGGAGACCAACGAACGGTTGGGATCTTCATTAATGATGCGACTGTCAAC	5399
Db	5441	GCTGTATTCGGAGACCAACGAACGGTTGGGATCTTCATTAATGATGCGACTGTCAAC	5499
QY	5400	AGCGTGCAGGTTTTCTGTTTCTGTTGTTGGGGTCAACCGGTACAAATGGTGTGGGAGTGAC	5459
Db	5500	AGCGTGCAGGTTTTCTGTTTCTGTTGTTGGGGTCAACCGGTACAAATGGTGTGGGAAATGAC	5559
QY	5460	GATGATGTGAATATTAGATGTACCATATTTTTTGTAAATATTTATGTTTCTTAAC	5519
Db	5560	GATGATGTGAATATTAGATGTACCATATTTTTTGTAAATATTTATGTTTCTTAAC	5619
QY	5520	AAATTTTATCGTATAGGTTGATGAACAGCTCATGTGTTTTTGGCAAAAGACTGTAATATTTAT	5579
Db	5620	AAATTTTATCGTATAGGTTGATGAACAGCTCATGTGTTTTTGGCAAAAGACTGTAATATTTAT	5679

Qy	5580	TTATGTGTTGCATGGTCAAAATTTACACACTGAAACCCCTGCACCTTAGCTAGAACCTCAT	5639
Db	5680	TTATGTGTTGCATGGTCAAAATTTACACACTGAAACCCCTGCACCTTAGCTAGAACCTCAT	5739
Qy	5640	TTTATAAGATTAAACAACAGGAAATAAATTTGTAATAAAGGTTTTCT	5684
Db	5740	TTTATAAGATTAAACAACAGGAAATAAATTTGTAATAAAGGTTTTCT	5784
RESULT 13			
US-10-269-909-78			
; Sequence 78, Application US/10269909			
; Publication No. US20030180747A1			
; GENERAL INFORMATION:			
; APPLICANT: HRUBAN, RALPH H.			
; APPLICANT: ASGANI, PEDRAM			
; APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE			
; TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES			
; FILE REFERENCE: 59303 (71699)			
; CURRENT APPLICATION NUMBER: US/10/269,909			
; CURRENT FILING DATE: 2003-10-11			
; PRIOR APPLICATION NUMBER: 60/328,609			
; PRIOR FILING DATE: 2001-10-11			
; PRIOR APPLICATION NUMBER: 60/332,754			
; PRIOR FILING DATE: 2001-11-19			
; NUMBER OF SEQ ID NOS: 87			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 78			
; LENGTH: 5784			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-269-909-78			
Query Match 97.9%; Score 5576.6; DB 14; Length 5784;			
Best Local Similarity 99.4%; Pred. No. 0;			
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;			
Qy	1	GACTACGCTGCACCTGCAGGCGCGGTCTCTCGCTCCAGCAGAGCCTGCGCCCTTCTGACTC	60
Db	109	GAGCATCTGCACCTGCAGGCGCGGTCTCTCGCTCCAGCAGAGCCTGCGCCCTTCTGACTC	168
Qy	61	GGTCCGGAACACTGAAACCAAGTATCATCTGCATCTTTTGGCAACACAGAGCTCAGCTG	120
Db	169	GGTCCGGAACACTGAAACCAAGTATCATCTGCATCTTTTGGCAACACAGAGCTCAGCTG	228
Qy	121	CAGGAGCAGAGTGGTCTCGAGGCTGGTCTCTGCTGGTCTCTGCTGGTCTGCGCCAGCAGC	180
Db	229	CAGGAGCAGAGTGGTCTCGAGGCTGGTCTCTGCTGGTCTCTGCTGGTCTGCGCCAGCAGC	288
Qy	181	AAGCTGTGTACAGGACAAAGACAGACCTTCAGCTTTTTCAGTATCAGCAATCAAC	240
Db	289	AAGCTGTGTACAGGACAAAGACAGACCTTCAGCTTTTTCAGTATCAGCAATCAAC	348
Qy	241	GCAAGACATTGGCGCCCAAGCAGTTCCGCGGGCCGACCCCGCGCTGCCGCTTACCGCT	300
Db	349	GCAAGACATTGGCGCCCAAGCAGTTCCGCGGGCCGACCCCGCGCTGCCGCTTACCGCT	408
Qy	301	TCGTGCGCTTGACTACATCCACCGGTGAACGAGATGACCTCAGCAAGTATCAAC	360
Db	409	TCGTGCGCTTGACTACATCCACCGGTGAACGAGATGACCTCAGCAAGTATCAAC	468
Qy	361	TCATGCGCGCAGAGGAGGGCTTCTTCTCAGCGGCCAGCTCAAGCAGGACGGCAAGTCCA	420
Db	469	TCATGCGCGCAGAGGAGGGCTTCTTCTCAGCGGCCAGCTCAAGCAGGACGGCAAGTCCA	528
Qy	421	GGGACAGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGCAGTTCGAGATCGTCT	480
Db	529	GGGACAGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGAGTTCGAGATCGTCT	588
Qy	481	CCAAACGGCCCCGGGACACGCTGGATCTCACCTACTGGATTCAGCGGACCCGGCATGTGG	540
Db	589	CCAAACGGCCCCGGGACACGCTGGATCTCACCTACTGGATTCAGCGGACCCGGCATGTGG	648

QY 961 TCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCCAGCTCAGCGAGAACCTCAAGAGAG 1020
Db 1069 TCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACCCAGCTCAGCGAGAACCTCAAGAGAG 1128
QY 1021 TGTGGAATGATAACCACTTTCTCTGGAGGCTCATTTGTGGCCCTCCCTAAAGCAAGGAACA 1080
Db 1129 TGTGGAATGATAACCACTTTCTCTGGAGGCTCATTTGTGGCCCTCCCTAAAGCAAGGAACA 1188
QY 1081 TGTGAGCTTGTGCGAGGATGCGCGTTCTTTTGGGAAATGAAACGTGGGTGGTGACA 1140
Db 1189 TGTGAGCTTGTGCGAGGATGCGCGTTCTTTTGGGAAATGAAACGTGGGTGGTGACA 1248
QY 1141 GCTGACCACTGTACCTGCAAGAAATTTAAACCATTTGCCACCAATCACCTGCCCGC 1200
Db 1249 GCTGACCACTGTACCTGCAAGAAATTTAAACCATTTGCCACCAATCACCTGCCCGC 1308
QY 1201 CTGCAACCTGCGCCAGTCCATCTCTTTGTGGAAGCGAATGCTGCCCTTCCTGCCCTCCACT 1260
Db 1309 CTGCAACCTGCGCCAGTCCATCTCTTTGTGGAAGCGAATGCTGCCCTTCCTGCCCTCCACT 1368
QY 1261 CGGTGGAGCGTGAAGAGGCTGTCTCGTGGGAGAGTGGACCCAGTGTCTCGTGACGT 1320
Db 1369 CGGTGGAGCGTGAAGAGGCTGTCTCGTGGGAGAGTGGACCCAGTGTCTCGTGACGT 1428
QY 1321 GTGGCTCTGGACCCAGCAGAGAGCGCGTCTGTGACGTCAACAGCAACACCTGCTTGG 1380
Db 1429 GTGGCTCTGGACCCAGCAGAGAGCGCGTCTGTGACGTCAACAGCAACACCTGCTTGG 1488
QY 1381 GGCCCTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGATCCGGCAGG 1440
Db 1489 GGCCCTCCATCCAGACACGGGCTTGCAGTCTGAGCAAGTGTGACACCCGATCCGGCAGG 1548
QY 1441 ACGCGGCTGAGCAGCACTGTGTCCTTGGTCTCATGCTGTGACCTGTGGAGTTGGCA 1500
Db 1549 ACGCGGCTGAGCAGCACTGTGTCCTTGGTCTCATGCTGTGACCTGTGGAGTTGGCA 1608
QY 1501 ATATCACACGATCCGCTCTGTGAACTCCCAAGTCCCGAGTGGCGGCGCAAGATTGCA 1560
Db 1609 ATATCACACGATCCGCTCTGTGAACTCCCAAGTCCCGAGTGGCGGCGCAAGATTGCA 1668
QY 1561 AAGGAGTGGCGGGAGACCAAGCCTGCCAGGGCGCCCATGCCCAATCGATGGCGCT 1620
Db 1669 AAGGAGTGGCGGGAGACCAAGCCTGCCAGGGCGCCCATGCCCAATCGATGGCGCT 1728
QY 1621 GGAGCCCTGTGCTCCCGTGTGTCGGCTGCACTGTGACCTGTGCGGTGGATCCGGGAGC 1680
Db 1729 GGAGCCCTGTGCTCCCGTGTGTCGGCTGCACTGTGACCTGTGCGGTGGATCCGGGAGC 1788
QY 1681 GCACCCGGGTGTGCAACAGCCCTGAGCCTGAGTACGAGGAGAGCCCTGCTGGGGGATG 1740
Db 1789 GCACCCGGGTGTGCAACAGCCCTGAGCCTGAGTACGAGGAGAGCCCTGCTGGGGGATG 1848
QY 1741 TGCAGGAGCGTCAGATGTGCAACAGAGAGCGTCCCGTGGATGGCTGTTATCCAAAC 1800
Db 1849 TGCAGGAGCGTCAGATGTGCAACAGAGAGCGTCCCGTGGATGGCTGTTATCCAAAC 1908
QY 1801 CCTGCTTCCGGGAGCCAGTGTGAGAGCTTCCCGGATGGGTCTGTGATGCGGCTCTCT 1860
Db 1909 CCTGCTTCCGGGAGCCAGTGTGAGAGCTTCCCGGATGGGTCTGTGATGCGGCTCTCT 1968
QY 1861 GCCCTGTGGGCTTCTTGGGCAATGACCCACTGTGAGGACCTGCGAGGTGTCGCCCTGG 1920
Db 1969 GCCCTGTGGGCTTCTTGGGCAATGACCCACTGTGAGGACCTGCGAGGTGTCGCCCTGG 2028
QY 1921 TCCCGACATCTGCTTCTCCACAGCAAGGTGCTCGCTGTGTCAACACTCAGCTGGCT 1980
Db 2029 TCCCGACATCTGCTTCTCCACAGCAAGGTGCTCGCTGTGTCAACACTCAGCTGGCT 2088
QY 1981 TCCACTGCTGCTGCGCCCGCCGATACAGAGGACCCAGCCGCTGGGGTGGCCCTGG 2040
Db 2089 TCCACTGCTGCTGCGCCCGCCGATACAGAGGAAACCAAGCCGCTGGGGTGGCCCTGG 2148

QY 2041 AAGCAGCCAAAGCGGAAAGCAAGTGTGTGAGCCCGGAAACCCATGCAAGGACAAAGACAC 2100
Db 2149 AAGCAGCCAAAGCGGAAAGCAAGTGTGTGAGCCCGGAAACCCATGCAAGGACAAAGACAC 2208
QY 2101 ACAACTGCCACAAAGCAGCGGAGTGCATCTACTGGGCCACTTTCAGCGACCCCATGTACA 2160
Db 2209 ACAACTGCCACAAAGCAGCGGAGTGCATCTACTGGGCCACTTTCAGCGACCCCATGTACA 2268
QY 2161 AGTGCAGAGTGCAGACAGGCTACGCGGGCGAGCGGCTCATCTGCGGGGAGGACTCGGACC 2220
Db 2269 AGTGCAGAGTGCAGACAGGCTACGCGGGCGAGCGGCTCATCTGCGGGGAGGACTCGGACC 2328
QY 2221 TCGACGGCTGGCCCAACCTCAATCTGTCTGGCCACCAAGCCACCTTACCACTGCATCA 2280
Db 2329 TCGACGGCTGGCCCAACCTCAATCTGTCTGGCCACCAAGCCACCTTACCACTGCATCA 2388
QY 2281 AGGATAACTGCCCCCATCTGCCAAATTTCTGGCAGGAAAGACTTTTCAAGGACGGGATTG 2340
Db 2389 AGGATAACTGCCCCCATCTGCCAAATTTCTGGCAGGAAAGACTTTTCAAGGACGGGATTG 2448
QY 2341 GCGATGCTGTGATGATGACGATGACAAATGACGGTGTGACCGATGAGAGGACAACTGCC 2400
Db 2449 GCGATGCTGTGATGATGACGATGACAAATGACGGTGTGACCGATGAGAGGACAACTGCC 2508
QY 2401 AGCTCTCTTCAATCCCGCCAGGCTGACTATGACAAAGGATGAGGTTGGGGACCCGCTGTG 2460
Db 2509 AGCTCTCTTCAATCCCGCCAGGCTGACTATGACAAAGGATGAGGTTGGGGACCCGCTGTG 2568
QY 2461 ACACTGCCCTTACGTGCAACCCCTGCCAGATCGACACAGCAACAAATGGAGAGGTTG 2520
Db 2569 ACACTGCCCTTACGTGCAACCCCTGCCAGATCGACACAGCAACAAATGGAGAGGTTG 2628
QY 2521 ACGCTGTCTCGTGGACATTTGATGGGACGATGCTTCAATGAACGAGACAAATTTGCCCT 2580
Db 2629 ACGCTGTCTCGTGGACATTTGATGGGACGATGCTTCAATGAACGAGACAAATTTGCCCT 2688
QY 2581 AGCTTTAACAACACTGACAGAGGACACGGATGTTGAGCGTGTGGGGGATCACTGTGACA 2640
Db 2689 AGCTTTAACAACACTGACAGAGGACACGGATGTTGAGCGTGTGGGGGATCACTGTGACA 2748
QY 2641 ACTGCCCTGTGTGACAACTGACAGCGGACCGCTGAGCGTGTGAGCAATCACCTTGTGGGGACC 2700
Db 2749 ACTGCCCTGTGTGACAACTGACAGCGGACCGCTGAGCGTGTGAGCAATCACCTTGTGGGGACC 2808
QY 2701 AGTGTGACAAACAGGACATAGATGACGCGCCACAGAACCAACAGGACAACTGCC 2760
Db 2809 AGTGTGACAAACAGGACATAGATGACGCGCCACAGAACCAACAGGACAACTGCC 2868
QY 2761 CCTACATCTCCAAACCGCCACCGGCTGACCATGACAGAGACGCGCCAGCGGACGCGCTGTG 2820
Db 2869 CCTACATCTCCAAACCGCCACCGGCTGACCATGACAGAGACGCGCCAGCGGACGCGCTGTG 2928
QY 2821 ACCCTGATGATGACAAACGATGGCGTCCCGGATGACAGGAGCAACTGCGCGCTTGTGTTCA 2880
Db 2929 ACCCTGATGATGACAAACGATGGCGTCCCGGATGACAGGAGCAACTGCGCGCTTGTGTTCA 2988
QY 2881 ACCAGACAGAGAGACTTGGACGCTGATGACCGGGTGATATTTGTAAGATGATTTG 2940
Db 2989 ACCAGACAGAGAGACTTGGACGCTGATGACCGGGTGATATTTGTAAGATGATTTG 3048
QY 2941 ACAATGACAAACATCCAGATATTGATGATGTGTCTGTAACCAATGCTCACTAGTGAGA 3000
Db 3049 ACAATGACAAACATCCAGATATTGATGATGTGTCTGTAACCAATGCTCACTAGTGAGA 3108
QY 3001 CAGACTTCAAGAACTTCCAGATGTTGCCCTTGGATCCCAAGAGGACCAACCAATTTGATC 3060
Db 3109 CAGACTTCAAGAACTTCCAGATGTTGCCCTTGGATCCCAAGAGGACCAACCAATTTGATC 3168
QY 3061 CCAACTGGGTCAATTCGCATCAAGCAAGGAGCTGTTTTCAGACAGCCAACTCGGACCCCG 3120
Db 3169 CCAACTGGGTCAATTCGCATCAAGCAAGGAGCTGTTTTCAGACAGCCAACTCGGACCCCG 3228
QY 3121 GCATCGCTGAGGTTTTCAGCGAGTTTGGGTCTGTGGAATTCAGTGGGCACTTCTACGTAA 3180

QY 5340 GCTGTATTCCCGAGACCAACGAAAGCGTTGGGATATCTTCAITTAATGTAGGAGCTGTCAAC 5399
Db 5441 GCTGTATTCCCGAGACCAACGAAAGCGTTGGGATATCTTCAITTAATGTAGGAGCTGTCAAC 5499
QY 5400 AGCGTGCAGGTTTCTGTTTCTGTTGTTGGGTCACCGGTACCAATGGTGGGAGTGAC 5459
Db 5500 AGCGTGCAGGTTTCTGTTTCTGTTGTTGGGTCACCGGTACCAATGGTGGGAGTGAC 5559
QY 5460 GATGATGTGAATATTAGAAATGTACCAATATTTTGTAAATATTTATGTTTCTAAAC 5519
Db 5560 GATGATGTGAATATTAGAAATGTACCAATATTTTGTAAATATTTATGTTTCTAAAC 5619
QY 5520 AAATTTATCGTATAGGTGATGAACGTCATGTTTGGCAAGAGCTGTAAATATTTAT 5579
Db 5620 AAATTTATCGTATAGGTGATGAACGTCATGTTTGGCAAGAGCTGTAAATATTTAT 5679
QY 5580 TTATGTTTCAATGTTCAAAATTTCAACCTGAAACCGTCACTTAGCTAGTAACCTCAT 5639
Db 5680 TTATGTTTCAATGTTCAAAATTTCAACCTGAAACCGTCACTTAGCTAGTAACCTCAT 5739
QY 5640 TTTTAAAGATTAAACACAGGAAATTAATTTGTAATAAGGTTTCT 5684
Db 5740 TTTTAAAGATTAAACACAGGAAATTAATTTGTAATAAGGTTTCT 5784

RESULT 15
US-10-007-781-1
; Sequence 1, Application US/10007781
; Publication No. US20030194703A1
; GENERAL INFORMATION:
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: Association of Thrombospondin
; TITLE OF INVENTION: Polymorphisms with Vascular Disease
; FILE REFERENCE: 2825-001
; CURRENT APPLICATION NUMBER: US/10/007,781
; PRIOR FILING DATE: 2002-05-13
; PRIOR FILING DATE: 2002-05-13
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/248,130
; PRIOR APPLICATION NUMBER: 60/300,158
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-781-1

Query Match 97.9%; Score 5576.6; DB 14; Length 5784;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5651; Conservative 0; Mismatches 24; Indels 10; Gaps 5;

QY 1 GACTACGTGCTACGAGGCGGTCCTCGCTCCAGCAGAGCCTGCGCCTTTCTGACTC 60
Db 109 GAGCATCTGCTGCTGAGGCGGTCCTCGCTCCAGCAGAGCCTGCGCCTTTCTGACTC 168
QY 61 GGTCCGGAACTGAAACCAAGTCATCATCTGATCTTTTGGCAACCAAGAGCTCAGCTG 120
Db 169 GGTCCGGAACTGAAACCAAGTCATCATCTGATCTTTTGGCAACCAAGAGCTCAGCTG 228
QY 121 CAGGAGGAGGAGTCTGAGGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 229 CAGGAGGAGGAGTCTGAGGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
QY 181 AAGCTGGTCAACAGGACAAAGACAGACCTTGCAGCTTTTTCAGTATCAGCAACATCAAC 240
Db 289 AAGCTGGTCAACAGGACAAAGACAGACCTTGCAGCTTTTTCAGTATCAGCAACATCAAC 348
QY 241 GMAAGACCATTTGGCGCAAGAGATTCCGGCGGCCGACCCCGGCTGCGGCTTACCGCT 300

Db 349 GCAAGACCATTTGGCGCCAAAGCAGTTCCGGCGGCGCCGACCCCGGCGTGGCGGCTTACCGCT 408
QY 301 TCGTGGCTTTGACTACATCCACCGGTGAACGAGATGACCTCAGCAAGATCACAAGA 360
Db 409 TCGTGGCTTTGACTACATCCACCGGTGAACGAGATGACCTCAGCAAGATCACAAGA 468
QY 361 TCATCGGCGAAGAGAGGCTTCTTCTCAGGCGCCAGCTCAAGCAGGACGCGCAAGTCCA 420
Db 469 TCATCGGCGAAGAGAGGCTTCTTCTCAGGCGCCAGCTCAAGCAGGACGCGCAAGTCCA 528
QY 421 GGGGCACCGCTGTGGCTCTGGAGGGCGCCCGGTCTCTCCAGAGGAGTTCGAGATCGTCT 480
Db 529 GGGGCACCGCTGTGGCTCTGGAGGGCGCCCGGTCTCTCCAGAGGAGTTCGAGATCGTCT 588
QY 481 CCNACGGCCCCCGGACACGCTGGATCTCACTACTGATTTGACGGCACCCGGCATGG 540
Db 589 CCNACGGCCCCCGGACACGCTGGATCTCACTACTGATTTGACGGCACCCGGCATGG 648
QY 541 TCTCCCTGGAGACGCTCGGCTCGGCTGACTCCAGTGGAAAGAACCTCAGCGTCGAGGTGG 600
Db 649 TCTCCCTGGAGACGCTCGGCTCGGCTGACTCCAGTGGAAAGAACCTCAGCGTCGAGGTGG 708
QY 601 CTGGCGAGACCTTACAGCTTGGAGCTGGGCTGGAGCTCATAGACAGCTTCGCTCTGGAGC 560
Db 709 CTGGCGAGACCTTACAGCTTGGAGCTGGGCTGGAGCTCATAGACAGCTTCGCTCTGGAGC 768
QY 661 AGCCCTTCTACGAGCACCTGCGAGGCGGAAAGAGCGGATGTACGTGGCCAAAGGCTCTG 720
Db 769 AGCCCTTCTACGAGCACCTGCGAGGCGGAAAGAGCGGATGTACGTGGCCAAAGGCTCTG 828
QY 721 CCAGAGAGAGTCACTTCAGGGGTTTGGCTTCAGAAAGTCCACCTAGTGTGAAAACCTG 780
Db 829 CCAGAGAGAGTCACTTCAGGGGTTTGGCTTCAGAAAGTCCACCTAGTGTGAAAACCTG 888
QY 781 TGGAGATATTCTAAGCAAGAGGTTGCGACAAAGCGAGGAGCTGAGATCAACGCCA 840
Db 889 TGGAGATATTCTAAGCAAGAGGTTGCGACAAAGCGAGGAGCTGAGATCAACGCCA 948
QY 841 TCAGTGAGAAACACAGAGACGCTGCGCTGGGTCGCGATGTACCAACCGAGTACGTGGGCG 900
Db 949 TCAGTGAGAAACACAGAGACGCTGCGCTGGGTCGCGATGTACCAACCGAGTACGTGGGCG 1008
QY 901 CCAGCTCAGAGAGGAGGCGCGAGGTGTGCGAAGCGTCTGTCGAGGAGCTGGGAAACATGG 960
Db 1009 CCAGCTCAGAGAGGAGGCGCGAGGTGTGCGAAGCGTCTGTCGAGGAGCTGGGAAACATGG 1068
QY 961 TCCAGGAGCTCTCGGGCTCCACGCTCTCGTGAACACAGCTCAGCGAGAACCTCAAGAGAG 1020
Db 1069 TCCAGGAGCTCTCGGGCTCCACGCTCTCGTGAACACAGCTCAGCGAGAACCTCAAGAGAG 1128
QY 1021 TGTGGAATGATTAACCAAGTTCCTGCGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGAACA 1080
Db 1129 TGTGGAATGATTAACCAAGTTCCTGCGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGAACA 1188
QY 1081 TGTGAGCTTGTGCGCAGGATGCGCGTTCTTTTGGGAAATGAAACGTCGGTGGTGACA 1140
Db 1189 TGTGAGCTTGTGCGCAGGATGCGCGTTCTTTTGGGAAATGAAACGTCGGTGGTGACA 1248
QY 1141 GCTGCAACAGCTGTACTGCAAGAAATTTAAACCAATTTGCCACCAATCACTGCGCGC 1200
Db 1249 GCTGCAACAGCTGTACTGCAAGAAATTTAAACCAATTTGCCACCAATCACTGCGCGCGC 1308
QY 1201 CTGCAACCTCGCGCAGTCCATCTTTGTGAAAGGCGAATGCTGCGCCCTTCTGCTCCACT 1260
Db 1309 CTGCAACCTCGCGCAGTCCATCTTTGTGAAAGGCGAATGCTGCGCCCTTCTGCTCCACT 1368
QY 1261 CGGTGAGCGGTGAGGAGGCTGCTCTCGTGGGAGAGTGGAGCCAGTGTCTCGGTGACGT 1320
Db 1369 CGGTGAGCGGTGAGGAGGCTGCTCTCGTGGGAGAGTGGAGCCAGTGTCTCGGTGACGT 1428
QY 1321 GTGGCTCTGGGACCCAGCAGAGAGGCGGTCTCTGTGACCTCACCAGCAACACACTGCTTGG 1380
Db 1429 GTGGCTCTGGGACCCAGCAGAGAGGCGGTCTCTGTGACCTCACCAGCAACACACTGCTTGG 1488

